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(54) **Title:** STRESS-RELATED POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

(57) **Abstract:** The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce transgenic plants having advantageous properties compared to a reference plant. Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods and is also disclosed.

STRESS-RELATED POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

This application claims the benefit of US Provisional Application No. 60/310,847, filed August 9, 2001, US Provisional Application No. 60/336,049, filed December 5, 2001, US Provisional Application No. 60/338,692, filed December 11, 2001, and US Non-provisional Application No. 10/171,468, filed June 14, 2002, the entire contents of which are hereby incorporated by reference.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

INTRODUCTION

A plant's traits, such as its biochemical, developmental, or phenotypic characteristics, may be controlled through a number of cellular processes. One important way to manipulate that control is through transcription factors - proteins that influence the expression of a particular gene or sets of genes. Transformed and transgenic plants that comprise cells having altered levels of at least one selected transcription factor, for example, possess advantageous or desirable traits. Strategies for manipulating traits by altering a plant cell's transcription factor content can therefore result in plants and crops with commercially valuable properties. Applicants have identified polynucleotides encoding transcription factors, developed numerous transgenic plants using these polynucleotides, and have analyzed the plants for a variety of important traits. In so doing, applicants have identified important polynucleotide and polypeptide sequences for producing commercially valuable plants and crops as well as the methods for making them and using them. Other aspects and embodiments of the invention are described below and can be derived from the teachings of this disclosure as a whole.

Background of the Invention

Transcription factors (TFs) can modulate gene expression, either increasing or decreasing (inducing or repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different

tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

The present invention provides novel transcription factors useful for modifying a plant's phenotype in desirable ways.

Summary of the Invention

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising a polypeptide sequence selected from those of the Sequence Listing, SEQ ID NOs: 2 to 2N, where N = 2-123, or those listed in Table 4, or a complementary nucleotide sequence thereof; (b) a nucleotide sequence encoding a polypeptide comprising a variant of a polypeptide of (a) having one or more, or between 1 and about 5, or between 1 and about 10, or between 1 and about 30, conservative amino acid substitutions; (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID NOs: 1 to (2N - 1), where N = 2-123, or those included in Table 4, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides of a sequence of any of (a)-(e), or at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides outside of a region encoding a conserved domain of any of (a)-(e); (g) a

nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's characteristic, functions as a transcription factor, or alters the level of transcription of a gene or transgene in a cell; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60%, or at least 70 %, or at least 80 %, or at least 90 %, or at least 95 % sequence identity to a nucleotide sequence of any of (a)-(g) or a 10 or 15 nucleotide, or at least about 20, or at least about 30 nucleotide region of a sequence of (a)-(g) that is outside of a region encoding a conserved domain; (j) a nucleotide sequence that encodes a polypeptide having at least 31% sequence identity to a polypeptide listed in Table 4, or the Sequence Listing; (k) a nucleotide sequence which encodes a polypeptide having at least 60%, or at least 70 %, or at least 80%, or at least 90 %, or at least 95 % sequence identity to a polypeptide listed in Table 4, or the Sequence Listing; and (l) a nucleotide sequence that encodes a conserved domain of a polypeptide having at least 85%, or at least 90%, or at least 95%, or at least 98% sequence identity to a conserved domain of a polypeptide listed in Table 4, or the Sequence Listing. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-specific promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above-described polynucleotides.

In a second aspect, the invention comprises an isolated or recombinant polypeptide comprising a subsequence of at least about 10, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above, or comprising a subsequence of at least about 8, or at least about 12, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids outside a conserved domain.

In a third aspect, the invention comprises an isolated or recombinant polynucleotide that encodes a polypeptide that is a paralog of the isolated polypeptide described above. In one aspect, the invention is a paralog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

In a fourth aspect, the invention comprises an isolated or recombinant polynucleotide that encodes a polypeptide that is an ortholog of the isolated polypeptide described above. In one aspect, the invention is an ortholog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

In a fifth aspect, the invention comprises an isolated polypeptide that is a paralog of the isolated polypeptide described above. In one aspect, the invention is a paralog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

In a sixth aspect, the invention comprises an isolated polypeptide that is an ortholog of the isolated polypeptide described above. In one aspect, the invention is an ortholog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

The present invention also encompasses transcription factor variants. A preferred transcription factor variant is one having at least 40% amino acid sequence identity, a more preferred transcription factor variant is one having at least 50% amino acid sequence identity and a most preferred transcription factor variant is one having at least 65% amino acid sequence identity to the transcription factor amino acid sequences SEQ ID NOs: 2 to 2N, where N = 2-123, and which contains at least one functional or structural characteristic of the transcription factor amino acid sequences. Sequences having lesser degrees of identity but comparable biological activity are considered to be equivalents.

In another aspect, the invention is a transgenic plant comprising one or more of the above-described isolated or recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above-described polypeptide. Further, the invention is a plant lacking a nucleotide sequence encoding a polypeptide described above or substantially lacking a polypeptide described above. The plant may be any plant, including, but not limited to, Arabidopsis, mustard, soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot,

cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, vegetable brassicas, and mint or other labiates. In yet another aspect, the inventions is an isolated plant material of a plant, including, but not limited to, plant tissue, fruit, seed, plant cell, embryo, protoplast, pollen, and the like. In yet another aspect, the invention is a transgenic plant tissue culture of regenerable cells, including, but not limited to, embryos, meristematic cells, microspores, protoplast, pollen, and the like.

In yet another aspect the invention is a transgenic plant comprising one or more of the above described polynucleotides wherein the encoded polypeptide is expressed and regulates transcription of a gene.

In a further aspect the invention provides a method of using the polynucleotide composition to breed a progeny plant from a transgenic plant including crossing plants, producing seeds from transgenic plants, and methods of breeding using transgenic plants, the method comprising transforming a plant with the polynucleotide composition to create a transgenic plant, crossing the transgenic plant with another plant, selecting seed, and growing the progeny plant from the seed.

In a further aspect, the invention provides a progeny plant derived from a parental plant wherein said progeny plant exhibits at least three fold greater messenger RNA levels than said parental plant, wherein the messenger RNA encodes a DNA-binding protein which is capable of binding to a DNA regulatory sequence and inducing expression of a plant trait gene, wherein the progeny plant is characterized by a change in the plant trait compared to said parental plant. In yet a further aspect, the progeny plant exhibits at least ten fold greater messenger RNA levels compared to said parental plant. In yet a further aspect, the progeny plant exhibits at least fifty fold greater messenger RNA levels compared to said parental plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having a modified trait. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for a modified trait. In one aspect, the plant is a monocot plant. In another aspect, the plant is a dicot plant. In another aspect the recombinant polynucleotide is from a dicot plant and the plant is a monocot plant. In yet another aspect the recombinant polynucleotide is from a monocot plant and the plant is a dicot plant. In yet another aspect the recombinant polynucleotide is from a monocot plant and the plant is a monocot plant. In yet another aspect the recombinant polynucleotide is from a dicot plant and the plant is a dicot plant.

In another aspect, the invention is a transgenic plant comprising an isolated or recombinant polynucleotide encoding a polypeptide wherein the polypeptide is selected from the group consisting of SEQ ID NOs: 2-2N where N = 2-123. In yet another aspect, the invention is a plant with altered expression levels of a polypeptide described above or a plant with altered expression or activity levels of an above-described polypeptide. Further, the invention is a plant lacking a polynucleotide sequence encoding a polypeptide described above or substantially lacking a polypeptide described above. The plant may be any plant, including, but not limited to, Arabidopsis, mustard, soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, vegetable brassicas, and mint or other labiates. In yet another aspect, the inventions is an isolated plant material of a plant, including, but not limited to, plant tissue, fruit, seed, plant cell, embryo, protoplast, pollen, and the like. In yet another aspect, the

invention is a transgenic plant tissue culture of regenerable cells, including, but not limited to, embryos, meristematic cells, microspores, protoplast, pollen, and the like.

In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization, or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant trait.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database, and querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant phenotype.

Brief Description of the Sequence Listing, Tables, and Figure

The Sequence Listing provides exemplary polynucleotide and polypeptide sequences of the invention. The traits associated with the use of the sequences are included in the Examples.

Diskette1 is a read-only memory computer-readable diskette and contains a copy of the Sequence Listing in ASCII text format. The Sequence Listing is named "SEQLIST514442002040" and is 895 kilobytes in size. The copy of the Sequence Listing on the diskette is hereby incorporated by reference in its entirety.

Table 4 shows the polynucleotides and polypeptides identified by SEQ ID NO; Mendel Gene ID No.; conserved domain of the polypeptide; and if the polynucleotide was tested in a transgenic assay. The first column shows the polynucleotide SEQ ID NO; the second column shows the Mendel Gene ID No., GID; the third column shows the trait(s) resulting from the knock out or overexpression of the polynucleotide in the transgenic plant; the fourth column shows the category of the trait; the fifth column shows the transcription factor family to which the polynucleotide belongs; the sixth column ("Comment"), includes specific effects and utilities conferred by the polynucleotide of the first column; the seventh column shows the SEQ ID NO of the polypeptide encoded by the polynucleotide; and the eighth column shows the amino acid residue positions of the conserved domain in amino acid (AA) co-ordinates.

Table 5 lists a summary of orthologous and homologous sequences identified using BLAST (tblastx program). The first column shows the polynucleotide sequence identifier (SEQ ID NO), the second column shows the corresponding cDNA identifier (Gene ID), the third column shows the orthologous or homologous polynucleotide GenBank Accession Number (Test Sequence ID), the fourth column shows the calculated probability value that the sequence identity is due to chance (Smallest Sum Probability), the fifth column shows the plant species from which the test sequence

was isolated (Test Sequence Species), and the sixth column shows the orthologous or homologous test sequence GenBank annotation (Test Sequence GenBank Annotation).

Figure 1 shows a phylogenic tree of related plant families adapted from Daly et al. (2001 *Plant Physiology* 127:1328-1333).

Detailed Description of Exemplary Embodiments

In an important aspect, the present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants. Throughout this disclosure, various information sources are referred to and/or are specifically incorporated. The information sources include scientific journal articles, patent documents, textbooks, and World Wide Web browser-inactive page addresses, for example. While the reference to these information sources clearly indicates that they can be used by one of skill in the art, applicants specifically incorporate each and every one of the information sources cited herein, in their entirety, whether or not a specific mention of "incorporation by reference" is noted. The contents and teachings of each and every one of the information sources can be relied on and used to make and use embodiments of the invention.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a plant" includes a plurality of such plants, and a reference to "a stress" is a reference to one or more stresses and equivalents thereof known to those skilled in the art, and so forth.

The polynucleotide sequences of the invention encode polypeptides that are members of well-known transcription factor families, including plant transcription factor families, as disclosed in Table 4. Generally, the transcription factors encoded by the present sequences are involved in cell differentiation and proliferation and the regulation of growth. Accordingly, one skilled in the art would recognize that by expressing the present sequences in a plant, one may change the expression of autologous genes or induce the expression of introduced genes. By affecting the expression of similar autologous sequences in a plant that have the biological activity

of the present sequences, or by introducing the present sequences into a plant, one may alter a plant's phenotype to one with improved traits. The sequences of the invention may also be used to transform a plant and introduce desirable traits not found in the wild-type cultivar or strain. Plants may then be selected for those that produce the most desirable degree of over- or underexpression of target genes of interest and coincident trait improvement.

The sequences of the present invention may be from any species, particularly plant species, in a naturally occurring form or from any source whether natural, synthetic, semi-synthetic or recombinant. The sequences of the invention may also include fragments of the present amino acid sequences. In this context, a "fragment" refers to a fragment of a polypeptide sequence which is at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity of a transcription factor. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

As one of ordinary skill in the art recognizes, transcription factors can be identified by the presence of a region or domain of structural similarity or identity to a specific consensus sequence or the presence of a specific consensus DNA-binding site or DNA-binding site motif (see, for example, Riechmann et al., (2000) *Science* 290: 2105-2110). The plant transcription factors may belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) *Plant Cell* 4:1575-1588); the zinc finger protein (Z) family (Klug and Schwabe (1995) *FASEB J. 9:* 597-604); the homeobox (HB) protein family (Buerglin in *Guidebook to the Homeobox Genes,* Duboule (ed.) (1994) Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996)

Mol. Gen. Genet. 1996 250:7-16); the NAM protein family (Souer et al. (1996) *Cell* 85:159-170); the IAA/AUX proteins (Rouse et al. (1998) *Science* 279:1371–1373); the HLH/MYC protein family (Littlewood et al. (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) *FASEB J.* 8:192-200); the Box P-binding protein (the BPF-1) family (da Costa e Silva et al. (1993) *Plant J.* 4:125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) *Prog. Nucl. Acids Res. Mol. Biol.* 54:35-100); the scarecrow (SCR) family (Di Laurenzio et al. (1996) *Cell* 86:423-433); the GF14 family (Wu et al. (1997) *Plant Physiol.* 114:1421-1431); the polycomb (PCOMB) family (Kennison (1995) *Annu. Rev. Genet.* 29:289-303); the teosinte branched (TEO) family (Luo et al. (1996) *Nature* 383:794-799; the ABI3 family (Giraudat et al. (1992) *Plant Cell* 4:1251-1261); the triple helix (TH) family (Dehesh et al. (1990) *Science* 250:1397-1399); the EIL family (Chao et al. (1997) *Cell* 89:1133-44); the AT-HOOK family (Reeves and Nissen (1990) *J. Biol. Chem.* 265:8573-8582); the S1FA family (Zhou et al. (1995) *Nucleic Acids Res.* 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) *Plant Physiol.* 109:723); the YABBY family (Bowman et al. (1999) *Development* 126:2387-96); the PAZ family (Bohmert et al. (1998) *EMBO J.* 17:170-80); a family of miscellaneous (MISC) transcription factors including the DPBF family (Kim et al. (1997) *Plant J.* 11:1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the golden (GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936), the TUBBY family (Boggin et al, (1999) *Science* 286:2119-2125), the heat shock family (Wu C (1995) *Annu Rev Cell Dev Biol* 11:441-469), the ENBP family (Christiansen et al (1996) *Plant Mol Biol* 32:809-821), the RING-zinc family (Jensen et al. (1998) *FEBS letters* 436:283-287), the PDBP family (Janik et al *Virology.* (1989) 168:320-329), the PCF family (Cubas P, et al. *Plant J.* (1999) 18:215-22), the SRS (SHI-related) family (Fridborg et al *Plant Cell* (1999) 11:1019-1032), the CPP (cysteine-rich polycomb-like) family (Cvitanich et al *Proc. Natl. Acad. Sci.* U S A. (2000) 97:8163-8168), the ARF (auxin response factor) family (Ulmasov, et al. (1999) *Proc. Natl. Acad. Sci.* USA 96: 5844-5849), the SWI/SNF family (Collingwood et al *J. Mol. End.* 23:255-275), the ACBF family (Seguin et al (1997) *Plant Mol Biol.* 35:281-291), PCGL (CG-1 like) family (da Costa e Silva et al. (1994) *Plant Mol Biol.* 25:921-924) the ARID family (Vazquez et al. (1999) *Development.* 126: 733-42), the Jumonji family, Balciunas et al (2000, *Trends*

Biochem Sci. 25: 274-276), the bZIP-NIN family (Schauser et al (1999) *Nature* 402: 191-195), the E2F family Kaelin et al (1992) *Cell* 70: 351-364) and the GRF-like family (Knaap et al (2000) *Plant Physiol.* 122: 695-704). As indicated by any part of the list above and as known in the art, transcription factors have been sometimes categorized by class, family, and sub-family according to their structural content and consensus DNA-binding site motif, for example. Many of the classes and many of the families and sub-families are listed here. However, the inclusion of one sub-family and not another, or the inclusion of one family and not another, does not mean that the invention does not encompass polynucleotides or polypeptides of a certain family or sub-family. The list provided here is merely an example of the types of transcription factors and the knowledge available concerning the consensus sequences and consensus DNA-binding site motifs that help define them as known to those of skill in the art (each of the references noted above are specifically incorporated herein by reference). A transcription factor may include, but is not limited to, any polypeptide that can activate or repress transcription of a single gene or a number of genes. This polypeptide group includes, but is not limited to, DNA-binding proteins, DNA-binding protein binding proteins, protein kinases, protein phosphatases, GTP-binding proteins, and receptors, and the like.

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like; as substrates for cloning e.g., including digestion or ligation reactions; and for identifying exogenous or endogenous modulators of the transcription factors. A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotides, e.g., at least about 15 consecutive polymerized nucleotides, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer

region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "polypeptide" is an amino acid sequence comprising a plurality of consecutive polymerized amino acid residues e.g., at least about 15 consecutive polymerized amino acid residues, optionally at least about 30 consecutive polymerized amino acid residues, at least about 50 consecutive polymerized amino acid residues. In many instances, a polypeptide comprises a polymerized amino acid residue sequence that is a transcription factor or a domain or portion or fragment thereof. Additionally, the polypeptide may comprise a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA-binding domain, or the like. The polypeptide optionally comprises modified amino acid residues, naturally occurring amino acid residues not encoded by a codon, non-naturally occurring amino acid residues.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. A "synthetic polypeptide" is a polypeptide created by consecutive polymerization of isolated amino acid residues using methods well known in the art. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

"Identity" or "similarity" refers to sequence similarity between two polynucleotide sequences or between two polypeptide sequences, with identity being a more strict comparison. The phrases "percent identity" and "% identity" refer to the percentage of sequence similarity found in a comparison of two or more polynucleotide sequences or two or more polypeptide sequences. Identity or similarity can be determined by comparing a position in each sequence that may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same nucleotide base or amino acid, then the molecules are identical at that position. A degree of similarity or identity between polynucleotide sequences is a function of the number of identical or matching nucleotides at positions shared by the polynucleotide sequences. A degree of identity of polypeptide sequences is a function of the number of identical amino acids at positions shared by the polypeptide sequences. A degree of homology or similarity of polypeptide sequences is a function of the number of amino acids, i.e., structurally related, at positions shared by the polypeptide sequences.

"Altered" nucleic acid sequences encoding polypeptide include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide encoding a polypeptide with at least one functional characteristic of the polypeptide. Included within this definition are polymorphisms that may or may not be readily detectable using a particular oligonucleotide probe of the

polynucleotide encoding polypeptide, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding polypeptide. The encoded polypeptide protein may also be "altered", and may contain deletions, insertions, or substitutions of amino acid residues that produce a silent change and result in a functionally equivalent polypeptide. Deliberate amino acid substitutions may be made on the basis of similarity in residue side chain chemistry, including, but not limited to, polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological activity of polypeptide is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine. Alignments between different polypeptide sequences may be used to calculate "percentage sequence similarity".

The term "plant" includes whole plants, shoot vegetative organs/structures (*e.g.*, leaves, stems and tubers), roots, flowers and floral organs/structures (*e.g.*, bracts, sepals, petals, stamens, carpels, anthers and ovules), seed (including embryo, endosperm, and seed coat) and fruit (the mature ovary), plant tissue (*e.g.*, vascular tissue, ground tissue, and the like) and cells (*e.g.*, guard cells, egg cells, and the like), and progeny of same. The class of plants that can be used in the method of the invention is generally as broad as the class of higher and lower plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), gymnosperms, ferns, horsetails, psilophytes, lycophytes, bryophytes, and multicellular algae. (See for example, Figure 1, adapted from Daly et al. 2001 *Plant Physiology* 127:1328-1333; and see also Tudge, C., The Variety of Life, Oxford University Press, New York, 2000, pp. 547-606.)

A "transgenic plant" refers to a plant that contains genetic material not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty.

Typically, the foreign genetic material has been introduced into the plant by human manipulation, but any method can be used as one of skill in the art recognizes.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

"Ectopic expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. The pattern of expression may also be compared with a reference expression pattern in a wild type plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

A "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the

intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA-binding site or domain that binds to a DNA promoter region, an activation domain, or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a polynucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically, of at least about 15 consecutive nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50 nucleotides, of any of the sequences provided herein.

The invention also encompasses production of DNA sequences that encode transcription factors and transcription factor derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding transcription factors or any fragment thereof.

A "conserved domain", with respect to a polypeptide, refers to a domain within a transcription factor family which exhibits a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% amino acid residue sequence identity of a polypeptide of consecutive amino acid residues. A fragment or domain can be referred to as outside a consensus sequence or outside a consensus DNA-binding site that is known to exist or that exists for a particular transcription factor class, family, or sub-family. In this case, the fragment or domain will not include the exact amino acids of a consensus sequence or consensus DNA-binding site of a transcription factor class, family or sub-family, or the exact amino acids of a particular transcription factor consensus sequence or consensus DNA-binding site. Furthermore, a particular fragment, region, or domain of a polypeptide, or a polynucleotide encoding a polypeptide, can be "outside a conserved domain" if all the amino acids of the

fragment, region, or domain fall outside of a defined conserved domain(s) for a polypeptide or protein. The conserved domains for each of polypeptides of SEQ ID NOs:2 - 2N, where N = 2-123, are listed in Table 4 as described in Example VII. Also, many of the polypeptides of Table 4 have conserved domains specifically indicated by start and stop sites. A comparison of the regions of the polypeptides in SEQ ID NOs:2 - 2N, where N = 2-123, or of those in Table 4, allows one of skill in the art to identify conserved domain(s) for any of the polypeptides listed or referred to in this disclosure, including those in Table 4 or Table 5.

A "trait" refers to a physiological, morphological, biochemical, or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch, or oil content of seed or leaves, or by observation of a metabolic or physiological process, e.g. by measuring uptake of carbon dioxide, or by the observation of the expression level of a gene or genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays, or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield, or pathogen tolerance. Any technique can be used to measure the amount of, comparative level of, or difference in any selected chemical compound or macromolecule in the transgenic plants, however.

"Trait modification" refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference compared with a wild type plant. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

I. Traits Which May Be Modified

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves, inflorescences, and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, osmotic sensitivity to soluble sugar concentrations, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

II. Transcription Factors Modify Expression Of Endogenous Genes

Expression of genes which encode transcription factors modify expression of endogenous genes, polynucleotides, and proteins are well known in the art. In addition, transgenic plants comprising isolated polynucleotides encoding transcription factors may also modify expression of endogenous genes, polynucleotides, and proteins. Examples include Peng et al. (1997, Genes and Development 11:3194-3205) and Peng et al. (1999, Nature, 400:256-261). In addition, many others have

demonstrated that an *Arabidopsis* transcription factor expressed in an exogenous plant species elicits the same or very similar phenotypic response. See, for example, Fu et al. (2001, Plant Cell 13:1791-1802); Nandi et al. (2000, Curr. Biol. 10:215-218); Coupland (1995, Nature 377:482-483); and Weigel and Nilsson (1995, Nature 377:482-500).

In another example, Mandel et al. (1992, Cell 71-133-143) and Suzuki et al. (2001, Plant J. 28:409-418) teach that a transcription factor expressed in another plant species elicits the same or very similar phenotypic response of the endogenous sequence, as often predicted in earlier studies of *Arabidopsis* transcription factors in *Arabidopsis* (see Mandel et al., 1992, *supra*; Suzuki et al., 2001, *supra*).

Other examples include Müller et al. (2001, Plant J. 28:169-179); Kim et al. (2001, Plant J. 25:247-259); Kyozuka and Shimamoto (2002, Plant Cell Physiol. 43:130-135); Boss and Thomas (2002, Nature, 416:847-850); He et al. (2000, Transgenic Res., 9:223-227); and Robson et al. (2001, Plant J. 28:619-631).

In yet another example, Gilmour et al. (1998, Plant J. 16:433-442) teach an Arabidopsis AP2 transcription factor, CBF1, which, when overexpressed in transgenic plants, increases plant freezing tolerance. Jaglo et al (2001, Plant Physiol. 127:910-917) further identified sequences in Brassica napus which encode CBF-like genes and that transcripts for these genes accumulated rapidly in response to low temperature. Transcripts encoding CBF-like proteins were also found to accumulate rapidly in response to low temperature in wheat, as well as in tomato. An alignment of the CBF proteins from Arabidopsis, B. napus, wheat, rye, and tomato revealed the presence of conserved amino acid sequences, PKK/RPAGRxKFxETRHP and DSAWR, that bracket the AP2/EREBP DNA binding domains of the proteins and distinguish them from other members of the AP2/EREBP protein family. (See Jaglo et al., supra.)

III. Polypeptides and Polynucleotides of the Invention

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides, or novel variant polypeptides or polynucleotides encoding novel variants of transcription factors derived from the specific sequences provided here. These polypeptides and polynucleotides may be employed to modify a plant's characteristic.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. In addition, further exemplary polynucleotides encoding the polypeptides of the invention were identified in the plant GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5′ and 3′ ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5′ and 3′ ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor or knockout plants and the changes in the characteristic(s) or trait(s) of the plants observed. Therefore, the polynucleotides and polypeptides can be employed to improve the characteristics of plants.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor plant cells and the changes in the expression levels of a number of genes, polynucleotides, and/or proteins of the plant cells observed. Therefore, the polynucleotides and polypeptides can be employed to change expression levels of a genes, polynucleotides, and/or proteins of plants.

IV. Producing Polypeptides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989

("Sambrook") and Current Protocols in Molecular Biology, F. M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger (supra), Sambrook (supra), and Ausubel (supra), as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. *See*, e.g., Ausubel, Sambrook and Berger, *all supra.*

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-1869; and Matthes et al. (1984) EMBO J. 3:801-805. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

V. Homologous Sequences

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, rape, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, Brussels sprouts, and kohlrabi). Other crops, fruits and vegetables whose phenotype can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such pine, poplar and eucalyptus, or mint or other labiates.

Orthologs And Paralogs

Several different methods are known by those of skill in the art for identifying and defining these functionally homologous sequences. Three general methods for defining paralogs and orthologs are described; a paralog or ortholog or homolog may be identified by one or more of the methods described below.

Orthologs and paralogs are evolutionarily related genes that have similar sequence and similar functions. Orthologs are structurally related genes in different species most likely derived from a common ancestral molecule prior to speciation. Paralogs are structurally related genes within a single species and are most likely a result of gene and/or chromosomal duplication.

Within a single plant species, gene duplication may causes two copies of a particular gene, giving rise to two or more genes with similar sequence and similar

function known as paralogs. A paralog is therefore a similar gene with a similar function within the same species. Paralogs typically cluster together or in the same clade (a group of similar genes) when a gene family phylogeny is analyzed using programs such as CLUSTAL (Thompson et al. (1994) Nucleic Acids Res. 22:4673-4680; Higgins et al. (1996) Methods Enzymol. 266 383-402). Groups of similar genes can also be identified using by pair-wise BLAST analysis (Feng and Doolittle (1987) J. Mol. Evol. 25:351-360). For example, a clade of very similar MADS domain transcription factors from Arabidopsis all share a common function in flowering time (Ratcliffe et al. (2001) Plant Physiol. 126:122-132), and a group of very similar AP2 domain transcription factors from Arabidopsis are involved in tolerance of plants to freezing (Gilmour et al. (1998) Plant J. 16:433-442). Analysis of groups of similar genes with similar function that fall within one clade can yield sub-sequences that are particular to the clade. These sub-sequences, known as consensus sequences, can not only be used to define the sequences within each clade, but define the functions of these genes, since genes within each clade typically share the same function. (See also, for example, Mount, D.W. (2001) Bioinformatics: Sequence and Genome Analysis Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York page 543.)

Speciation, the production of new species from a parental species, can also give rise to two or more genes with similar sequence and similar function. These genes, termed orthologs, often have an identical function within their host plants and are often interchangeable between species without losing function. Because plants have common ancestors, many genes in any plant species will have a corresponding orthologous gene in another plant species. Once a phylogenic tree for a gene family of one species has been constructed using a program such as CLUSTAL (Thompson et al. (1994) Nucleic Acids Res. 22:4673-4680; Higgins et al. (1996) Methods Enzymol. 266:383-402), potential orthologous sequences can placed into the phylogenetic tree and its relationship to genes from the species of interest can be determined. Once the ortholog pair has been identified, the function of the test ortholog can be determined by determining the function of the reference ortholog.

Transcription factors that are homologous to the listed sequences will typically share at least about 30% amino acid sequence identity, or at least about 30% amino

acid sequence identity outside of a known consensus sequence or consensus DNA-binding site. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences, or with the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site, or with the listed sequences excluding one or all conserved domain. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences, or to the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site or outside one or all conserved domain. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences, or to a listed sequence but excluding or outside a known consensus sequence or consensus DNA-binding site, or outside one or all conserved domain. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity. Transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence identity over the entire length of the polypeptide or the homolog. In addition, transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence similarity over the entire length of the polypeptide or the homolog.

Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Inc. Madison, Wis.). The MEGALIGN program

can create alignments between two or more sequences according to different methods, e.g., the clustal method. (See, e.g., Higgins, D. G. and P. M. Sharp (1988) Gene 73:237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. Other alignment algorithms or programs may be used, including FASTA, BLAST, or ENTREZ, FASTA and BLAST. These are available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with or without default settings. ENTREZ is available through the National Center for Biotechnology Information. In one embodiment, the percent identity of two sequences can be determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences (see USPN 6,262,333).

Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., San Diego, Calif., USA. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See Methods Mol. Biol. 70: 173-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid-encoded amino acid sequences can be used to search both protein and DNA databases.

The percentage similarity between two polypeptide sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between polynucleotide sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) Methods Enzymol.

183:626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions (see US Patent Application No. 20010010913).

Thus, the invention provides methods for identifying a sequence similar or paralogous or orthologous or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

In addition, one or more polynucleotide sequences or one or more polypeptides encoded by the polynucleotide sequences may be used to search against a BLOCKS (Bairoch et al. (1997) Nucleic Acids Res. 25:217-221), PFAM, and other databases which contain previously identified and annotated motifs, sequences and gene functions. Methods that search for primary sequence patterns with secondary structure gap penalties (Smith et al. (1992) Protein Engineering 5:35-51) as well as algorithms such as Basic Local Alignment Search Tool (BLAST; Altschul, S. F. (1993) J. Mol. Evol. 36:290-300; Altschul et al. (1990) *supra*), BLOCKS (Henikoff, S. and Henikoff, G. J. (1991) Nucleic Acids Research 19:6565-6572), Hidden Markov Models (HMM; Eddy, S. R. (1996) Cur. Opin. Str. Biol. 6:361-365; Sonnhammer et al. (1997) Proteins 28:405-420), and the like, can be used to manipulate and analyze polynucleotide and polypeptide sequences encoded by polynucleotides. These databases, algorithms and other methods are well known in the art and are described in Ausubel et al. (1997; Short Protocols in Molecular Biology, John Wiley & Sons, New York N.Y., unit 7.7) and in Meyers, R. A. (1995; Molecular Biology and Biotechnology, Wiley VCH, New York N.Y., p 856-853).

Furthermore, methods using manual alignment of sequences similar or homologous to one or more polynucleotide sequences or one or more polypeptides encoded by the polynucleotide sequences may be used to identify regions of similarity and conserved domains. Such manual methods are well-known of those of skill in the

art and can include, for example, comparisons of tertiary structure between a polypeptide sequence encoded by a polynucleotide which comprises a known function with a polypeptide sequence encoded by a polynucleotide sequence which has a function not yet determined. Such examples of tertiary structure may comprise predicted alpha helices, beta-sheets, amphipathic helices, leucine zipper motifs, zinc finger motifs, proline-rich regions, cysteine repeat motifs, and the like.

VI. Identifying Polynucleotides or Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing and tables can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physical-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number thereof), as described in more detail in the references cited above. Encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NOs: 26; 46; 176; 114; 142; 144; 82; 50; 72; 96; 18; 22; 26; and 240, and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G. M. and S. L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A. R. (1987) Methods Enzymol. 152:507-511.) Estimates of homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (Hames and Higgins, Eds. (1985) Nucleic Acid Hybridisation, IRL Press, Oxford, U.K.). Stringency conditions can be adjusted to screen for moderately similar fragments, such as homologous sequences from distantly related organisms, to highly similar fragments, such as genes that duplicate functional enzymes from closely related organisms. Post-hybridization washes determine stringency conditions.

In addition to the nucleotide sequences listed in Tables 4 and 5, full length cDNA, orthologs, paralogs and homologs of the present nucleotide sequences may be identified and isolated using well known methods. The cDNA libraries orthologs, paralogs and homologs of the present nucleotide sequences may be screened using hybridization methods to determine their utility as hybridization target or amplification probes.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C. For example, high stringency is about 0.2 x SSC, 0.1% SDS at 65° C. Ultra-high stringency will be the same conditions except the wash temperature is raised about 3 to about 5° C, and ultra-ultra-high stringency will be the same conditions except the wash temperature is raised about 6 to about 9° C. For identification of less closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC, as known in the art.

In another example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30° C, more preferably of at least about 37° C, and most preferably of at least about 42° C. Varying additional parameters, such as

hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment, hybridization will occur at 30° C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37° C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 μg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42° C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50% formamide, and 200 μg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps that follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25° C, more preferably of at least about 42° C. Another preferred set of highly stringent conditions uses two final washes in 0.1X SSC, 0.1% SDS at 65° C. The most preferred high stringency washes are of at least about 68° C. For example, in a preferred embodiment, wash steps will occur at 25° C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42° C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, the wash steps will occur at 68° C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art (see U.S. Patent Application No. 20010010913).

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to

noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radioactive label, or the like.

Alternatively, transcription factor homolog polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

VII. Sequence Variations

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing. Nucleic acids having a sequence that differs from the sequences

shown in the Sequence Listing, or complementary sequences, that encode functionally equivalent peptides (i.e., peptides having some degree of equivalent or similar biological activity) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code, are also within the scope of the invention.

Altered polynucleotide sequences encoding polypeptides include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide encoding a polypeptide with at least one functional characteristic of the instant polypeptides. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding the instant polypeptides, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding the instant polypeptides.

Allelic variant refers to any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (i.e., no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant is also used herein to denote a protein encoded by an allelic variant of a gene. Splice variant refers to alternative forms of RNA transcribed from a gene. Splice variation arises naturally through use of alternative splicing sites within a transcribed RNA molecule, or less commonly between separately transcribed RNA molecules, and may result in several mRNAs transcribed from the same gene. Splice variants may encode polypeptides having altered amino acid sequence. The term splice variant is also used herein to denote a protein encoded by a splice variant of an mRNA transcribed from a gene.

Those skilled in the art would recognize that the polypeptide sequence G481, SEQ ID NO: 114, represents a single transcription factor; allelic variation and alternative splicing may be expected to occur. Allelic variants of the polynucleotide sequence of SEQ ID NO: 113 can be cloned by probing cDNA or genomic libraries from different individual organisms according to standard procedures. Allelic variants of the DNA sequence shown in SEQ ID NO:113, including those containing

silent mutations and those in which mutations result in amino acid sequence changes, are within the scope of the present invention, as are proteins which are allelic variants of SEQ ID NO: 114. cDNAs generated from alternatively spliced mRNAs, which retain the properties of the transcription factor are included within the scope of the present invention, as are polypeptides encoded by such cDNAs and mRNAs. Allelic variants and splice variants of these sequences can be cloned by probing cDNA or genomic libraries from different individual organisms or tissues according to standard procedures known in the art (see USPN 6,388,064).

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acid			Possible Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	TGC	TGT				
Aspartic acid	Asp	D	GAC	GAT				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	TTC	TTT				
Glycine	Gly	G	GGA	GGC	GGG	GGT		
Histidine	His	H	CAC	CAT				
Isoleucine	Ile	I	ATA	ATC	ATT			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	Met	M	ATG					
Asparagine	Asn	N	AAC	AAT				
Proline	Pro	P	CCA	CCC	CCG	CCT		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	Thr	T	ACA	ACC	ACG	ACT		
Valine	Val	V	GTA	GTC	GTG	GTT		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG

and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Similar substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 3 when it is desired to maintain the activity of the protein. Table 3 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as structural and functional substitutions. For example, a residue in column 1 of Table 3 may be substituted with residue in column 2; in addition, a residue in column 2 of Table 3 may be substituted with the residue of column 1.

Table 3

Residue	Similar Substitutions
Ala	Ser; Thr; Gly; Val; Leu; Ile
Arg	Lys; His; Gly
Asn	Gln; His; Gly; Ser; Thr
Asp	Glu, Ser; Thr
Gln	Asn; Ala
Cys	Ser; Gly
Glu	Asp
Gly	Pro; Arg
His	Asn; Gln; Tyr; Phe; Lys; Arg
Ile	Ala; Leu; Val; Gly; Met
Leu	Ala; Ile; Val; Gly; Met
Lys	Arg; His; Gln; Gly; Pro
Met	Leu; Ile; Phe
Phe	Met; Leu; Tyr; Trp; His; Val; Ala
Ser	Thr; Gly; Asp; Ala; Val; Ile; His
Thr	Ser; Val; Ala; Gly
Trp	Tyr; Phe; His
Tyr	Trp; Phe; His
Val	Ala; Ile; Leu; Gly; Thr; Ser; Glu

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a

hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

VIII. Further Modifying Sequences of the Invention – Mutation/Forced Evolution

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. The modified sequences may be created using purified natural polynucleotides isolated from any organism or may be synthesized from purified compositions and chemicals using chemical means well know to those of skill in the art. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, for example, by Stemmer (1994) Nature 370:389-391, Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751, and U.S. Patents 5,811,238, 5,837,500, and 6,242,568. Methods for engineering synthetic transcription factors and other polypeptides are described, for example, by Zhang et al. (2000) J. Biol. Chem. 275:33850-33860, Liu et al. (2001) J. Biol. Chem. 276:11323-11334, and Isalan et al. (2001) Nature Biotechnol. 19:656-660. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by

the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *Saccharomyces cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA-binding domain derived from a transcription factor of the invention

can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA-binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

IX. Expression and Modification of Polypeptides

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

X. Vectors, Promoters, and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts that describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in

Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see,* e.g., Odell et al. (1985) Nature 313:810-812); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547-552); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977-984).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorable be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al, (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wunI*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using

promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acid, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those

previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cell expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants that include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing

polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

XI. Modified Amino Acid Residues

Polypeptides of the invention may contain one or more modified amino acid residues. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid residue(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid residue include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acid residues are replete throughout the literature.

The modified amino acid residues may prevent or increase affinity of the polypeptide for another molecule, including, but not limited to, polynucleotide, proteins, carbohydrates, lipids and lipid derivatives, and other organic or synthetic compounds.

XII. Identification of Additional Factors

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phentoype or trait of interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a

transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA-binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien et al. ((1991), Proc. Natl. Acad. Sci. USA 88:9578-9582) and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are

transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

XIII. Identification of Modulators

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northerns, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998, and supplements through 2001). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the

cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175; Furka, (1991) Int. J. Pept. Prot. Res. 37:487-493; and Houghton et al. (1991) Nature 354:84-88). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators that inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any

additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention. Modulation of expression or activity of a polynucleotide or polypeptide of the invention may also be caused by molecular elements in a signal transduction second messenger pathway and such modulation can affect similar elements in the same or another signal transduction second messenger pathway.

XIV. Subsequences

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra-high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A

nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

To be encompassed by the present invention, an expressed polypeptide which comprises such a polypeptide subsequence performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a specific DNA promoter region, an activation domain or a domain for protein-protein interactions.

XV. Production of Transgenic Plants

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of

trait modification, improved characteristics, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Arabidopsis as a model system

Arabidopsis thaliana is the object of rapidly growing attention as a model for genetics and metabolism in plants. Arabidopsis has a small genome, and well documented studies are available. It is easy to grow in large numbers and mutants defining important genetically controlled mechanisms are either available, or can readily be obtained. Various methods to introduce and express isolated homologous genes are available (see Koncz, et al., eds. *Methods in Arabidopsis Research*. et al. (1992), World Scientific, New Jersey, New Jersey, in "Preface"). Because of its small size, short life cycle, obligate autogamy and high fertility, *Arabidopsis* is also a choice organism for the isolation of mutants and studies in morphogenetic and development pathways, and control of these pathways by transcription factors (Koncz, *supra*, p. 72). A number of studies introducing transcription factors into *A. thaliana* have demonstrated the utility of this plant for understanding the mechanisms of gene regulation and trait alteration in plants. See, for example, Koncz, *supra*, and U.S. Patent Number 6,417,428).

Arabidopsis genes in transgenic plants.

Expression of genes which encode transcription factors modify expression of endogenous genes, polynucleotides, and proteins are well known in the art. In addition, transgenic plants comprising isolated polynucleotides encoding transcription factors may also modify expression of endogenous genes, polynucleotides, and proteins. Examples include Peng et al. (1997, Genes and Development 11:3194-3205) and Peng et al. (1999, Nature, 400:256-261). In addition, many others have demonstrated that an *Arabidopsis* transcription factor expressed in an exogenous plant species elicits the same or very similar phenotypic response. See, for example, Fu et al. (2001, Plant Cell 13:1791-1802); Nandi et al. (2000, Curr. Biol. 10:215-218); Coupland (1995, Nature 377:482-483); and Weigel and Nilsson (1995, Nature 377:482-500).

Homologous genes introduced into transgenic plants.

Homologous genes that may be derived from any plant, or from any source whether natural, synthetic, semi-synthetic or recombinant, and that share significant sequence identity or similarity to those provided by the present invention, may be introduced into plants, for example, crop plants, to confer desirable or improved traits. Consequently, transgenic plants may be produced that comprise a recombinant expression vector or cassette with a promoter operably linked to one or more sequences homologous to presently disclosed sequences. The promoter may be, for example, a plant or viral promoter.

The invention thus provides for methods for preparing transgenic plants, and for modifying plant traits. These methods include introducing into a plant a recombinant expression vector or cassette comprising a functional promoter operably linked to one or more sequences homologous to presently disclosed sequences. Plants and kits for producing these plants that result from the application of these methods are also encompassed by the present invention.

The complete descriptions of the traits associated with each polynucleotide of the invention is fully disclosed in Table 4, Table 5, and Table 6.

Table 4

Polynucleotide SEQ ID NO:	GID No.	Trait	Category	Family	Comment	Polypeptide SEQ ID NO:	Conserved Domains
1	G1322	Cold	Abiotic stress	MYB-(R1)R2R3	Increased seedling vigor	2	(26-130)
3	G2130	Cold; heat; Botrytis	Abiotic stress; disease	AP2	Increased susceptibility to chilling; better germination in heat; increased susceptibilty to Botrytis	4	(93-160)
5	G256	Cold	Abiotic stress	MYB-(R1)R2R3	Better germination and growth in cold	6	(13-115)
7	G394	Cold	Abiotic stress	HB	More sensitive to chilling.	8	(121-182)
9	G664	Cold	Abiotic stress	MYB-(R1)R2R3	Better germination and growth in cold	10	(13-116)
11	G864	Cold; heat	Abiotic stress	AP2	Adult stage chilling sensitivity; better germination in heat	12	(119-186)
13	G1820	Drought; osmotic; hormone sensitivity	Abiotic stress; hormone sensitivity	CAAT	Increased tolerance to drought; better germination in high salt; reduced ABA sensitivity	14	(70-133)
15	G912	Drought; freezing	Abiotic stress	AP2	Increased survival in drought condtions, freezing tolerant	16	(51-118)
17	G2583	Drought; low humidity; insect resistance	Abiotic stress; disease	AP2	Tolerance to drought and/or low humidity; resistance to insects	18	(4-71)
19	G975	Drought; low humidity; insect resistance	Abiotic stress; disease	AP2	Tolerance to drought and/or low humidity; resistance to insects	20	(4-71)
21	G1322	Drought; low humidity; insect resistance	Abiotic stress; disease	MYB-(R1)R2R3	Tolerance to drought and/or low humidity; resistance to insects	22	(26-130)
23	G303	Drought; low humidity; insect resistance	Abiotic stress; disease	HLH/MYC	Tolerance to drought and/or low humidity; resistance to insects	24	(92-161)
25	G720	Freezing	Abiotic stress	GARP	Knockout: increased susceptibility to freezing (knockout); overexpressor: slightly more freezing tolerant	26	(301-349)
27	G913	Freezing	Abiotic stress	AP2	Increased tolerance to freezing	28	(62-128)
29	G1305	Heat	Abiotic stress	MYB-(R1)R2R3	Reduced chlorosis	30	(15-118)
31	G1645	Heat	Abiotic stress	MYB-(R1)R2R3	Reduced germination vigor	32	(90-210)
33	G1841	Heat	Abiotic stress	AP2	Better germination under heat stress	34	(83-150)
35	G2430	Heat	Abiotic stress	GARP	Increased tolerance	36	(425-478)
37	G3	Heat	Abiotic stress	AP2	More sensitive	38	(28-95)
39	G464	Heat	Abiotic stress	IAA	Better germination and growth in heat	40	(20-28, 71-82, 126-142, 187-224)
41	G682	Heat	Abiotic stress	MYB-related	Better germination and growth in heat	42	(27-63)
43	G964	Heat	Abiotic stress	HB	Better germination and growth	44	(126-186)
45	G1792	Nutrient uptake; Botrytis; Erysiphe; Fusarium	Abiotic stress; disease	AP2	Increased tolerance to nitrogen-limited medium; increased fungal disease resistance	46	(17-85)
47	G1794	Nutrient uptake; osmotic	Abiotic stress	AP2	Reduced root growth; increased sensitivity to osmotic stress	48	(182-248)
49	G1946	Nutrient uptake	Abiotic stress	HS	Increased root growth on phosphate-free media	50	(32-130)
51	G225	Nutrient uptake	Abiotic stress	MYB-related	Increased tolerance to nitrogen-limited medium	52	(39-76)
53	G226	Nutrient uptake; sodium chloride	Abiotic stress	MYB-related	Increased tolerance to nitrogen-limited medium; susceptible to high salt	54	(28-78)
55	G419	Nutrient uptake	Abiotic stress	HB	Increased tolerance to potassium-free medium	56	(392-452)

Table 4

57	G545	Nutrient uptake; sodium chloride; Erysiphe; Fusarium; Pseudomonas	Abiotic stress; disease	Z-C2H2	Increased tolerance to phosphate-free medium, high salt; increased susceptibility to disease	58	(82-102, 136-154)
59	G561	Nutrient uptake	Abiotic stress	bZIP	Increased tolerance to potassium-free medium	60	(248-308)
61	G911	Nutrient uptake	Abiotic stress	RING/C3H2C3	Increased growth on potassium-free medium	62	(86-129)
63	G1069	Osmotic; hormone sensitivity	Abiotic stress; hormone sensitivity	AT-hook	Better germination under osmotic stress; reduced ABA sensitivity	64	(67-74)
65	G1089	Osmotic	Abiotic stress	BZIPT2	Better germination under osmotic stress	66	(425-500)
67	G1452	Osmotic; hormone sensitivity	Abiotic stress; hormone sensitivity	NAC	Better germination on sucrose and salt; reduced sensitivity to ABA	68	(30-177)
69	G175	Osmotic	Abiotic stress	WRKY	Increased tolerance	70	(178-234, 372-428)
71	G1852	Osmotic	Abiotic stress	AKR	Better root growth	72	(1-601)
73	G1863	Osmotic	Abiotic stress	GRF-like	Decreased germination under salt stress	74	(TBD)
75	G188	Osmotic; Fusarium	Abiotic stress; disease	WRKY	Better germination under osmotic stress; increased susceptibilty	76	(175-222)
77	G1930	Osmotic	Abiotic stress	AP2	Better germination under osmotic stress	78	(59-124)
79	G2053	Osmotic	Abiotic stress	NAC	Increased root growth	80	(10-149)
81	G2140	Osmotic; hormone sensitivity	Abiotic stress; hormone sensitivity	HLH/MYC	Better germination on NaCl and sucrose; decreased sensitivity to ABA	82	(167-242)
83	G2153	Osmotic	Abiotic stress	AT-hook	Better germination	84	(75-94, 162-206)
85	G2379	Osmotic	Abiotic stress	TH	Increased seedling vigor on high sucrose media	86	(19-110, 173-232)
87	G2701	Osmotic	Abiotic stress	MYB-related	Better germination on high NaCl and sucrose	88	(33-81, 129-183)
89	G2719	Osmotic	Abiotic stress	MYB-(R1)R2R3	Increased seedling vigor on high sucrose	90	(56-154)
91	G2789	Osmotic; hormone sensitivity	Abiotic stress; hormone sensitivity	AT-hook	Better germination on high sucrose; reduced ABA sensitivity	92	(53-73, 121-165)
93	G303	Osmotic	Abiotic stress	HLH/MYC	Better germination on high sucrose and high NaCl	94	(92-161)
95	G325	Osmotic	Abiotic stress	Z-CO-like	Slightly better germination on high sucrose and high NaCl	96	(5-28, 48-71)
97	G353	Osmotic	Abiotic stress	Z-C2H2	Increased seedling vigor on PEG	98	(41-61, 84-104)
99	G47	Osmotic	Abiotic stress	AP2	Better root growth	100	(11-80)
101	G489	Osmotic	Abiotic stress	CAAT	Increased tolerance to osmotic stress	102	(57-156)
103	G502	Osmotic	Abiotic stress	NAC	Increased sensitivity to osmotic stress	104	(10-155)
105	G526	Osmotic	Abiotic stress	NAC	Increased sensitivity to osmotic stress	106	(21-149)
107	G921	Osmotic	Abiotic stress	WRKY	Increased sensitivity to osmotic stress	108	(146-203)
109	G922	Osmotic; sodium chloride	Abiotic stress	SCR	Better germination on high sucrose; better germination and increased root growth on high salt	110	(225-242)
111	G926	Osmotic; hormone sensitivity	Abiotic stress; hormone sensitivity	CAAT	Increased tolerance to osmotic stress (salt and sucrose); reduced sensitivity to ABA	112	(131-225)
113	G481	Osmotic	Abiotic stress	CAAT	Overexpressors more tolerant to high sucrose in a germination assay	114	(20-109)
115	G1807	Oxidative	Abiotic stress	bZIP	More sensitive to acifluorfen	116	(249-297)

Table 4

117	G477	Oxidative; Sclerotina	Abiotic stress; disease	SBP	Increased sensitivity to oxidative stress; increased susceptibility to Sclerotinia-caused disease	118	(108-233)
119	G789	Oxidative; Sclerotina	Abiotic stress; disease	HLH/MYC	Increased sensitivity to oxidative stress; increased susceptibility to Sclerotina-caused disease	120	(253-313)
121	G1836	Sodium chloride	Abiotic stress	CAAT	Better germination in high salt	122	(30-164)
123	G196	Sodium chloride	Abiotic stress	WRKY	Increased tolerance	124	(223-283)
125	G2110	Sodium chloride	Abiotic stress	WRKY	Increased tolerance	126	(239-298)
127	G22	Sodium chloride	Abiotic stress	AP2	Increased tolerance to high salt	128	(89-157)
129	G2713	Sodium chloride	Abiotic stress	TUBBY	Increased root growth	130	(59-270, 400-445)
131	G312	Sodium chloride	Abiotic stress	SCR	Slightly better germination on high NaCl	132	(320-336)
133	G482	Sodium chloride	Abiotic stress	CAAT	Increased tolerance to high salt	134	(25-116)
135	G801	Sodium chloride	Abiotic stress	PCF	Better germination on NaCl	136	(32-93)
137	G867	Sodium chloride	Abiotic stress	AP2	Better seedling vigor	138	(59-124)
139	G884	Sodium chloride	Abiotic stress	WRKY	Increased root growth	140	(227-285, 407-465)
141	G2133	Glyphosate	Herbicide sensitivity	AP2	Increased tolerance	142	(11-83)
143	G2517	Glyphosate	Herbicide sensitivity	WRKY	Increased tolerance	144	(TBD)
145	G343	Glyphosate	Herbicide sensitivity	GATA/Zn	Increase in resistance	146	(178-214)
147	G1062	Hormone sensitivity	Hormone sensitivity	HLH/MYC	Altered response to the growth hormone ethylene	148	(308-359)
149	G1095	Hormone sensitivity	Hormone sensitivity	RING/C3H2C3	Increased sensitivity to ACC	150	(134-159)
151	G1134	Hormone sensitivity	Hormone sensitivity	HLH/MYC	Altered response to the growth hormone ethylene	152	(198-247)
153	G12	Hormone sensitivity	Hormone sensitivity	AP2	Increased sensitivity to ACC	154	(TBD)
155	G1330	Hormone sensitivity	Hormone sensitivity	MYB-(R1)R2R3	Altered response to ethylene	156	(28-134)
157	G1666	Hormone sensitivity	Hormone sensitivity	HLH/MYC	Increased sensitivity to ACC	158	(353-420)
159	G546	Hormone sensitivity	Hormone sensitivity	RING/C3H2C3	Decreased sensitivity to ABA	160	(114-155)
161	G760	Hormone sensitivity	Hormone sensitivity	NAC	hypersensitive to ACC	162	(12-156)
163	G913	Hormone sensitivity	Hormone sensitivity	AP2	Increased sensitivity to ACC	164	(62-128)
165	G1064	Botrytis	Disease	PCF	Increased sensitivity	166	(116-179)
167	G1084	Botrytis	Disease	BZIPT2	Increased susceptibility	168	(TBD)
169	G1196	Botrytis	Disease	AKR	Increased susceptibility	170	(179-254)
171	G1255	Botrytis	Disease	Z-CO-like	Increased susceptibility	172	(18-56)
173	G1514	Botrytis	Disease	RING/C3HC4	Increased susceptibility	174	(20-50)
175	G1756	Botrytis	Disease	WRKY	Increased susceptibility	176	(TBD)
177	G1880	Botrytis	Disease	Z-C2H2	Increased resistance	178	(69-89, 111-139)
179	G1919	Botrytis	Disease	RING/C3HC4	Increased tolerance	180	(214-287)
181	G1936	Botrytis; Sclerotina	Disease	PCF	Increased susceptibility	182	(64-129)
183	G1950	Botrytis	Disease	AKR	Increased tolerance	184	(65-228)
185	G2069	Botrytis	Disease	bZIP	Increased susceptibility	186	(TBD)
187	G207	Botrytis	Disease	MYB-(R1)R2R3	Increased susceptibility	188	(6-106)
189	G2380	Botrytis	Disease	TH	Increased susceptibility	190	(107-181)
191	G248	Botrytis	Disease	MYB-(R1)R2R3	Increased susceptibility	192	(264-332)
193	G2555	Botrytis	Disease	HLH/MYC	Increased susceptibility	194	(175-245)

Table 4

195	G28	Botrytis; Sclerotina; Erysiphe	Disease	AP2	Botrytis, Sclerotina: increased tolerance; Erysiphe: increased resistance	196	(145-213)
197	G371	Botrytis	Disease	RING/C3HC4	Increased susceptibility	198	(21-74)
199	G812	Botrytis	Disease	HS	Increased tolerance	200	(31-120)
201	G865	Botrytis	Disease	AP2	Increased susceptibility	202	(36-103)
203	G940	Botrytis	Disease	EIL	Increased susceptibility	204	(86-96)
205	G558	Defense gene expression	Disease	bZIP	Increased expression of defense genes	206	(45-105)
207	G569	Defense gene expression	Disease	bZIP	Decreased expression of defense genes	208	(90-153)
209	G1266	Erysiphe	Disease	AP2	Increased tolerance	210	(79-147)
211	G19	Erysiphe	Disease	AP2	Increased tolerance; repressed by methyl jasmonate and induced by ACC	212	(76-145)
213	G237	Erysiphe	Disease	MYB-(R1)R2R3	Increased tolerance	214	(11-113)
215	G378	Erysiphe	Disease	RING/C3H2C3	Increased resistance	216	(196-237)
217	G409	Erysiphe	Disease	HB	Increased tolerance	218	(64-124)
219	G591	Erysiphe	Disease	HLH/MYC	Increased tolerance	220	(143-240)
221	G616	Erysiphe	Disease	TEO	Increased tolerance	222	(39-95)
223	G869	Erysiphe	Disease	AP2	Increased tolerance	224	(109-177)
225	G881	Erysiphe	Disease	WRKY	Increased susceptibility	226	(176-233)
227	G1047	Fusarium	Disease	bZIP	Increased tolerance	228	(129-180)
229	G1363	Fusarium	Disease	CAAT	Increased tolerance	230	(174-226)
231	G147	Fusarium	Disease	MADS	Increased susceptibility	232	(2-57)
233	G896	Fusarium	Disease	Z-LSDlike	Increased susceptibility	234	(18-39)
235	G418	Pseudomonas	Disease	HB	Increased tolerance	236	(500-560)
237	G525	Pseudomonas	Disease	NAC	Increased tolerance	238	(23-167)
239	G1927	Sclerotinia	Disease	NAC	Increased tolerance	240	(17-188)
241	G278	Sclerotinia	Disease	AKR	Increased susceptibility	242	(2-593)
243	G594	Sclerotinia	Disease	HLH/MYC	Increased susceptibility	244	(140-204)
245	G805	Sclerotinia	Disease	PCF	Increased susceptibility	246	(51-114)

Table 5

SEQ ID NO	GID	Test Sequence ID	Smallest Sum Probability	Test Sequence Species	Test Sequence GenBank Annotation
25	G720	BG450227	3.20E-31	[Medicago truncatula]	NF015E11DT1F1087 Drought Medicago trunc
25	G720	AF318580	3.60E-26	[Zea mays]	putative transcription factor ZmGLK1 (Glk1) mRNA,
25	G720	AF318581	1.50E-22	[Oryza sativa]	putative transcription factor OsGLK1 (Glk1) mR
25	G720	AW906970	5.50E-20	[Solanum tuberosum]	EST343197 potato stolon, Cornell Universi
25	G720	BE330069	2.20E-15	[Glycine max]	so73a08.y1 Gm-c1040 Glycine max cDNA clone GENO
25	G720	AI896489	4.20E-15	[Lycopersicon esculentum]	EST265932 tomato callus, TAMU Lycop
25	G720	BI070070	4.70E-14	[Populus tremula x Populus tremuloides]	C013P55U Populus stra
25	G720	AW618051	3.10E-11	[Lycopersicon pennellii]	EST314101 L. pennellii trichome, Cor
25	G720	BG049455	1.80E-09	[Sorghum bicolor]	OV1_20_B11.g1_A002 Ovary 1 (OV1) Sorghum bi
25	G720	AW719680	1.20E-08	[Lotus japonicus]	LjNEST8C3r Lotus japonicus nodule library 5
25	G720	gi11177540	1.30E-28	[Zea mays]	putative transcription factor Golden2.
25	G720	gi13940498	6.90E-28	[Oryza sativa]	putative transcription factor OsGLK1.
25	G720	gi4519671	5.60E-05	[Nicotiana tabacum]	transfactor.
25	G720	gi6942190	0.0022	[Mesembryanthemum crystallinum]	CDPK substrate protein 1; C
25	G720	gi5916207	0.0053	[Chlamydomonas reinhardtii]	regulatory protein of P-starvat
25	G720	gi1247386	0.23	[Nicotiana alata]	PRP2.
25	G720	gi169878	0.24	[Sesbania rostrata]	nodulin.
25	G720	gi1808688	0.3	[Sporobolus stapfianus]	hypothetical protein.
25	G720	gi99948	0.61	[Glycine max]	proline-rich protein 2 precursor - soybean.
25	G720	gi82091	0.7	[Lycopersicon esculentum]	hydroxyproline-rich glycoprotein
45	G1792	AI776626	1.20E-32	[Lycopersicon esculentum]	EST257726 tomato resistant, Cornell
45	G1792	BF646324	1.30E-29	[Medicago truncatula]	NF074E05EC1F1038 Elicited cell culture
45	G1792	BM178875	4.60E-29	[Glycine max]	saj60f01.y1 Gm-c1072 Glycine max cDNA clone SOY
45	G1792	AC025907	4.20E-27	[Oryza sativa]	chromosome 10 clone nbxb0094K20, *** SEQUENCIN
45	G1792	AP004623	1.90E-22	[Oryza sativa (japonica cultivar-group)]	( ) chromosome 8 clo
45	G1792	BM268956	2.10E-22	[Zea mays]	MEST402-H11.univ ISUM5-RN Zea mays cDNA clone MEST
45	G1792	AF245119	3.80E-22	[Mesembryanthemum crystallinum]	AP2-related transcription fac
45	G1792	BH517030	2.10E-21	[Brassica oleracea]	BOHRB76TF BOHR Brassica oleracea genomic
45	G1792	BM437083	5.00E-21	[Vitis vinifera]	VVA014A06_53661 An expressed sequence tag da
45	G1792	BF275652	5.90E-21	[Gossypium arboreum]	GA__Eb0024J23f Gossypium arboreum 7-10 d
45	G1792	gi1732406	1.00E-24	[Nicotiana tabacum]	S25-XP1 DNA binding protein.
45	G1792	gi12597874	1.70E-24	[Oryza sativa]	putative ethylene-responsive element binding
45	G1792	gi7528276	3.60E-24	[Mesembryanthemum crystallinum]	AP2-related transcription f
45	G1792	gi2213783	3.30E-23	[Lycopersicon esculentum]	Pti5.
45	G1792	gi19034045	8.60E-23	[Oryza sativa (japonica cultivar-group)]	putative DNA bindi
45	G1792	gi8980313	8.60E-23	[Catharanthus roseus]	AP2-domain DNA-binding protein.
45	G1792	gi8809571	8.60E-23	[Nicotiana sylvestris]	ethylene-responsive element binding

Table 5

45	G1792	gi17385636	5.50E-21	[Matricaria chamomilla]	ethylene-responsive element binding
45	G1792	gi8571476	5.00E-20	[Atriplex hortensis]	apetala2 domain-containing protein.
45	G1792	gi1688233	1.30E-19	[Solanum tuberosum]	DNA binding protein homolog.
175	G1756	AV423663	6.50E-34	[Lotus japonicus]	AV423663 Lotus japonicus young plants (two-
175	G1756	AW596933	3.10E-30	[Glycine max]	sj84f07.y1 Gm-c1034 Glycine max cDNA clone GENO
175	G1756	AW447931	8.40E-24	[Triticum aestivum]	BRY_1082 BRY Triticum aestivum cDNA clone
175	G1756	BI266533	1.50E-22	[Medicago truncatula]	NF100A09IN1F1097 Insect herbivory Medic
175	G1756	AW218278	1.10E-19	[Lycopersicon esculentum]	EST303459 tomato radicle, 5 d post-
175	G1756	AP002744	2.60E-18	[Oryza sativa]	genomic DNA, chromosome 1, PAC clone:P0006C01,
175	G1756	BG600477	3.00E-15	[Solanum tuberosum]	EST505372 cSTS Solanum tuberosum cDNA clo
175	G1756	gi11761072	7.10E-23	[Oryza sativa]	hypothetical protein.
175	G1756	gi4322940	3.10E-15	[Nicotiana tabacum]	DNA-binding protein 2.
175	G1756	gi1432056	9.00E-12	[Petroselinum crispum]	WRKY3.
175	G1756	gi4894963	2.00E-11	[Avena sativa]	DNA-binding protein WRKY3.
175	G1756	gi927025	7.40E-11	[Cucumis sativus]	SPF1-like DNA-binding protein.
175	G1756	gi13620227	2.50E-10	[Lycopersicon esculentum]	hypothetical protein.
175	G1756	gi11993901	6.10E-10	[Dactylis glomerata]	somatic embryogenesis related protein.
175	G1756	gi1159877	7.20E-10	[Avena fatua]	DNA-binding protein.
175	G1756	gi484261	8.60E-10	[Ipomoea batatas]	SPF1 protein.
175	G1756	gi3420906	1.30E-09	[Pimpinella brachycarpa]	zinc finger protein; WRKY1.
113	G481	BG440251	9.00E-42	[Gossypium arboreum]	GA__Ea0006K20f Gossypium arboreum 7-10 d
113	G481	BM887558	3.90E-41	[Glycine max]	sam40c09.y1 Gm-c1068 Glycine max cDNA clone SOY
113	G481	ZMNFYB	1.70E-40	[Zea mays]	Z.mays mRNA for CAAT-box DNA binding protein subun
113	G481	AI728916	2.40E-40	[Gossypium hirsutum]	BNLGHi12022 Six-day Cotton fiber Gossypi
113	G481	AW775623	3.80E-40	[Medicago truncatula]	EST334688 DSIL Medicago truncatula cDNA
113	G481	AW738727	9.80E-40	[Lycopersicon esculentum]	EST340154 tomato flower buds, anthe
113	G481	BG599785	1.70E-38	[Solanum tuberosum]	EST504680 cSTS Solanum tuberosum cDNA clo
113	G481	BE413647	2.50E-38	[Triticum aestivum]	SCU001.E10.R990714 ITEC SCU Wheat Endospe
113	G481	BF065056	5.80E-38	[Hordeum vulgare]	HV_CEb0022M01f Hordeum vulgare seedling gre
113	G481	BG314203	1.00E-37	[Triticum monococcum]	WHE2460_E10_I20ZS Triticum monococcum i
113	G481	gi22380	1.10E-45	[Zea mays]	CAAT-box DNA binding protein subunit B (NF-YB).
113	G481	gi15408794	2.60E-30	[Oryza sativa]	putative CCAAT-binding transcription factor
113	G481	gi16902054	1.00E-28	[Vernonia galamensis]	CCAAT-box binding factor HAP3 B domai
113	G481	gi16902050	2.70E-28	[Glycine max]	CCAAT-box binding factor HAP3 B domain.
113	G481	gi16902056	4.30E-28	[Argemone mexicana]	CCAAT-box binding factor HAP3 B domain.
113	G481	gi16902058	1.50E-23	[Triticum aestivum]	CCAAT-box binding factor HAP3 B domain.
141	G2133	BE320193	1.20E-22	[Medicago truncatula]	NF024B04RT1F1029 Developing root Medica
141	G2133	AP003379	2.10E-20	[Oryza sativa]	chromosome 1 clone P0408G07, *** SEQUENCING IN
141	G2133	BG832521	1.50E-16	[Pinus taeda]	NXPV_073_H03_F NXPV (Nsf Xylem Planings wood Ve

Table 5

141	G2133	BG046836	1.50E-15	[Glycine max]	saa62d08.y1 Gm-c1060 Glycine max cDNA clone GEN
141	G2133	BG321374	1.60E-15	[Descurainia sophia]	Ds01_06d08_R Ds01_AAFC_ECORC_cold_stress
141	G2133	BE432190	4.00E-15	[Lycopersicon esculentum]	EST398719 tomato breaker fruit, TIG
141	G2133	BI431368	6.70E-15	[Solanum tuberosum]	EST534129 P. infestans-challenged leaf So
141	G2133	AU085418	1.20E-14	[Cryptomeria japonica]	AU085418 Cryptomeria japonica inner ba
141	G2133	BG446456	2.80E-14	[Gossypium arboreum]	GA__Eb0034M18f Gossypium arboreum 7-10 d
141	G2133	AI728590	3.10E-14	[Gossypium hirsutum]	BNLGHi11133 Six-day Cotton fiber Gossypi
141	G2133	gi8571476	2.50E-16	[Atriplex hortensis]	apetala2 domain-containing protein.
141	G2133	gi14140155	3.30E-15	[Oryza sativa]	putative AP2 domain transcription factor.
141	G2133	gi5616086	3.00E-14	[Brassica napus]	dehydration responsive element binding pro
141	G2133	gi12225916	1.10E-13	[Zea mays]	unnamed protein product.
141	G2133	gi10798644	4.20E-13	[Nicotiana tabacum]	AP2 domain-containing transcription fac
141	G2133	gi8980313	1.90E-12	[Catharanthus roseus]	AP2-domain DNA-binding protein.
141	G2133	gi2213785	1.30E-11	[Lycopersicon esculentum]	Pti6.
141	G2133	gi6478845	7.30E-11	[Matricaria chamomilla]	ethylene-responsive element binding
141	G2133	gi12658319	1.20E-10	[Hordeum vulgare]	CBF1-like protein BCBF1.
141	G2133	gi8809573	1.50E-10	[Nicotiana sylvestris]	ethylene-responsive element binding
143	G2517	BI470088	1.50E-35	[Glycine max]	saf38f09.y3 Gm-c1077 Glycine max cDNA clone GEN
143	G2517	BI208323	2.60E-31	[Lycopersicon esculentum]	EST526363 cTOS Lycopersicon esculen
143	G2517	BE445081	4.40E-28	[Triticum aestivum]	WHE1131_B06_D11ZS Wheat etiolated seedlin
143	G2517	AV408330	2.40E-26	[Lotus japonicus]	AV408330 Lotus japonicus young plants (two-
143	G2517	BE362650	7.10E-26	[Sorghum bicolor]	DG1_88_H02.b1_A002 Dark Grown 1 (DG1) Sorgh
143	G2517	BI308031	4.70E-25	[Medicago truncatula]	EST529441 GPOD Medicago truncatula cDNA
143	G2517	AP002839	2.00E-23	[Oryza sativa]	genomic DNA, chromosome 1, PAC clone:P0688A04,
143	G2517	BE216050	4.60E-21	[Hordeum vulgare]	HV_CEb0009E04f Hordeum vulgare seedling gre
143	G2517	BG889690	8.70E-21	[Solanum tuberosum]	EST515541 cSTD Solanum tuberosum cDNA clo
143	G2517	L35779	7.50E-19	[Brassica rapa]	BNAESTG Mustard flower buds Brassica rapa cDN
143	G2517	gi11761085	2.10E-25	[Oryza sativa]	putative DNA-binding protein homolog.
143	G2517	gi9187622	1.10E-20	[Solanum tuberosum]	WRKY DNA binding protein.
143	G2517	gi4322940	6.70E-17	[Nicotiana tabacum]	DNA-binding protein 2.
143	G2517	gi1432058	5.40E-15	[Petroselinum crispum]	WRKY2.
143	G2517	gi1159877	5.10E-14	[Avena fatua]	DNA-binding protein.
143	G2517	gi3420906	5.80E-13	[Pimpinella brachycarpa]	zinc finger protein; WRKY1.
143	G2517	gi13620227	1.50E-12	[Lycopersicon esculentum]	hypothetical protein.
143	G2517	gi927025	6.40E-12	[Cucumis sativus]	SPF1-like DNA-binding protein.
143	G2517	gi4894963	1.40E-11	[Avena sativa]	DNA-binding protein WRKY3.
143	G2517	gi6723482	4.70E-11	[Betula pendula]	wrky-type DNA binding protein.
81	G2140	AI488313	4.80E-59	[Lycopersicon esculentum]	EST246635 tomato ovary, TAMU Lycope
81	G2140	BE020519	6.10E-55	[Glycine max]	sm44g03.y1 Gm-c1028 Glycine max cDNA clone GENO

Table 5

81	G2140	AU093196	9.70E-46	[Oryza sativa subsp. japonica]	AU093196 Rice callus Oryza sat
81	G2140	AP003908	8.00E-39	[Oryza sativa]	chromosome 8 clone OJ1300_C09, *** SEQUENCING
81	G2140	BF647687	5.30E-37	[Medicago truncatula]	NF025A04EC1F1024 Elicited cell culture
81	G2140	AI054433	1.70E-26	[Mesembryanthemum crystallinum]	R6-R97 Ice plant Lambda Uni-Z
81	G2140	BE922838	1.70E-24	[Solanum tuberosum]	EST426607 potato leaves and petioles Sola
81	G2140	AU085144	1.80E-16	[Cryptomeria japonica]	AU085144 Cryptomeria japonica inner ba
81	G2140	BG275442	1.90E-13	[Pinus taeda]	NXSI_141_F07_F NXSI (Nsf Xylem Side wood Inclin
81	G2140	BE051300	6.30E-13	[Zea mays]	za74h04.b50 Maize Glume cDNAs Library Zea mays cDN
81	G2140	gi8570062	1.70E-27	[Oryza sativa]	ESTs C26093(C11622),AU090634(C12429) corresp
81	G2140	gi527655	0.00014	[Pennisetum glaucum]	myc-like regulatory R gene product.
81	G2140	gi22472	0.0055	[Zea mays]	R-S protein (AA 1-612).
81	G2140	gi527665	0.017	[Sorghum bicolor]	myc-like regulatory R gene product.
81	G2140	gi1086526	0.058	[Oryza australiensis]	transcriptional activator Ra homolog.
81	G2140	gi1086534	0.081	[Oryza officinalis]	transcriptional activator Ra homolog.
81	G2140	gi10998404	0.15	[Petunia x hybrida]	anthocyanin 1.
81	G2140	gi527663	0.15	[Tripsacum australe]	myc-like regulatory R gene product.
81	G2140	gi1086536	0.4	[Oryza rufipogon]	transcriptional activator Ra homolog.
81	G2140	gi1086530	0.49	[Oryza longistaminata]	transcriptional activator Ra homolog
49	G1946	LPHSF8	1.10E-119	[Lycopersicon peruvianum]	L.peruvianum Lp-hsf8 mRNA for heat
49	G1946	AC087771	4.10E-112	[Medicago truncatula]	clone 8D15, *** SEQUENCING IN PROGRESS
49	G1946	LEHSF8	5.90E-103	[Lycopersicon esculentum]	L.esculentum Le-hsf8 gene for heat
49	G1946	AW569138	3.10E-75	[Glycine max]	si63g09.y1 Gm-r1030 Glycine max cDNA clone GENO
49	G1946	BG890899	1.30E-70	[Solanum tuberosum]	EST516750 cSTD Solanum tuberosum cDNA clo
49	G1946	AC027658	4.60E-53	[Oryza sativa]	subsp. japonica BAC nbxb0006I13, chromosome 10
49	G1946	AV833112	4.90E-52	[Hordeum vulgare subsp. vulgare]	AV833112 K. Sato unpublished
49	G1946	gi19492	2.80E-121	[Lycopersicon peruvianum]	heat shock transcription factor 8
49	G1946	gi19260	5.10E-106	[Lycopersicon esculentum]	heat stress transcription factor
49	G1946	gi662924	2.00E-47	[Glycine max]	heat shock transcription factor 21.
49	G1946	gi5821138	9.70E-46	[Nicotiana tabacum]	heat shock factor.
49	G1946	gi11761077	2.90E-40	[Oryza sativa]	putative heat shock factor protein 1 (HSF 1)
49	G1946	gi886742	3.20E-40	[Zea mays]	heat shock factor.
49	G1946	gi7158882	2.70E-38	[Medicago sativa]	heat shock transcription factor.
49	G1946	gi3550588	1.90E-30	[Pisum sativum]	heat shock transcription factor (HSFA).
49	G1946	gi100546	0.46	[Avena sativa]	avenin precursor - oat.
49	G1946	gi14190783	1	[Apium graveolens]	putative phloem transcription factor M1.
71	G1852	AF220204	2.00E-95	[Malus domestica]	unknown mRNA.
71	G1852	BG597959	3.30E-95	[Solanum tuberosum]	EST496637 cSTS Solanum tuberosum cDNA clo
71	G1852	AC077693	4.50E-93	[Oryza sativa]	chromosome 10 clone OSJNBa0095C07, *** SEQUENC
71	G1852	BG445922	5.90E-91	[Gossypium arboreum]	GA__Ea0030A23f Gossypium arboreum 7-10 d

Table 5

71	G1852	BG581705	1.60E-90	[Medicago truncatula]	EST483440 GVN Medicago truncatula cDNA
71	G1852	BF009089	5.30E-86	[Glycine max]	ss73d04.y1 Gm-c1062 Glycine max cDNA clone GENO
71	G1852	BE434670	2.20E-71	[Lycopersicon esculentum]	EST405748 tomato breaker fruit, TIG
71	G1852	BG317894	5.90E-56	[Pinus taeda]	NXPV_006_H10_F NXPV (Nsf Xylem Planings wood Ve
71	G1852	AV422410	1.20E-55	[Lotus japonicus]	AV422410 Lotus japonicus young plants (two-
71	G1852	AI055434	1.20E-50	[Gossypium hirsutum]	coau0003P22 Cotton Boll Abscission Zone
71	G1852	gi5734619	1.30E-103	[Oryza sativa]	Similar to Arabidopsis thaliana BAC F15P23 (
71	G1852	gi6752888	1.80E-98	[Malus x domestica]	unknown.
71	G1852	gi498042	0.81	[Senecio odorus]	ORF.
71	G1852	gi4432741	1	[Dioscorea tenuipes]	phosphoglucose isomerase.
95	G325	AB001888	9.20E-43	[Oryza sativa]	mRNA for zinc finger protein, complete cds,
95	G325	BE558327	5.40E-30	[Hordeum vulgare]	HV_CEb0017D19f Hordeum vulgare seedling gre
95	G325	BG644908	1.80E-29	[Medicago truncatula]	EST506527 KV3 Medicago truncatula cDNA
95	G325	BG605313	3.10E-29	[Triticum aestivum]	WHE2331_C04_F07ZS Wheat pre-anthesis spik
95	G325	BG459023	1.60E-28	[Zea mays]	947052H08.y1 947 - 2 week shoot from Barkan lab Ze
95	G325	BG590826	3.20E-28	[Solanum tuberosum]	EST498668 P. infestans-challenged leaf So
95	G325	BG412316	4.40E-27	[Sorghum bicolor]	OV2_40_D10.b1_A002 Ovary 2 (OV2) Sorghum bi
95	G325	BG127619	1.50E-25	[Lycopersicon esculentum]	EST473181 tomato shoot/meristem Lyc
95	G325	AW399335	7.70E-22	[Lycopersicon pennellii]	EST309835 L. pennellii trichome, Cor
95	G325	AW780799	3.90E-21	[Glycine max]	sl76c08.y1 Gm-c1027 Glycine max cDNA clone GENO
95	G325	gi3618320	5.60E-49	[Oryza sativa]	zinc finger protein.
95	G325	gi3341723	1.40E-13	[Raphanus sativus]	CONSTANS-like 1 protein.
95	G325	gi11037311	5.00E-13	[Brassica nigra]	constans-like protein.
95	G325	gi2303683	6.00E-13	[Brassica napus]	unnamed protein product.
95	G325	gi4091806	2.80E-12	[Malus x domestica]	CONSTANS-like protein 2.
95	G325	gi10946337	7.00E-11	[Ipomoea nil]	CONSTANS-like protein.
95	G325	gi4557093	6.50E-10	[Pinus radiata]	zinc finger protein.
17	G2583	AW928465	1.40E-43	[Lycopersicon esculentum]	EST337253 tomato flower buds 8 mm t
17	G2583	BE023297	2.40E-42	[Glycine max]	sm80e10.y1 Gm-c1015 Glycine max cDNA clone GENO
17	G2583	AP003615	1.60E-30	[Oryza sativa]	chromosome 6 clone P0486H12, *** SEQUENCING IN
17	G2583	AU088998	2.90E-21	[Lotus japonicus]	AU088998 Lotus japonicus flower bud cDNA Lo
17	G2583	AT001828	4.60E-20	[Brassica rapa subsp. pekinensis]	AT001828 Flower bud cDNA Br
17	G2583	BG415973	2.40E-18	[Hordeum vulgare]	HVSMEk0009E06f Hordeum vulgare testa/perica
17	G2583	BF647090	3.80E-17	[Medicago truncatula]	NF007A06EC1F1038 Elicited cell culture
17	G2583	BG560598	2.90E-16	[Sorghum propinquum]	RHIZ2_59_D07.b1_A003 Rhizome2 (RHIZ2) So
17	G2583	AW011200	6.60E-16	[Pinus taeda]	ST17H08 Pine TriplEx shoot tip library Pinus ta
17	G2583	BF479478	1.60E-15	[Mesembryanthemum crystallinum]	L48-3155T3 Ice plant Lambda U
17	G2583	gi19507	1.40E-16	[Lupinus polyphyllus]	put. pPLZ2 product (AA 1-164).
17	G2583	gi10798644	1.00E-12	[Nicotiana tabacum]	AP2 domain-containing transcription fac

Table 5

17	G2583	gi8571476	4.70E-12	[Atriplex hortensis]	apetala2 domain-containing protein.
17	G2583	gi2213783	8.40E-12	[Lycopersicon esculentum]	Pti5.
17	G2583	gi8809573	5.30E-11	[Nicotiana sylvestris]	ethylene-responsive element binding
17	G2583	gi4099914	8.40E-11	[Stylosanthes hamata]	ethylene-responsive element binding p
17	G2583	gi6478845	8.90E-11	[Matricaria chamomilla]	ethylene-responsive element binding
17	G2583	gi15290041	9.40E-11	[Oryza sativa]	hypothetical protein.
17	G2583	gi12225884	1.70E-10	[Zea mays]	unnamed protein product.
17	G2583	gi3264767	3.40E-10	[Prunus armeniaca]	AP2 domain containing protein.
21	G1322	AW032656	3.60E-43	[Lycopersicon esculentum]	EST276215 tomato callus, TAMU Lycop
21	G1322	BF649523	5.40E-42	[Medicago truncatula]	NF080G02EC1F1019 Elicited cell culture
21	G1322	BG369720	1.50E-41	[Hordeum vulgare]	HVSMEi0025K10f Hordeum vulgare 20 DAP spike
21	G1322	BF325282	2.60E-41	[Glycine max]	su20e03.y1 Gm-c1066 Glycine max cDNA clone GENO
21	G1322	CPU33917	6.40E-41	[Craterostigma plantagineum]	myb-related transcription factor
21	G1322	AW255388	2.40E-40	[Mentha x piperita]	ML407 peppermint glandular trichome Menth
21	G1322	AB052230	1.30E-39	[Arabis gemmifera]	gene for MYB transcription factor Atmyb2,
21	G1322	AY026332	9.40E-39	[Oryza sativa]	Myb transcription factor JAMyb mRNA, complete
21	G1322	PSMYB26	1.10E-37	[Pisum sativum]	P.sativum mRNA for Myb-like protein (Myb26).
21	G1322	AI055122	4.30E-37	[Gossypium hirsutum]	coau0003B15 Cotton Boll Abscission Zone
21	G1322	gi1002796	5.50E-49	[Craterostigma plantagineum]	Cpm10.
21	G1322	gi13177578	3.00E-46	[Oryza sativa]	Myb transcription factor JAMyb.
21	G1322	gi1841475	1.50E-39	[Pisum sativum]	Myb26.
21	G1322	gi14249015	9.00E-39	[Gossypium hirsutum]	myb-like transcription factor Myb 5.
21	G1322	gi82306	3.10E-37	[Antirrhinum majus]	myb protein 305 - garden snapdragon.
21	G1322	gi8247759	7.40E-34	[Triticum aestivum]	GAMyb protein.
21	G1322	gi2130046	2.30E-33	[Hordeum vulgare]	MybHv5 protein - barley.
21	G1322	gi15082210	7.50E-33	[Fragaria x ananassa]	transcription factor MYB1.
21	G1322	gi5139806	1.10E-31	[Glycine max]	GmMYB29A2.
21	G1322	gi1732247	2.90E-31	[Nicotiana tabacum]	transcription factor Myb1.
23	G303	BE021887	5.70E-28	[Glycine max]	sm63g05.y1 Gm-c1028 Glycine max cDNA clone GENO
23	G303	BI480474	8.60E-28	[Triticum aestivum]	WHE2903_F02_L03ZS Wheat aluminum-stressed
23	G303	AC079935	5.40E-27	[Oryza sativa]	clone OSJNBa0095C06, *** SEQUENCING IN PROGRES
23	G303	AW573949	1.50E-22	[Medicago truncatula]	EST316540 GVN Medicago truncatula cDNA
23	G303	BF200153	1.30E-21	[Triticum monococcum]	WHE2252_F02_K04ZE Triticum monococcum s
23	G303	CAR011013	2.20E-18	[Cicer arietinum]	epicotyl EST, clone Can133.
23	G303	BE357342	2.60E-11	[Sorghum bicolor]	DG1_148_D06.g1_A002 Dark Grown 1 (DG1) Sorg
23	G303	BG275269	3.10E-11	[Pinus taeda]	NXSI_138_F10_F NXSI (Nsf Xylem Side wood Inclin
23	G303	BF588006	7.50E-10	[Sorghum propinquum]	FM1_35_E08.g1_A003 Floral-Induced Merist
23	G303	AI491136	2.00E-09	[Lycopersicon esculentum]	EST241845 tomato shoot, Cornell Lyc
23	G303	gi3641870	1.40E-22	[Cicer arietinum]	hypothetical protein.

Table 5

23	G303	gi1086538	9.60E-05	[Oryza rufipogon]	transcriptional activator Rb homolog.
23	G303	gi1086534	0.00082	[Oryza officinalis]	transcriptional activator Ra homolog.
23	G303	gi527661	0.0015	[Phyllostachys acuta]	myc-like regulatory R gene product.
23	G303	gi527653	0.005	[Pennisetum glaucum]	myc-like regulatory R gene product.
23	G303	gi22195	0.0078	[Zea mays]	regulatory protein.
23	G303	gi13161337	0.014	[Oryza sativa]	putative transcription activator.
23	G303	gi10998404	0.014	[Petunia x hybrida]	anthocyanin 1.
23	G303	gi1086526	0.052	[Oryza australiensis]	transcriptional activator Ra homolog.
23	G303	gi527665	0.072	[Sorghum bicolor]	myc-like regulatory R gene product.
239	G1927	BG350410	3.30E-63	[Solanum tuberosum]	091B07 Mature tuber lambda ZAP Solanum tu
239	G1927	BF066070	8.80E-48	[Hordeum vulgare]	HV_CEb0014M06f Hordeum vulgare seedling gre
239	G1927	AW736414	1.80E-47	[Medicago truncatula]	EST332428 KV3 Medicago truncatula cDNA
239	G1927	BG159075	7.10E-47	[Sorghum propinquum]	RHIZ2_17_E07.b1_A003 Rhizome2 (RHIZ2) So
239	G1927	BI543350	7.70E-39	[Beta vulgaris]	S1A_F6 Sugar Beet peroxide germination cDNA l
239	G1927	BE131060	9.20E-38	[Mesembryanthemum crystallinum]	L48-1010T3 Ice plant Lambda U
239	G1927	BI140602	1.00E-37	[Sorghum bicolor]	IP1_51_D12.b1_A002 Immature pannicle 1 (IP1
239	G1927	AI779001	4.30E-37	[Lycopersicon esculentum]	EST259880 tomato susceptible, Corne
239	G1927	BF484725	6.40E-36	[Triticum aestivum]	WHE2319_A01_B01ZS Wheat pre-anthesis spik
239	G1927	BE449422	7.30E-35	[Lycopersicon hirsutum]	EST356181 L. hirsutum trichome, Corne
239	G1927	gi7716952	4.10E-40	[Medicago truncatula]	NAC1.
239	G1927	gi6175246	1.10E-35	[Lycopersicon esculentum]	jasmonic acid 2.
239	G1927	gi15148914	4.70E-35	[Phaseolus vulgaris]	NAC domain protein NAC2.
239	G1927	gi1279640	3.30E-34	[Petunia x hybrida]	NAM.
239	G1927	gi6730938	4.70E-34	[Oryza sativa]	OsNAC4 protein.
239	G1927	gi14485513	4.10E-31	[Solanum tuberosum]	putative NAC domain protein.
239	G1927	gi6732156	4.20E-31	[Triticum monococcum]	unnamed protein product.
239	G1927	gi4218535	1.30E-30	[Triticum sp.]	GRAB1 protein.
239	G1927	gi4996349	6.30E-25	[Nicotiana tabacum]	NAC-domain protein.
239	G1927	gi2982275	2.60E-08	[Picea mariana]	ATAF1-like protein.

Traits of interest

Examples of some of the traits that may be desirable in plants, and that may be provided by transforming the plants with the presently disclosed sequences, are listed in Table 6.

Table 6. Genes, traits and utilities that affect plant characteristics

Trait Category	Traits	Transcription factor genes that impact traits	Utility Gene effect on:
Resistance and tolerance	Salt stress resistance	G22; G196; G226; G303; G312; G325; G353; G482; G545; G801; G867; G884; G922; G926; G1452; G1794; G1820; G1836; G1843; G1863; G2053; G2110; G2140; G2153; G2379; G2701; G2713; G2719; G2789	Germination rate, survivability, yield; extended growth range
	Osmotic stress resistance	G47; G175; G188; G303; G325; G353; G489; G502; G526; G921; G922; G926; G1069; G1089; G1452; G1794; G1930; G2140; G2153; G2379; G2701; G2719; G2789;	Germination rate, survivability, yield
	Cold stress resistance; cold germination	G256; G394; G664;G864;G1322; G2130	Germination, growth, earlier planting
	Tolerance to freezing	G303; G325; G353; G720; G912; G913; G1794; G2053; G2140; G2153; G2379; G2701; G2719; G2789	Survivability, yield, appearance, extended range
	Heat stress resistance	G3; G464; G682; G864; G964; G1305; G1645; G2130 G2430	Germination, growth, later planting
	Drought, low humidity resistance	G303; G325; G353; G720; G912; G926; G1452; G1794; G1820; G1843; G2053; G2140; G2153; G2379; G2583; G2701; G2719; G2789	Survivability, yield, extended range
	Radiation resistance	G1052	Survivability, vigor, appearance
	Decreased herbicide sensitivity	G343; G2133; G2517	Resistant to increased herbicide use
	Increased herbicide sensitivity	G374; G877;G1519	Use as a herbicide target

	Oxidative stress	G477; G789; G1807; G2133; G2517	Improved yield, appearance, reduced senescence
	Light response	G183; G354; G375; G1062; G1322; G1331; G1488; G1494; G1521; G1786; G1794; G2144; G2555;	Germination, growth, development, flowering time
Development, morphology	Overall plant architecture	G24; G27; G31; G33; G47; G147; G156; G160; G182; G187; G195; G196; G211; G221; G237; G280; G342; G352; G357; G358; G360; G362; G364; G365; G367; G373; G377; G396; G431; G447; G479; G546; G546; G551; G578; G580; G596; G615; G617; G620; G625; G638; G658; G716; G725; G727; G730; G740; G770; G858; G865; G869; G872; G904; G910; G912; G920; G939; G963; G977; G979; G987; G988; G993; G1007; G1010; G1014; G1035; G1046; G1049; G1062; G1069; G1070; G1076; G1089; G1093; G1127; G1131; G1145; G1229; G1246; G1304; G1318; G1320; G1330; G1331; G1352; G1354; G1360; G1364; G1379; G1384; G1399; G1415; G1417; G1442; G1453; G1454; G1459; G1460; G1471; G1475; G1477; G1487; G1487; G1492; G1499; G1499; G1531; G1540; G1543; G1543; G1544; G1548; G1584; G1587; G1588; G1589; G1636; G1642; G1747; G1749; G1749; G1751; G1752; G1763; G1766; G1767; G1778; G1789; G1790; G1791; G1793; G1794; G1795; G1800; G1806; G1811; G1835; G1836; G1838; G1839; G1843; G1853; G1855; G1865; G1881; G1882; G1883; G1884; G1891; G1896; G1898; G1902; G1904; G1906; G1913; G1914; G1925; G1929; G1930; G1954; G1958; G1965; G1976;	Vascular tissues, lignin content; cell wall content; appearance

		G2057; G2107; G2133; G2134; G2151; G2154; G2157; G2181; G2290; G2299; G2340; G2340; G2346; G2373; G2376; G2424; G2465; G2505; G2509; G2512; G2513; G2519; G2520; G2533; G2534; G2573; G2589; G2687; G2720; G2787; G2789; G2893	
	Size: increased stature	G189; G1073; G1435; G2430	
	Size: reduced stature or dwarfism	G3; G5; G21; G23; G39; G165; G184; G194; G258; G280; G340; G343; G353; G354; G362; G363; G370; G385; G396; G439; G440; G447; G450; G550; G557; G599; G636; G652; G670; G671; G674; G729; G760; G804; G831; G864; G884; G898; G900; G912; G913; G922; G932; G937; G939; G960; G962; G977; G991; G1000; G1008; G1020; G1023; G1053; G1067; G1075; G1137; G1181; G1198; G1228; G1266; G1267; G1275; G1277; G1309; G1311; G1314; G1317; G1322; G1323; G1326; G1332; G1334; G1367; G1381; G1382; G1386; G1421; G1488; G1494; G1537; G1545; G1560; G1586; G1641; G1652; G1655; G1671; G1750; G1756; G1757; G1782; G1786; G1794; G1839; G1845; G1879; G1886; G1888; G1933; G1939; G1943; G1944; G2011; G2094; G2115; G2130; G2132; G2144; G2145; G2147; G2156; G2294; G2313; G2344; G2431; G2510; G2517; G2521; G2893; G2893	Ornamental; small stature provides wind resistance; creation of dwarf varieties
	Fruit size and number	G362	Biomass, yield, cotton boll fiber density
	Flower structure, inflorescence	G47; G259; G353; G354; G671; G732; G988; G1000; G1063; G1140; G1326; G1449; G1543; G1560; G1587; G1645; G1947; G2108; G2143; G2893	Ornamental horticulture; production of saffron or other edible flowers
	Number and development of trichomes	G225; G226; G247; G362; G585; G634; G676; G682; G1014; G1332; G1452; G1795;	Resistance to pests and desiccation; essential oil

		G2105	production
	Seed size, color, and number	G156; G450; G584; G652; G668; G858; G979; G1040; G1062; G1145; G1255; G1494; G1531; G1534; G1594; G2105; G2114;	Yield
	Root development, modifications	G9; G1482; G1534; G1794; G1852; G2053; G2136; G2140	
	Modifications to root hairs	G225; G226	Nutrient, water uptake, pathogen resistance
	Apical dominance	G559; G732; G1255; G1275; G1411; G1488; G1635; G2452; G2509	Ornamental horticulture
	Branching patterns	G568; G988; G1548	Ornamental horticulture, knot reduction, improved windscreen
	Leaf shape, color, modifications	G375; G377; G428; G438; G447; G464; G557; G577; G599; G635; G671; G674; G736; G804; G903; G977; G921; G922; G1038; G1063; G1067; G1073; G1075; G1146; G1152; G1198; G1267; G1269; G1452; G1484; G1586; G1594; G1767; G1786; G1792; G1886; G2059; G2094; G2105; G2113; G2117; G2143; G2144; G2431; G2452; G2465; G2587; G2583; G2724;	Appealing shape or shiny leaves for ornamental agriculture, increased biomass or photosynthesis
	Silique	G1134	Ornamental
	Stem morphology	G47; G438; G671; G748; G988; G1000	Ornamental; digestibility
	Shoot modifications	G390; G391	Ornamental stem bifurcations
Disease, Pathogen Resistance	Bacterial	G211; G347; G367; G418; G525; G545; G578; G1049	Yield, appearance, survivability, extended range
	Fungal	G19; G28; G28; G28; G147; G188; G207; G211; G237; G248; G278; G347; G367; G371; G378; G409; G477; G545; G545; G558; G569; G578; G591; G594; G616; G789; G805; G812; G865; G869; G872; G881; G896;	Yield, appearance, survivability, extended range

		G940; G1047; G1049; G1064; G1084; G1196; G1255; G1266; G1363; G1514; G1756; G1792; G1792; G1792; G1792; G1880; G1919; G1919; G1927; G1927; G1936; G1936; G1950; G2069; G2130; G2380; G2380; G2555	
Nutrients	Increased tolerance to nitrogen-limited soils	G225; G226; G1792	
	Increased tolerance to phosphate-limited soils	G419; G545; G561; G1946	
	Increased tolerance to potassium-limited soils	G561; G911	
Hormonal	Hormone sensitivity	G12; G546; G926; G760; G913; G926; G1062; G1069; G1095; G1134; G1330; G1452; G1666; G1820; G2140; G2789	Seed dormancy, drought tolerance; plant form, fruit ripening
Seed biochemistry	Production of seed prenyl lipids, including tocopherol	G214; G259; G490; G652; G748; G883; G1052; G1328; G1930; G2509; G2520	Antioxidant activity, vitamin E
	Production of seed sterols	G20	Precursors for human steroid hormones; cholesterol modulators
	Production of seed glucosinolates	G353; G484; G674; G1272; G1506; G1897; G1946; G2113; G2117; G2155; G2290; G2340	Defense against insects; putative anticancer activity; undesirable in animal feeds
	Modified seed oil content	G162; G162; G180; G192; G241; G265; G286; G291; G427; G509; G519; G561; G567; G590; G818; G849; G892; G961; G974; G1063; G1143; G1190; G1198; G1226; G1229; G1323; G1451; G1471; G1478; G1496; G1526; G1543; G1640; G1644; G1646; G1672; G1677; G1750; G1765; G1777; G1793; G1838; G1902; G1946; G1948; G2059; G2123; G2138; G2139; G2343; G2792; G2830	Vegetable oil production; increased caloric value for animal feeds; lutein content
	Modified seed oil	G217; G504; G622; G778;	Heat stability,

	composition	G791; G861; G869; G938; G965; G1417; G2192	digestibility of seed oils
	Modified seed protein content	G162; G226; G241; G371; G427; G509; G567; G597; G732; G849; G865; G892; G963; G988; G1323; G1323; G1419; G1478; G1488; G1634; G1637; G1641; G1644; G1652; G1677; G1777; G1777; G1818; G1820; G1903; G1909; G1946; G1946; G1958; G2059; G2117; G2417; G2509	Reduced caloric value for humans
Leaf biochemistry	Production of flavonoids	G1666*	Ornamental pigment production; pathogen resistance; health benefits
	Production of leaf glucosinolates	G264; G353; G484; G652; G674; G681; G1069; G1198; G1322; G1421; G1657; G1794; G1897; G1946; G2115; G2117; G2144; G2155; G2155; G2340; G2512; G2520; G2552	Defense against insects; putative anticancer activity; undesirable in animal feeds
	Production of diterpenes	G229	Induction of enzymes involved in alkaloid biosynthesis
	Production of anthocyanin	G546	Ornamental pigment
	Production of leaf phytosterols, inc. stigmastanol, campesterol	G561; G2131; G2424	Precursors for human steroid hormones; cholesterol modulators
	Leaf fatty acid composition	G214; G377; G861; G962; G975; G987; G1266; G1337; G1399; G1465; G1512; G2136; G2147; G2192	Nutritional value; increase in waxes for disease resistance
	Production of leaf prenyl lipids, including tocopherol	G214; G259; G280; G652; G987; G1543; G2509; G2520	Antioxidant activity, vitamin E
Biochemistry, general	Production of miscellaneous secondary metabolites	G229; G663	
	Sugar, starch, hemicellulose composition,	G158; G211; G211; G237; G242; G274; G598; G1012; G1266; G1309; G1309; G1641;	Food digestibility, hemicellulose & pectin content;

		G1765; G1865; G2094; G2094; G2589; G2589	fiber content; plant tensile strength, wood quality, pathogen resistance, pulp production; tuber starch content
Sugar sensing	Plant response to sugars	G26; G38; G43; G207; G218; G241; G254; G263; G308; G536; G567; G567; G680; G867; G912; G956; G996; G1068; G1225; G1314; G1314; G1337; G1759; G1804; G2153; G2379	Photosynthetic rate, carbohydrate accumulation, biomass production, source-sink relationships, senescence
Growth, Reproduction	Plant growth rate and development	G447; G617; G674; G730; G917; G937; G1035; G1046; G1131; G1425; G1452; G1459; G1492; G1589; G1652; G1879; G1943; G2430; G2431; G2465; G2521	Faster growth, increased biomass or yield, improved appearance; delay in bolting
	Embryo development	G167	
	Seed germination rate	G979; G1792; G2130	Yield
	Plant, seedling vigor	G561; G2346	Survivability, yield
	Senescence; cell death	G571; G636; G878; G1050; G1463; G1749; G1944; G2130; G2155; G2340; G2383	Yield, appearance; response to pathogens;
	Modified fertility	G39; G340; G439; G470; G559; G615; G652; G671; G779; G962; G977; G988; G1000; G1063; G1067; G1075; G1266; G1311; G1321; G1326; G1367; G1386; G1421; G1453; G1471; G1453; G1560; G1594; G1635; G1750; G1947; G2011; G2094; G2113; G2115; G2130; G2143; G2147; G2294; G2510; G2893	Prevents or minimizes escape of the pollen of GMOs
	Early flowering	G147; G157; G180; G183; G183; G184; G185; G208; G227; G294; G390; G390; G390; G391; G391; G427; G427; G490; G565; G590; G592; G720; G789; G865; G898; G898; G989; G989; G1037; G1037; G1142; G1225; G1225; G1226; G1242; G1305;	Faster generation time; synchrony of flowering; potential for introducing new traits to single variety

		G1305; G1380; G1380; G1480; G1480; G1488; G1494; G1545; G1545; G1649; G1706; G1760; G1767; G1767; G1820; G1841; G1841; G1842; G1843; G1843; G1946; G1946; G2010; G2030; G2030; G2144; G2144; G2295; G2295; G2347; G2348; G2348; G2373; G2373; G2509; G2509; G2555; G2555	
	Delayed flowering	G8; G47; G192; G214; G234; G361; G362; G562; G568; G571; G591; G680; G736; G748; G859; G878; G910; G912; G913; G971; G994; G1051; G1052; G1073; G1079; G1335; G1435; G1452; G1478; G1789; G1804; G1865; G1865; G1895; G1900; G2007; G2133; G2155; G2291; G2465	Delayed time to pollen production of GMO plants; synchrony of flowering; increased yield
	Extended flowering phase	G1947	
	Flower and leaf development	G259; G353; G377; G580; G638 G652; G858; G869; G917; G922; G932; G1063; G1075; G1140; G1425; G1452; G1499; G1548; G1645; G1865; G1897; G1933; G2094; G2124; G2140; G2143; G2535; G2557	Ornamental applications; decreased fertility
	Flower abscission	G1897	Ornamental: longer retention of flowers

* When co-expressed with G669 and G663

Significance of modified plant traits

Currently, the existence of a series of maturity groups for different latitudes represents a major barrier to the introduction of new valuable traits. Any trait (e.g. disease resistance) has to be bred into each of the different maturity groups separately, a laborious and costly exercise. The availability of single strain, which could be grown at any latitude, would therefore greatly increase the potential for introducing new traits to crop species such as soybean and cotton.

For many of the traits, listed in Table 6 and below, that may be conferred to plants, a single transcription factor gene may be used to increase or decrease, advance

or delay, or improve or prove deleterious to a given trait. For example, overexpression of a transcription factor gene that naturally occurs in a plant may cause early flowering relative to non-transformed or wild-type plants. By knocking out the gene, or suppressing the gene (with, for example, antisense suppression) the plant may experience delayed flowering. Similarly, overexpressing or suppressing one or more genes can impart significant differences in production of plant products, such as different fatty acid ratios. Thus, suppressing a gene that causes a plant to be more sensitive to cold may improve a plant's tolerance of cold.

Salt stress resistance. Soil salinity is one of the more important variables that determines where a plant may thrive. Salinity is especially important for the successful cultivation of crop plants, particular in many parts of the world that have naturally high soil salt concentrations, or where the soil has been over-utilized. Thus, presently disclosed transcription factor genes that provide increased salt tolerance during germination, the seedling stage, and throughout a plant's life cycle would find particular value for imparting survivability and yield in areas where a particular crop would not normally prosper.

Osmotic stress resistance. Presently disclosed transcription factor genes that confer resistance to osmotic stress may increase germination rate under adverse conditions, which could impact survivability and yield of seeds and plants.

Cold stress resistance. The potential utility of presently disclosed transcription factor genes that increase tolerance to cold is to confer better germination and growth in cold conditions. The germination of many crops is very sensitive to cold temperatures. Genes that would allow germination and seedling vigor in the cold would have highly significant utility in allowing seeds to be planted earlier in the season with a high rate of survivability. Transcription factor genes that confer better survivability in cooler climates allow a grower to move up planting time in the spring and extend the growing season further into autumn for higher crop yields.

Tolerance to freezing. The presently disclosed transcription factor genes that impart tolerance to freezing conditions are useful for enhancing the survivability and appearance of plants conditions or conditions that would otherwise cause extensive

cellular damage. Thus, germination of seeds and survival may take place at temperatures significantly below that of the mean temperature required for germination of seeds and survival of non-transformed plants. As with salt tolerance, this has the added benefit of increasing the potential range of a crop plant into regions in which it would otherwise succumb. Cold tolerant transformed plants may also be planted earlier in the spring or later in autumn, with greater success than with non-transformed plants.

Heat stress tolerance. The germination of many crops is also sensitive to high temperatures. Presently disclosed transcription factor genes that provide increased heat tolerance are generally useful in producing plants that germinate and grow in hot conditions, may find particular use for crops that are planted late in the season, or extend the range of a plant by allowing growth in relatively hot climates.

Drought, low humidity tolerance. Strategies that allow plants to survive in low water conditions may include, for example, reduced surface area or surface oil or wax production. A number of presently disclosed transcription factor genes increase a plant's tolerance to low water conditions and provide the benefits of improved survivability, increased yield and an extended geographic and temporal planting range.

Radiation resistance. Presently disclosed transcription factor genes have been shown to increase lutein production. Lutein, like other xanthophylls such as zeaxanthin and violaxanthin, are important in the protection of plants against the damaging effects of excessive light. Lutein contributes, directly or indirectly, to the rapid rise of non-photochemical quenching in plants exposed to high light. Increased tolerance of field plants to visible and ultraviolet light impacts survivability and vigor, particularly for recent transplants. Also affected are the yield and appearance of harvested plants or plant parts. Crop plants engineered with presently disclosed transcription factor genes that cause the plant to produce higher levels of lutein therefore would have improved photoprotection, leading to less oxidative damage and increase vigor, survivability and higher yields under high light and ultraviolet light conditions.

Decreased herbicide sensitivity. Presently disclosed transcription factor genes that confer resistance or tolerance to herbicides (e.g., glyphosate) may find use in providing means to increase herbicide applications without detriment to desirable plants. This would allow for the increased use of a particular herbicide in a local environment, with the effect of increased detriment to undesirable species and less harm to transgenic, desirable cultivars.

Increased herbicide sensitivity. Knockouts of a number of the presently disclosed transcription factor genes have been shown to be lethal to developing embryos. Thus, these genes are potentially useful as herbicide targets.

Oxidative stress. In plants, as in all living things, abiotic and biotic stresses induce the formation of oxygen radicals, including superoxide and peroxide radicals. This has the effect of accelerating senescence, particularly in leaves, with the resulting loss of yield and adverse effect on appearance. Generally, plants that have the highest level of defense mechanisms, such as, for example, polyunsaturated moieties of membrane lipids, are most likely to thrive under conditions that introduce oxidative stress (e.g., high light, ozone, water deficit, particularly in combination). Introduction of the presently disclosed transcription factor genes that increase the level of oxidative stress defense mechanisms would provide beneficial effects on the yield and appearance of plants. One specific oxidizing agent, ozone, has been shown to cause significant foliar injury, which impacts yield and appearance of crop and ornamental plants. In addition to reduced foliar injury that would be found in ozone resistant plant created by transforming plants with some of the presently disclosed transcription factor genes, the latter have also been shown to have increased chlorophyll fluorescence (Yu-Sen Chang et al. Bot. Bull. Acad. Sin. (2001) 42: 265-272).

Heavy metal tolerance. Heavy metals such as lead, mercury, arsenic, chromium and others may have a significant adverse impact on plant respiration. Plants that have been transformed with presently disclosed transcription factor genes that confer improved resistance to heavy metals, through, for example, sequestering or reduced uptake of the metals will show improved vigor and yield in soils with relatively high concentrations of these elements. Conversely, transgenic transcription factors may

also be introduced into plants to confer an increase in heavy metal uptake, which may benefit efforts to clean up contaminated soils.

Light response. Presently disclosed transcription factor genes that modify a plant's response to light may be useful for modifying a plant's growth or development, for example, photomorphogenesis in poor light, or accelerating flowering time in response to various light intensities, quality or duration to which a non-transformed plant would not similarly respond. Examples of such responses that have been demonstrated include leaf number and arrangement, and early flower bud appearances.

Overall plant architecture. Several presently disclosed transcription factor genes have been introduced into plants to alter numerous aspects of the plant's morphology. For example, it has been demonstrated that a number of transcription factors may be used to manipulate branching, such as the means to modify lateral branching, a possible application in the forestry industry. Transgenic plants have also been produced that have altered cell wall content, lignin production, flower organ number, or overall shape of the plants. Presently disclosed transcription factor genes transformed into plants may be used to affect plant morphology by increasing or decreasing internode distance, both of which may be advantageous under different circumstances. For example, for fast growth of woody plants to provide more biomass, or fewer knots, increased internode distances are generally desirable. For improved wind screening of shrubs or trees, or harvesting characteristics of, for example, members of the Gramineae family, decreased internode distance may be advantageous. These modifications would also prove useful in the ornamental horticulture industry for the creation of unique phenotypic characteristics of ornamental plants.

Increased stature. For some ornamental plants, the ability to provide larger varieties may be highly desirable. For many plants, including t fruit-bearing trees or trees and shrubs that serve as view or wind screens, increased stature provides obvious benefits. Crop species may also produce higher yields on larger cultivars.

Reduced stature or dwarfism. Presently disclosed transcription factor genes that decrease plant stature can be used to produce plants that are more resistant to damage by wind and rain, or more resistant to heat or low humidity or water deficit. Dwarf plants are also of significant interest to the ornamental horticulture industry, and particularly for home garden applications for which space availability may be limited.

Fruit size and number. Introduction of presently disclosed transcription factor genes that affect fruit size will have desirable impacts on fruit size and number, which may comprise increases in yield for fruit crops, or reduced fruit yield, such as when vegetative growth is preferred (e.g., with bushy ornamentals, or where fruit is undesirable, as with ornamental olive trees).

Flower structure, inflorescence, and development. Presently disclosed transgenic transcription factors have been used to create plants with larger flowers or arrangements of flowers that are distinct from wild-type or non-transformed cultivars. This would likely have the most value for the ornamental horticulture industry, where larger flowers or interesting presentations generally are preferred and command the highest prices. Flower structure may have advantageous effects on fertility, and could be used, for example, to decrease fertility by the absence, reduction or screening of reproductive components. One interesting application for manipulation of flower structure, for example, by introduced transcription factors could be in the increased production of edible flowers or flower parts, including saffron, which is derived from the stigmas of *Crocus sativus*.

Number and development of trichomes. Several presently disclosed transcription factor genes have been used to modify trichome number and amount of trichome products in plants. Trichome glands on the surface of many higher plants produce and secrete exudates that give protection from the elements and pests such as insects, microbes and herbivores. These exudates may physically immobilize insects and spores, may be insecticidal or ant-microbial or they may act as allergens or irritants to protect against herbivores. Trichomes have also been suggested to decrease transpiration by decreasing leaf surface air flow, and by exuding chemicals that protect the leaf from the sun.

Seed size, color and number. The introduction of presently disclosed transcription factor genes into plants that alter the size or number of seeds may have a significant impact on yield, both when the product is the seed itself, or when biomass of the vegetative portion of the plant is increased by reducing seed production. In the case of fruit products, it is often advantageous to modify a plant to have reduced size or number of seeds relative to non-transformed plants to provide seedless or varieties with reduced numbers or smaller seeds. Presently disclosed transcription factor genes have also been shown to affect seed size, including the development of larger seeds. . Seed size, in addition to seed coat integrity, thickness and permeability, seed water content and by a number of other components including antioxidants and oligosaccharides, may affect seed longevity in storage. This would be an important utility when the seed of a plant is the harvested crops, as with, for example, peas, beans, nuts, etc. Presently disclosed transcription factor genes have also been used to modify seed color, which could provide added appeal to a seed product.

Root development, modifications. By modifying the structure or development of roots by transforming into a plant one or more of the presently disclosed transcription factor genes, plants may be produced that have the capacity to thrive in otherwise unproductive soils. For example, grape roots that extend further into rocky soils, or that remain viable in waterlogged soils, would increase the effective planting range of the crop. It may be advantageous to manipulate a plant to produce short roots, as when a soil in which the plant will be growing is occasionally flooded, or when pathogenic fungi or disease-causing nematodes are prevalent.

Modifications to root hairs. Presently disclosed transcription factor genes that increase root hair length or number potentially could be used to increase root growth or vigor, which might in turn allow better plant growth under adverse conditions such as limited nutrient or water availability.

Apical dominance. The modified expression of presently disclosed transcription factors that control apical dominance could be used in ornamental horticulture, for example, to modifying plant architecture.

Branching patterns. Several presently disclosed transcription factor genes have been used to manipulate branching, which could provide benefits in the forestry industry. For example, reduction in the formation of lateral branches could reduce knot formation. Conversely, increasing the number of lateral branches could provide utility when a plant is used as a windscreen, or may also provide ornamental advantages.

Leaf shape, color and modifications. It has been demonstrated in laboratory experiments that overexpression of some of the presently disclosed transcription factors produced marked effects on leaf development. At early stages of growth, these transgenic seedlings developed narrow, upward pointing leaves with long petioles, possibly indicating a disruption in circadian-clock controlled processes or nyctinastic movements. Other transcription factor genes can be used to increase plant biomass; large size would be useful in crops where the vegetative portion of the plant is the marketable portion.

Siliques. Genes that later silique conformation in brassicates may be used to modify fruit ripening processes in brassicates and other plants, which may positively affect seed or fruit quality.

Stem morphology and shoot modifications. Laboratory studies have demonstrated that introducing several of the presently disclosed transcription factor genes into plants can cause stem bifurcations in shoots, in which the shoot meristems split to form two or three separate shoots. This unique appearance would be desirable in ornamental applications.

Diseases, pathogens and pests. A number of the presently disclosed transcription factor genes have been shown to or are likely to confer resistance to various plant diseases, pathogens and pests. The offending organisms include fungal pathogens *Fusarium oxysporum, Botrytis cinerea, Sclerotinia sclerotiorum,* and *Erysiphe orontii*. Bacterial pathogens to which resistance may be conferred include *Pseudomonas syringae*. Other problem organisms may potentially include nematodes, mollicutes, parasites, or herbivorous arthropods. In each case, one or more transformed transcription factor genes may provide some benefit to the plant to

help prevent or overcome infestation. The mechanisms by which the transcription factors work could include increasing surface waxes or oils, surface thickness, local senescence, or the activation of signal transduction pathways that regulate plant defense in response to attacks by herbivorous pests (including, for example, protease inhibitors).

Increased tolerance of plants to nutrient-limited soils. Presently disclosed transcription factor genes introduced into plants may provide the means to improve uptake of essential nutrients, including nitrogenous compounds, phosphates, potassium, and trace minerals. The effect of these modifications is to increase the seedling germination and range of ornamental and crop plants. The utilities of presently disclosed transcription factor genes conferring tolerance to conditions of low nutrients also include cost savings to the grower by reducing the amounts of fertilizer needed, environmental benefits of reduced fertilizer runoff; and improved yield and stress tolerance. In addition, this gene could be used to alter seed protein amounts and/or composition that could impact yield as well as the nutritional value and production of various food products.

Hormone sensitivity. One or more of the presently disclosed transcription factor genes have been shown to affect plant abscisic acid (ABA) sensitivity. This plant hormone is likely the most important hormone in mediating the adaptation of a plant to stress. For example, ABA mediates conversion of apical meristems into dormant buds. In response to increasingly cold conditions, the newly developing leaves growing above the meristem become converted into stiff bud scales that closely wrap the meristem and protect it from mechanical damage during winter. ABA in the bud also enforces dormancy; during premature warm spells, the buds are inhibited from sprouting. Bud dormancy is eliminated after either a prolonged cold period of cold or a significant number of lengthening days. Thus, by affecting ABA sensitivity, introduced transcription factor genes may affect cold sensitivity and survivability. ABA is also important in protecting plants from drought tolerance.

Several other of the present transcription factor genes have been used to manipulate ethylene signal transduction and response pathways. These genes can thus

be used to manipulate the processes influenced by ethylene, such as seed germination or fruit ripening, and to improve seed or fruit quality.

Production of seed and leaf prenyl lipids, including tocopherol. Prenyl lipids play a role in anchoring proteins in membranes or membranous organelles. Thus modifying the prenyl lipid content of seeds and leaves could affect membrane integrity and function. A number of presently disclosed transcription factor genes have been shown to modify the tocopherol composition of plants. Tocopherols have both anti-oxidant and vitamin E activity.

Production of seed and leaf phytosterols: Presently disclosed transcription factor genes that modify levels of phytosterols in plants may have at least two utilities. First, phytosterols are an important source of precursors for the manufacture of human steroid hormones. Thus, regulation of transcription factor expression or activity could lead to elevated levels of important human steroid precursors for steroid semi-synthesis. For example, transcription factors that cause elevated levels of campesterol in leaves, or sitosterols and stigmasterols in seed crops, would be useful for this purpose. Phytosterols and their hydrogenated derivatives phytostanols also have proven cholesterol-lowering properties, and transcription factor genes that modify the expression of these compounds in plants would thus provide health benefits.

Production of seed and leaf glucosinolates. Some glucosinolates have anti-cancer activity; thus, increasing the levels or composition of these compounds by introducing several of the presently disclosed transcription factors might be of interest from a nutraceutical standpoint. (3) Glucosinolates form part of a plants natural defense against insects. Modification of glucosinolate composition or quantity could therefore afford increased protection from predators. Furthermore, in edible crops, tissue specific promoters might be used to ensure that these compounds accumulate specifically in tissues, such as the epidermis, which are not taken for consumption.

Modified seed oil content. The composition of seeds, particularly with respect to seed oil amounts and/or composition, is very important for the nutritional value and production of various food and feed products. Several of the presently disclosed transcription factor genes in seed lipid saturation that alter seed oil content could be

used to improve the heat stability of oils or to improve the nutritional quality of seed oil, by, for example, reducing the number of calories in seed, increasing the number of calories in animal feeds, or altering the ratio of saturated to unsaturated lipids comprising the oils.

Seed and leaf fatty acid composition. A number of the presently disclosed transcription factor genes have been shown to alter the fatty acid composition in plants, and seeds in particular. This modification may find particular value for improving the nutritional value of, for example, seeds or whole plants. Dietary fatty acids ratios have been shown to have an effect on, for example, bone integrity and remodeling (see, for example, Weiler, H.A., *Pediatr Res* (2000) 47:5 692-697). The ratio of dietary fatty acids may alter the precursor pools of long-chain polyunsaturated fatty acids that serve as precursors for prostaglandin synthesis. In mammalian connective tissue, prostaglandins serve as important signals regulating the balance between resorption and formation in bone and cartilage. Thus dietary fatty acid ratios altered in seeds may affect the etiology and outcome of bone loss.

Modified seed protein content. As with seed oils, the composition of seeds, particularly with respect to protein amounts and/or composition, is very important for the nutritional value and production of various food and feed products. A number of the presently disclosed transcription factor genes modify the protein concentrations in seeds would provide nutritional benefits, and may be used to prolong storage, increase seed pest or disease resistance, or modify germination rates.

Production of flavonoids in leaves and other plant parts. Expression of presently disclosed transcription factor genes that increase flavonoid production in plants, including anthocyanins and condensed tannins, may be used to alter in pigment production for horticultural purposes, and possibly increasing stress resistance. Flavonoids have antimicrobial activity and could be used to engineer pathogen resistance. Several flavonoid compounds have health promoting effects such as the inhibition of tumor growth and cancer, prevention of bone loss and the prevention of the oxidation of lipids. Increasing levels of condensed tannins, whose biosynthetic pathway is shared with anthocyanin biosynthesis, in forage legumes is an important agronomic trait because they prevent pasture bloat by collapsing protein foams within

the rumen. For a review on the utilities of flavonoids and their derivatives, refer to Dixon et al. (1999) Trends Plant Sci. 4:394-400.

Production of diterpenes in leaves and other plant parts. Depending on the plant species, varying amounts of diverse secondary biochemicals (often lipophilic terpenes) are produced and exuded or volatilized by trichomes. These exotic secondary biochemicals, which are relatively easy to extract because they are on the surface of the leaf, have been widely used in such products as flavors and aromas, drugs, pesticides and cosmetics. Thus, the overexpression of genes that are used to produce diterpenes in plants may be accomplished by introducing transcription factor genes that induce said overexpression. One class of secondary metabolites, the diterpenes, can effect several biological systems such as tumor progression, prostaglandin synthesis and tissue inflammation. In addition, diterpenes can act as insect pheromones, termite allomones, and can exhibit neurotoxic, cytotoxic and antimitotic activities. As a result of this functional diversity, diterpenes have been the target of research several pharmaceutical ventures. In most cases where the metabolic pathways are impossible to engineer, increasing trichome density or size on leaves may be the only way to increase plant productivity.

Production of anthocyanin in leaves and other plant parts. Several presently disclosed transcription factor genes can be used to alter anthocyanin production in numerous plant species. The potential utilities of these genes include alterations in pigment production for horticultural purposes, and possibly increasing stress resistance in combination with another transcription factor.

Production of miscellaneous secondary metabolites. Microarray data suggests that flux through the aromatic amino acid biosynthetic pathways and primary and secondary metabolite biosynthetic pathways are up-regulated. Presently disclosed transcription factors have been shown to be involved in regulating alkaloid biosynthesis, in part by up-regulating the enzymes indole-3-glycerol phosphatase and strictosidine synthase. Phenylalanine ammonia lyase, chalcone synthase and trans-cinnamate mono-oxygenase are also induced, and are involved in phenylpropenoid biosynthesis.

Sugar, starch, hemicellulose composition. Overexpression of the presently disclosed transcription factors that affect sugar content resulted in plants with altered leaf insoluble sugar content. Transcription factors that alter plant cell wall composition have several potential applications including altering food digestibility, plant tensile strength, wood quality, pathogen resistance and in pulp production. The potential utilities of a gene involved in glucose-specific sugar sensing are to alter energy balance, photosynthetic rate, carbohydrate accumulation, biomass production, source-sink relationships, and senescence.

Hemicellulose is not desirable in paper pulps because of its lack of strength compared with cellulose. Thus modulating the amounts of cellulose vs. hemicellulose in the plant cell wall is desirable for the paper/lumber industry. Increasing the insoluble carbohydrate content in various fruits, vegetables, and other edible consumer products will result in enhanced fiber content. Increased fiber content would not only provide health benefits in food products, but might also increase digestibility of forage crops. In addition, the hemicellulose and pectin content of fruits and berries affects the quality of jam and catsup made from them. Changes in hemicellulose and pectin content could result in a superior consumer product.

Plant response to sugars and sugar composition. In addition to their important role as an energy source and structural component of the plant cell, sugars are central regulatory molecules that control several aspects of plant physiology, metabolism and development. It is thought that this control is achieved by regulating gene expression and, in higher plants, sugars have been shown to repress or activate plant genes involved in many essential processes such as photosynthesis, glyoxylate metabolism, respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, flowering and senescence. The mechanisms by which sugars control gene expression are not understood.

Because sugars are important signaling molecules, the ability to control either the concentration of a signaling sugar or how the plant perceives or responds to a signaling sugar could be used to control plant development, physiology or metabolism. For example, the flux of sucrose (a disaccharide sugar used for systemically transporting carbon and energy in most plants) has been shown to affect

gene expression and alter storage compound accumulation in seeds. Manipulation of the sucrose signaling pathway in seeds may therefore cause seeds to have more protein, oil or carbohydrate, depending on the type of manipulation. Similarly, in tubers, sucrose is converted to starch which is used as an energy store. It is thought that sugar signaling pathways may partially determine the levels of starch synthesized in the tubers. The manipulation of sugar signaling in tubers could lead to tubers with a higher starch content.

Thus, the presently disclosed transcription factor genes that manipulate the sugar signal transduction pathway may lead to altered gene expression to produce plants with desirable traits. In particular, manipulation of sugar signal transduction pathways could be used to alter source-sink relationships in seeds, tubers, roots and other storage organs leading to increase in yield.

Plant growth rate and development. A number of the presently disclosed transcription factor genes have been shown to have significant effects on plant growth rate and development. These observations have included, for example, more rapid or delayed growth and development of reproductive organs. This would provide utility for regions with short or long growing seasons, respectively. Accelerating plant growth would also improve early yield or increase biomass at an earlier stage, when such is desirable (for example, in producing forestry products).

Embryo development. Presently disclosed transcription factor genes that alter embryo development has been used to alter seed protein and oil amounts and/or composition which is very important for the nutritional value and production of various food products. Seed shape and seed coat may also be altered by these genes, which may provide for improved storage stability.

Seed germination rate. A number of the presently disclosed transcription factor genes have been shown to modify seed germination rate, including when the seeds are in conditions normally unfavorable for germination (e.g., cold, heat or salt stress, or in the presence of ABA), and may thus be used to modify and improve germination rates under adverse conditions.

Plant, seedling vigor. Seedlings transformed with presently disclosed transcription factors have been shown to possess larger cotyledons and appeared somewhat more advanced than control plants. This indicates that the seedlings developed more rapidly that the control plants. Rapid seedling development is likely to reduce loss due to diseases particularly prevalent at the seedling stage (e.g., damping off) and is thus important for survivability of plants germinating in the field or in controlled environments.

Senescence, cell death. Presently disclosed transcription factor genes may be used to alter senescence responses in plants. Although leaf senescence is thought to be an evolutionary adaptation to recycle nutrients, the ability to control senescence in an agricultural setting has significant value. For example, a delay in leaf senescence in some maize hybrids is associated with a significant increase in yields and a delay of a few days in the senescence of soybean plants can have a large impact on yield. Delayed flower senescence may also generate plants that retain their blossoms longer and this may be of potential interest to the ornamental horticulture industry.

Modified fertility. Plants that overexpress a number of the presently disclosed transcription factor genes have been shown to possess reduced fertility. This could be a desirable trait, as it could be exploited to prevent or minimize the escape of the pollen of genetically modified organisms (GMOs) into the environment.

Early and delayed flowering. Presently disclosed transcription factor genes that accelerate flowering could have valuable applications in such programs since they allow much faster generation times. In a number of species, for example, broccoli, cauliflower, where the reproductive parts of the plants constitute the crop and the vegetative tissues are discarded, it would be advantageous to accelerate time to flowering. Accelerating flowering could shorten crop and tree breeding programs. Additionally, in some instances, a faster generation time might allow additional harvests of a crop to be made within a given growing season. A number of *Arabidopsis* genes have already been shown to accelerate flowering when constitutively expressed. These include LEAFY, APETALA1 and CONSTANS (Mandel, M. et al., 1995, Nature 377, 522-524; Weigel, D. and Nilsson, O., 1995, Nature 377, 495-500; Simon et al., 1996, Nature 384, 59-62).

By regulating the expression of potential flowering using inducible promoters, flowering could be triggered by application of an inducer chemical. This would allow flowering to be synchronized across a crop and facilitate more efficient harvesting. Such inducible systems could also be used to tune the flowering of crop varieties to different latitudes. At present, species such as soybean and cotton are available as a series of maturity groups that are suitable for different latitudes on the basis of their flowering time (which is governed by day-length). A system in which flowering could be chemically controlled would allow a single high-yielding northern maturity group to be grown at any latitude. In southern regions such plants could be grown for longer, thereby increasing yields, before flowering was induced. In more northern areas, the induction would be used to ensure that the crop flowers prior to the first winter frosts.

In a sizeable number of species, for example, root crops, where the vegetative parts of the plants constitute the crop and the reproductive tissues are discarded, it would be advantageous to delay or prevent flowering. Extending vegetative development with presently disclosed transcription factor genes could thus bring about large increases in yields.. Prevention of flowering might help maximize vegetative yields and prevent escape of genetically modified organism (GMO) pollen.

Extended flowering phase. Presently disclosed transcription factors that extend flowering time have utility in engineering plants with longer-lasting flowers for the horticulture industry, and for extending the time in which the plant is fertile.

Flower and leaf development. Presently disclosed transcription factor genes have been used to modify the development of flowers and leaves. This could be advantageous in the development of new ornamental cultivars that present unique configurations. In addition, some of these genes have been shown to reduce a plant's fertility, which is also useful for helping to prevent development of pollen of GMOs.

Flower abscission. Presently disclosed transcription factor genes introduced into plants have been used to retain flowers for longer periods. This would provide a significant benefit to the ornamental industry, for both cut flowers and woody plant

varieties (of, for example, maize), as well as have the potential to lengthen the fertile period of a plant, which could positively impact yield and breeding programs.

A listing of specific effects and utilities that the presently disclosed transcription factor genes have on plants, as determined by direct observation and assay analysis, is provided in Table 4.

XVI. Antisense and Co-suppression

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University Press, Oxford, U.K.. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector

will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating it's activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription

factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation. Such methods are well known to those of skill in the art. (See for example Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific.)

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802-803).

A plant trait can also be modified by using the Cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (*See*, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA-binding specificity of zinc finger proteins by changing particular amino acids in the DNA-binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledenous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcurbitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species, Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation.

Transformation means introducing a nucleotide sequence into a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

XVII. Integrated Systems – Sequence Identity

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such improved characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP,

FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PHYTOSEQ sequence database (Incyte Genomics, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85:2444-2448, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods for determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (see internet website at ncbi.nlm.nih.gov). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to

find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915). Unless otherwise indicated, "sequence identity" here refers to the % sequence identity generated from a tblastx using the NCBI version of the algorithm at the default settings using gapped alignments with the filter "off" (see, for example, internet website at ncbi.nlm.nih.gov).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see,* e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element that displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

XVIII. Examples

The following examples are intended to illustrate but not limit the present invention. The complete descriptions of the traits associated with each polynucleotide of the invention is fully disclosed in Table 4, Table 5, and Table 6.

Example I: Full Length Gene Identification and Cloning

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of –4 or –5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ^{32}P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M $NaPO_4$ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60°C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single

primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

Example II: Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-1558) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, Valencia CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, Beverly MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma, St. Louis, MO). Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen).

Example III: Transformation of *Agrobacterium* with the Expression Vector

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 μl chilled buffer

(1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad, Hercules, CA). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

Example IV: Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an optical absorbance at 600 nm wavelength over 1 cm (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 µM benzylamino purine (Sigma), 200 µl/l Silwet L-77 (Lehle Seeds) until an A_{600} of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 μE/m^2/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

Example V: Identification of *Arabidopsis* Primary Transformants

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H_2O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H_2O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 μE/m^2/sec) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1

generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T_2) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

Example VI: Identification of *Arabidopsis* Plants with Transcription Factor Gene Knockouts

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

Example VII: Identification of Modified Phenotypes in Overexpression or Gene Knockout Plants

Experiments were performed to identify those transformants or knockouts that exhibited modified biochemical characteristics. Among the biochemicals that were assayed were insoluble sugars, such as arabinose, fucose, galactose, mannose, rhamnose or xylose or the like; prenyl lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or alpha-, delta- or gamma-

tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0 , 18:3 (linolenic acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, glucosinolates, protein or oil levels.

Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H_2SO_4 and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane:H_2SO_4 (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were analyzed with a Supelco SP-2330 column.

Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is and after heating at 95°C for a further 10 minutes, the extraction solvent is applied to a DEAE Sephadex column which had been previously equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 ul water and analyzed by reverse phase HPLC monitoring at 226 nm.

For wax alkanes, samples were extracted using an identical method as fatty acids and extracts were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were chromatographically isolated on a J&W DB35 mass spectrometer (J&W Scientific).

To measure prenyl lipids levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol determination. For leaves, an aliquot was removed and diluted with methanol and chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining optical absorbance at

665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters uBondapak C18 column (4.6 mm x 150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in hexane was added to the tubes and the samples were then extracted with one ml of water. The upper phase was removed, dried, and resuspended in 400 ul of 2% methylene chloride in hexane and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25 um phase, J&W Scientific).

Suppression of endogenous transcription factor gene expression can also be achieved using RNA interference , or RNAi. RNAi is a post-transcriptional, targeted gene-silencing technique that uses double-stranded RNA (dsRNA) to incite degradation of messenger RNA (mRNA) containing the same sequence as the dsRNA (Constans, (2002*) The Scientist* 16:36). Small interfering RNAs, or siRNAs are produced in at least two steps: an endogenous ribonuclease cleaves longer dsRNA into shorter, 21-23 nucleotide-long RNAs. The siRNA segments then mediate the degradation of the target mRNA (Zamore, (2001) *Nature Struct. Biol.*, 8:746-50). RNAi has been used for gene function determination in a manner similar to antisense oligonucleotides (Constans, (2002*) The Scientist* 16:36). Expression vectors that continually express siRNAs in transiently and stably transfected have been engineered to express small hairpin RNAs (shRNAs), which get processed in vivo into siRNAs-like molecules capable of carrying out gene-specific silencing (Brummelkamp et al., (2002) *Science* 296:550-553, and Paddison, et al. (2002) *Genes & Dev.* 16:948-958). Post-transcriptional gene silencing by double-stranded RNA is discussed in further detail by Hammond et al. (2001) *Nature Rev Gen* 2: 110-119, Fire et al. (1998) *Nature* 391: 806-811 and Timmons and Fire (1998) *Nature* 395: 854.--

Insoluble sugar levels were measured by the method essentially described by Reiter et al., Plant Journal 12:335-345. This method analyzes the neutral sugar composition of cell wall polymers found in *Arabidopsis* leaves. Soluble sugars were

separated from sugar polymers by extracting leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated by the hydrolysis were then reduced to the corresponding alditols by treatment with NaBH4, then were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID. Identity of the peaks was determined by comparing the retention times of known sugars converted to the corresponding alditol acetates with the retention times of peaks from wild-type plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x 250 um x 0.2 um) using a temperature program beginning at 180° C for 2 minutes followed by an increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven temperature is increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2 progeny plants were subjected to analysis by Near Infrared Reflectance Spectroscopy (NIRS) using a Foss NirSystems Model 6500 with a spinning cup transport system. NIRS is a non-destructive analytical method used to determine seed oil and protein composition. Infrared is the region of the electromagnetic spectrum located after the visible region in the direction of longer wavelengths. 'Near infrared' owns its name for being the infrared region near to the visible region of the electromagnetic spectrum. For practical purposes, near infrared comprises wavelengths between 800 and 2500 nm. NIRS is applied to organic compounds rich in O-H bonds (such as moisture, carbohydrates, and fats), C-H bonds (such as organic compounds and petroleum derivatives), and N-H bonds (such as proteins and amino acids). The NIRS analytical instruments operate by statistically correlating NIRS signals at several wavelengths with the characteristic or property intended to be measured. All biological substances contain thousands of C-H, O-H, and N-H bonds. Therefore, the exposure to near infrared radiation of a biological sample, such as a seed, results in a complex spectrum which contains qualitative and quantitative information about the physical and chemical composition of that sample.

The numerical value of a specific analyte in the sample, such as protein content or oil content, is mediated by a calibration approach known as chemometrics.

Chemometrics applies statistical methods such as multiple linear regression (MLR), partial least squares (PLS), and principle component analysis (PCA) to the spectral data and correlates them with a physical property or other factor, that property or factor is directly determined rather than the analyte concentration itself. The method first provides "wet chemistry" data of the samples required to develop the calibration.

Calibration for Arabidopsis seed oil composition was performed using accelerated solvent extraction using 1 g seed sample size and was validated against certified canola seed. A similar wet chemistry approach was performed for seed protein composition calibration.

Data obtained from NIRS analysis was analyzed statistically using a nearest-neighbor (N-N) analysis. The N-N analysis allows removal of within-block spatial variability in a fairly flexible fashion which does not require prior knowledge of the pattern of variability in the chamber. Ideally, all hybrids are grown under identical experimental conditions within a block (rep). In reality, even in many block designs, significant within-block variability exists. Nearest-neighbor procedures are based on assumption that environmental effect of a plot is closely related to that of its neighbors. Nearest-neighbor methods use information from adjacent plots to adjust for within-block heterogeneity and so provide more precise estimates of treatment means and differences. If there is within-plot heterogeneity on a spatial scale that is larger than a single plot and smaller than the entire block, then yields from adjacent plots will be positively correlated. Information from neighboring plots can be used to reduce or remove the unwanted effect of the spatial heterogeneity, and hence improve the estimate of the treatment effect. Data from neighboring plots can also be used to reduce the influence of competition between adjacent plots. The Papadakis N-N analysis can be used with designs to remove within-block variability that would not be removed with the standard split plot analysis (Papadakis, 1973, Inst. d'Amelior. Plantes Thessaloniki (Greece) Bull. Scientif., No. 23; Papadakis, 1984, Proc. Acad. Athens, 59, 326-342).

Experiments were performed to identify those transformants or knockouts that exhibited an improved pathogen tolerance. For such studies, the transformants were exposed to biotropic fungal pathogens, such as *Erysiphe orontii*, and necrotropic

fungal pathogens, such as *Fusarium oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on Petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection.

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20°C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20°C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

Botrytis cinerea is a necrotrophic pathogen. Botrytis cinerea was grown on potato dextrose agar in the light. A spore culture was made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105 spores/ml) was used to spray 10 day-old seedlings grown under sterile conditions on MS (minus sucrose) media. Symptoms were evaluated every day up to approximately 1 week.

Infection with bacterial pathogens Pseudomonas syringae pv maculicola (Psm) strain 4326 and pv maculicola strain 4326 was performed by hand inoculation at two doses. Two inoculation doses allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants were grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 was hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005. Disease

scoring occurred at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

In some instances, expression patterns of the pathogen-induced genes (such as defense genes) was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Methods Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999; supra).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imagene, a software purchased from BioDiscovery (Los Angeles, CA).

Experiments were performed to identify those transformants or knockouts that exhibited an improved environmental stress tolerance. For such studies, the transformants were exposed to a variety of environmental stresses. Plants were exposed to chilling stress (6 hour exposure to 4-8° C), heat stress (6 hour exposure to 32-37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (Nitrogen: all components of MS medium remained constant except N was reduced to 20 mg/l of NH_4NO_3, or Phosphate: All components of MS medium except KH_2PO_4, which was

replaced by K_2SO_4, Potassium: All components of MS medium except removal of KNO_3 and KH_2PO_4, which were replaced by NaH_4PO_4).

Experiments were performed to identify those transformants or knockouts that exhibited a modified structure and development characteristics. For such studies, the transformants were observed by eye to identify novel structural or developmental characteristics associated with the ectopic expression of the polynucleotides or polypeptides of the invention.

Experiments were performed to identify those transformants or knockouts that exhibited modified sugar-sensing. For such studies, seeds from transformants were germinated on media containing 5%, glucose or 9.4% sucrose which normally partially restrict hypocotyl elongation. Plants with altered sugar sensing may have either longer or shorter hypocotyls than normal plants when grown on this media. Additionally, other plant traits may be varied such as root mass.

Flowering time was measured by the number of rosette leaves present when a visible inflorescence of approximately 3 cm is apparent Rosette and total leaf number on the progeny stem are tightly correlated with the timing of flowering (Koornneef et al (1991) *Mol. Gen. Genet* 229:57-66. The vernalization response was measured. For vernalization treatments, seeds were sown to MS agar plates, sealed with micropore tape, and placed in a 4°C cold room with low light levels for 6-8 weeks. The plates were then transferred to the growth rooms alongside plates containing freshly sown non-vernalized controls. Rosette leaves were counted when a visible inflorescence of approximately 3 cm was apparent.

Modified phenotypes observed for particular overexpressor or knockout plants are provided in Table 4. For a particular overexpressor that shows a less beneficial characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

The sequences of the Sequence Listing or those in Tables 4 or 5 or those disclosed here can be used to prepare transgenic plants and plants with altered traits. The specific transgenic plants listed below are produced from the sequences of the Sequence Listing, as noted. Table 4 provides exemplary polynucleotide and polypeptide sequences of the invention. Table 4 includes, from left to right for each sequence: the first column shows the polynucleotide SEQ ID NO; the second column shows the Mendel Gene ID No., GID; the third column shows the trait(s) resulting from the knock out or overexpression of the polynucleotide in the transgenic plant; the fourth column shows the category of the trait; the fifth column shows the transcription factor family to which the polynucleotide belongs; the sixth column ("Comment"), includes specific effects and utilities conferred by the polynucleotide of the first column; the seventh column shows the SEQ ID NO of the polypeptide encoded by the polynucleotide; and the eighth column shows the amino acid residue positions of the conserved domain in amino acid (AA) co-ordinates.

G720: The complete sequence of G720 (SEQ ID NO: 25); similar to a portion of APRR2, Arabidopsis pseudo-response regulator (APRR2; Makino et al. 2000 Plant Cell Physiol. 41:791-803) was determined. A line homozygous for a T-DNA insertion in G720 and lines overexpressing G720 under the 35S promoter were used to determine the function of this gene. The T-DNA insertion in G720 was approximately half-way into the coding sequence, just before the conserved domain, and therefore should result in a null mutation. G720 knockout mutants were slightly more sensitive to freezing than the wild-type controls when the seedlings were cold-acclimated prior to freezing. G720 overexpressing lines were slightly more tolerant to freezing. When seedlings were frozen at $-10^{\circ}C$ for 20 hours, the G720 plants recovered slightly better compared to the wild-type control in two separate experiments. G720 was induced by ABA, salt, osmotic stress, drought, heat, and auxin. The combination of enhanced sensitivity to freezing in the knockout mutants, enhanced resistance in the overexpressing lines, and the induction pattern of G720 comprised strong evidence that G720 functions in regulation of dehydration tolerance, as freezing is a form of dehydration stress.

Plants overexpressing G720 also showed reduced time to flowering in the T1 generation. One third of the 35S::G720 T1 seedlings, from each of two separate

batches, flowered markedly earlier (up to 1 week sooner, 24-hour light conditions) than controls plants. All of the T1 lines showed high levels of G720 overexpression (determined by RT-PCR). Three early flowering T1 plants were selected for further study. However, none of these lines flowered early in the T2, suggesting that activity of the transgene might have been reduced between the generations.

Closely Related Genes from Other Species

G720 showed significant similarity to a drought-induced M. truncatula EST, GenBank accession number BG450227, that encodes a pseudo-receiver domain. The sequence similarity is high enough to suggest that the two proteins are orthologs, and the fact that G720 was also drought-induced is consistent with this hypothesis. Other ESTs from tomato and potato (BG642566, BG128919, BG129142, and BG887673) also showed high similarity to G720 and represent potential orthologs.

G1792: G1792 (SEQ ID NO: 45) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G1792 plants were more tolerant to the fungal pathogens Fusarium oxysporum and Botrytis cinerea and showed fewer symptoms after inoculation with a low dose of each pathogen. This result was confirmed using individual T2 lines. The effect of G1792 overexpression in increasing tolerance to pathogens received further, incidental confirmation. T2 plants of 35S::G1792 lines 5 and 12 had been growing in a room that suffered a serious powdery mildew infection. For each line, a pot of 6 plants was present in a flat containing 9 other pots of lines from unrelated genes. In either of the two different flats, the only plants that were free from infection were those from the 35S::G1792 line. This observation suggests that G1792 overexpression might increase resistance to powdery mildew. Additional experiments confirmed that 35S::G1792 plants showed increased tolerance to Erysiphe. G1792 was ubiquitously expressed, but appears to be induced by salicylic acid.

35S::G1792 overexpressing plants also showed more tolerance to growth under nitrogen-limiting conditions. In a root growth assay under conditions of limiting N, 35S::G1792 lines were slightly less stunted. In a germination assay that monitors the effect of C on N signaling through anthocyanin production on high sucrose plus and

minus glutamine the 35S::G1792 lines make less anthocyanin on high sucrose plus glutamine, suggesting that the gene could be involved in the plants ability to monitor their carbon and nitrogen status.

G1792 overexpressing plants showed several mild morphological alterations: leaves were dark green and shiny, and plants bolted, subsequently senesced, slightly later than wild-type controls. Among the T1plants, additional morphological variation (not reproduced later in the T2 plants) was observed: many showed reductions in size as well as aberrations in leaf shape, phyllotaxy, and flower development.

Closely Related Genes from Other Species

G1792 shows sequence similarity, outside the conserved AP2 domain, with a portion of a predicted protein from tomato, represented by EST sequence AI776626 (AI776626 EST257726 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER19A14, mRNA sequence).

G1756: G1756 (SEQ ID NO:175) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1756 caused alterations in plant growth and development, reducing overall plant size and fertility. In addition, 35S::G1756 overexpressing lines show more disease symptoms following inoculation with a low dose of the fungal pathogen Botrytis cinerea compared to the wild-type controls. G1756 was ubiquitously expressed and transcript levels were altered by a variety of environmental or physiological conditions; G1756 expression can be induced by auxin, cold, and Fusarium.

Closely Related Genes from Other Species

G1756 shows some sequence similarity with known genes from other plant species within the conserved WRKY domain.

G481: Northern blot data from five different tissue samples indicates that G481 (SEQ ID NO: 113) was primarily expressed in flower and/or silique, and root

tissue. G481 was analyzed through its ectopic overexpression in pl overexpressors were more tolerant to high sucrose in a germination phenotype of G481 was mild; however, there was a consistent difference in the hypocotyl and root elongation in the overexpressor plants compared to wild-type controls. Sucrose-sensing has been implicated in the regulation of source-sink relationships in plants. Consistent with the sugar sensing phenotype of the G481 overexpressors were the results from the biochemical analysis of G481 overexpressor plants suggesting that line 14 had higher amounts of seed oils and lower amounts of seed protein. This suggested that G481 was involved in the allocation of storage compounds to the seed. G481 overexpressor line 8 was darker green in the T2 generation which could mean a higher photosynthetic rate consistent with the possible role of G481 in sugar sensing.

Closely Related Genes from Other Species

There are several sequences from higher plants that show significant homology to G481 including, X59714 from corn, and two ESTs from tomato, AI486503 and AI782351.

G2133: G2133 (SEQ ID NO: 141) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2133 caused a variety of alterations in plant growth and development: delayed flowering, altered inflorescence architecture, and a decrease in overall size and fertility. At early stages, 35S::G2133 transformants were markedly smaller than controls and displayed curled, dark-green leaves. Most of these plants remained in a vegetative phase of development substantially longer than controls, and produced an increased number of leaves before bolting. In the most severely affected plants, bolting occurred more than a month later than in wild type (24-hour light). In addition, the plants displayed a reduction in apical dominance and formed large numbers of shoots simultaneously, from the axils of rosette leaves. These inflorescence stems had short internodes, and carried increased numbers of cauline leaf nodes, giving them a very leafy appearance. The fertility of 35S::G2133 plants was generally very low. In addition, G2133 overexpressing lines were more resistant to the herbicide glyphosate. In a repeat experiment, lines 4 and 5 were more tolerant

while line 2 was wild-type. G2133 expression was detected in a va flower, leaf, embryo, and silique samples. Its expression was altere conditions, including auxin treatment, osmotic stress, and Fusarium infection. G2133 can be used for the generation of glyphosate resistant plants, and to increase plant resistance to oxidative stress.

Closely Related Genes from Other Species

G2133 shows some sequence similarity with known genes from other plant species within the conserved AP2/EREBP domain.

G2517: G2517 (SEQ ID NO: 143) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2517 caused alterations in plant growth and development: size variation was apparent in the 35S::G2517 T1 generation, with at least half the lines being very small. Additionally, 4/12 T1 plants formed flower buds marginally earlier than wild type. Three T1 lines (#8,11,12) were examined in the T2 generation, and all three T2 populations were slightly smaller than controls. In the physiological analysis of the T2 populations, G2517 overexpressing lines were more resistant to the herbicide glyphosate. G2517 can be used for the generation of glyphosate resistant plants, and to increase plant resistance to oxidative stress.

Closely Related Genes from Other Species

G2517 shows some sequence similarity with known genes from other plant species within the conserved WRKY domain.

G2140: The complete sequence of G2140 (SEQ ID NO: 81) was determined. G2140 was expressed throughout the plant. It showed repression by salicylic acid and Erysiphe infection. Overexpressing G2140 in Arabidopsis resulted in seedlings that were more tolerant to osmotic stress conditions. In germination assays where seedlings were exposed to high concentrations of sucrose or NaCl, all three lines tested showed better cotyledon expansion and seedling vigor. Additionally, G2140 overexpressing plants showed insensitivity to ABA in a germination assay. In

general, G2140 overexpressing plants were small and sickly with sh grown in Petri plates. The combination of ABA insensitivity and re: osmotic stress at germination had also been observed for other genes, for example, G1820 (SEQ ID NO:13) and G926 (SEQ ID NO:111). Significantly, the ABA resistance was detected in a germination assay. ABA is involved in maintaining seed dormancy, and it is possible that ABA insensitivity at the germination stage promotes germination despite unfavorable conditions.

When grown in soil, G2140 overexpressing plants displayed marked changes in Arabidopsis leaf and root morphology. All twenty of the 35S::G2140 primary transformants displayed, to various extents, leaves with upcurled margins. In the most severe cases, the leaves became highly contorted and the plants were slightly small and grew more slowly than controls. Three T1 lines (#12, 15 and 16) that showed substantial levels of G2140 overexpression (determined by RT-PCR) were chosen for further study. The T2 seedlings from each of these lines exhibited stunted roots compared with controls. Seedlings from two of the lines (#15,16) also showed upcurled cotyledons. At later stages, however, T2-16 plants appeared wild type. Plants from the T2-12 and T2-15 populations were rather varied in size and showed hints of leaf curling later in development. However, this effect was less severe than that seen in the T1 lines. To verify the leaf-curling phenotype, two further T2 populations (#3,18) were morphologically examined; seedlings from T2-3 were extremely tiny with thickened hypocotyls and short stunted roots. Such plants were too small for transfer to soil. However, T2-18 plants showed slightly contorted cotyledons and formed severely upcurled leaves, confirming the effects seen in the T1 generation.

G2140 is useful for creating plants that germinate better under conditions of high salt. Evaporation from the soil surface causes upward water movement and salt accumulation in the upper soil layer where the seeds are placed. Thus, germination normally takes place at a salt concentration much higher than the mean salt concentration in the whole soil profile. Increased salt tolerance during the germination stage of a crop plant will impact survivability and yield. In addition, G2140 can be used to alter a plant's response to water deficit conditions and,

therefore, can be used to engineer plants with enhanced tolerance to freezing.

Closely Related Genes from Other Species

G2140 proteins show extensive sequence similarity with a tomato ovary cDNA; TAMU Lycopersicon esculentum (AI488313) and a Glycine max cDNA clone (BE020519).

G1946: G1946 (SEQ ID NO:49) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1946 resulted in accelerated flowering, with 35S::G1946 transformants producing flower buds up to a week earlier than wild-type controls (24-hour light conditions). These effects were seen in 12/20 primary transformants and in two independent plantings of each of the three T2 lines. Unlike many early flowering Arabidopsis transgenic lines, which are dwarfed, 35S::G1946 transformants often reached full-size at maturity, and produced large quantities of seeds, although the plants were slightly pale in coloration and had slightly flat leaves compared to wild-type. In addition, 35S::G1946 plants showed an altered response to phosphate deprivation. Seedlings of G1946 overexpressors showed more secondary root growth on phosphate-free media, when compared to wild-type control. In a repeat experiment, all three lines showed the phenotype. Overexpression of G1946 in Arabidopsis also resulted in an increase in seed glucosinolate M39501 in T2 lines 1and 3. An increase in seed oil and a decrease in seed protein was also observed in these two lines. G1946 was ubiquitously expressed, and did not appear to be significantly induced or repressed by any of the biotic and abiotic stress conditions tested, with the exception of cold, which repressed G1946 expression. G1946 can be used to modify flowering time, as well as to improve the plant's performance in conditions of limited phosphate, and to alter seed oil, protein, and glucosinolate composition.

Closely Related Genes from Other Species

A comparison of the amino acid sequence of G1946 with sequences available from GenBank showed strong similarity with plant HSFs of several species

(Lycopersicon peruvianum, Medicago truncatula, Lycopersicon esc
max, Solanum tuberosum, Oryza sativa and Hordeum vulgare subsp

G1852: G1852 (SEQ ID NO:71) was analyzed through its ectopic overexpression in plants. Analysis of the endogenous level of G1852 transcripts by RT-PCR revealed expression in all tissues tested. G1852 expression was induced in response to ABA, heat and drought treatment. 35S::G1852 overexpressor plants were more tolerant to osmotic stress in a root growth assay on PEG (polyethylene glycol)-containing media compared with wild-type controls. Seedlings were slightly larger and have more root growth. G1852 can be used to alter a plant's response to water deficit conditions and therefore, be used to engineer plants with enhanced tolerance to drought, salt stress, and freezing.

Closely Related Genes from Other Species

A comparison of the amino acid sequence of G1852 with entries available from GenBank shows strong similarity with plant ankyrins of several species (Malus domestica, Solanum tuberosum, Oryza sativa, Gossypium arboreum, Medicago truncatula, Glycine max, Lycopersicon esculentum, Pinus taeda, Lotus japonicus and Gossypium hirsutum).

G325: G325 (SEQ ID NO:95) was analyzed using transgenic plants in which G325 was expressed under the control of the 35S promoter. G325 overexpressing plants showed more tolerance to osmotic stress in a germination assay in three separate experiments. They showed more seedling vigor than wild-type control when germinated on plates containing high salt and high sucrose. G325 was expressed at high levels in flowers and cauline leaves, and at lower levels in shoots, rosette leaves, and seedlings. G325 was induced by auxin, cold and heat stress. Expression of G325 was reduced in response to Fusarium infection or salicylic acid treatment. G325 can be useful for enhancing seed germination under high salt conditions or other conditions of osmotic stress. Evaporation from the soil surface causes upward water movement and salt accumulation in the upper soil layer where the seeds are placed. Thus, germination normally takes place at a salt concentration much higher than the mean salt concentration of in the whole soil profile. Increased salt tolerance during the germination stage of a crop plant will impact survivability and yield. G325 can

also be used to engineer plants with enhanced tolerance to drought, freezing at later stages during growth and development.

Closely Related Genes from Other Species

G325 showed homology to non-Arabidopsis proteins within the conserved domain.

G2583: G2583 (SEQ ID NO: 17) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G2583 plants exhibited extremely glossy leaves. At early stages, 35S::G2583 seedlings appeared normal, but by about two weeks after sowing, the plants exhibited very striking shiny leaves, which were apparent until very late in development. Many lines displayed a variety of other effects such as a reduction in overall size, narrow curled leaves, or various non-specific floral abnormalities, which reduced fertility. These effects on leaf appearance were observed in 18/20 primary transformants, and in all the plants from 4/6 of the T2 lines (#2,4,9 and 15) examined. The glossy nature of the leaves from 35S::G2583 plants can be a consequence of changes in epicuticular wax content or composition. G2583 belongs to a small clade within the large AP2/EREBP Arabidopsis family that also contains G975 (SEQ ID NO: 19), G1387 (SEQ ID NO: 21), and G977 (SEQ ID NO: 23). Overexpression of G975 caused a substantial increase in leaf wax components, as well as morphological phenotypes resembling those observed in 35S::G2583 plants. G2583 was ubiquitously expressed, at higher levels in root, flower, embryo, and silique tissues. G2583 can be used to modify plant appearance (shiny leaves). In addition, it can be used to manipulate wax composition, amount, or distribution, which in turn can modify plant tolerance to drought and/or low humidity or resistance to insects.

Closely Related Genes from Other Species

G2583 showed some sequence similarity with known genes from other plant species within the conserved AP2/EREBP domain.

G1322: G1322 (SEQ ID NO: 21) was analyzed using transger the gene was expressed under the control of the 35S promoter. 35S transgenic plants were wild-type in phenotype with respect to the biochemical analyses performed. Overexpression of G1322 produced changes in overall plant size and leaf development. At all stages, 35S::G1322 plants were distinctly smaller than controls and developed curled dark-green leaves. Following the switch to flowering, the plants formed relatively thin inflorescence stems and had a rather poor seed yield. In addition, overexpression of G1322 resulted in plants with an altered etiolation response as well as enhanced tolerance to germination under chilling conditions. When germinated in the dark, G1322 overexpressing transgenic plant lines had open, slightly green cotyledons. Under chilling conditions, all three transgenic lines displayed a similar germination response, seedlings were slightly larger and had longer roots. In addition, an increase in the leaf glucosinolate M39480 was observed in all three T2 lines. According to RT-PCR analysis, G1322 was expressed primarily in flower tissue. The utilities of G1322 include altering a plant's chilling sensitivity and altering a plant's light response. The germination of many crops is very sensitive to cold temperatures. A gene that will enhance germination and seedling vigor in the cold has tremendous utility in allowing seeds to be planted earlier in the season with a higher survival rate. G1322 can also be useful for altering leaf glucosinolate composition. Increases or decreases in specific glucosinolates or total glucosinolate content are desirable depending upon the particular application. Modification of glucosinolate composition or quantity can therefore afford increased protection from predators. Furthermore, in edible crops, tissue specific promoters can be used to ensure that these compounds accumulate specifically in tissues, such as the epidermis, which are not taken for consumption.

Closely Related Genes from Other Species

G1322 shows some sequence similarity with known genes from other plant species within the conserved Myb domain.

G303: The complete sequence of G303 (SEQ ID NO: 23) was determined. G303 was detected at very low levels in roots and rosette leaves. G303 was analyzed using transgenic plants in which G303 was expressed under the control of the 35S

promoter. G303 overexpressing plants showed more tolerance to o germination assay in three separate experiments. They showed mo than wild-type control when germinated on plates containing high salt and high sucrose. G303 are useful for enhancing seed germination under high salt conditions or other conditions of osmotic stress. Evaporation from the soil surface causes upward water movement and salt accumulation in the upper soil layer where the seeds are placed. Thus, germination normally takes place at a salt concentration much higher than the mean salt concentration in the whole soil profile. Increased salt tolerance during the germination stage of a crop plant will impact survivability and yield. G303 can also be used to engineer plants with enhanced tolerance to drought, salt stress, and freezing.

Closely Related Genes from Other Species

G303 shows some sequence similarity with known genes from other plant species within the conserved basic HLH domain.

G1927:G1927 (SEQ ID NO: 239) was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1927 in Arabidopsis resulted in plants that had an altered response to pathogen. Plants overexpressing G1927 showed fewer disease symptoms following infection with the fungal pathogen Sclerotinia sclerotiorum compared with control plants. The experiment was repeated on individual lines, and all three lines showed the enhanced pathogen tolerance phenotype. G1927 expression appeared to be ubiquitous according to RT-PCR analysis. G1927 can be used to manipulate the defense response in order to generate pathogen-resistant plants.

Closely Related Genes from Other Species

G1927 showed extensive sequence similarity to a NAC protein from tomato (BG350410).

Example VIII: Identification of Homologous Sequences

Homologous sequences from *Arabidopsis* and plant species ot *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified non-Arabidopsis sequences homologous to the *Arabidopsis* sequences are provided in Table 5. The percent sequence identity among these sequences can be as low as 47%, or even lower sequence identity. The entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences are compared to sequences representing genes of SEQ IDs NOs:2 - 2N, where N = 2-123, using the Washington University TBLASTX algorithm (version 2.0a19MP) at the default settings using gapped alignments with the filter "off". For each gene of SEQ IDs NOs:2 - 2N, where N = 2-123, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of 3.6e-40 is 3.6×10^{-40}. In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. Examples of sequences so identified are presented in Table 5. Homologous or orthologous sequences are readily identified and available in GenBank by Accession number (Table 5; Test sequence ID)The identified homologous polynucleotide and polypeptide sequences and homologues of the *Arabidopsis* polynucleotides and polypeptides may be orthologs of the *Arabidopsis* polynucleotides and polypeptides.

Example IX Introduction of polynucleotides into dicots

SEQ ID NOs:1-(2N - 1), wherein N = 2-123, paralogous, orthologous, and homologous sequences recombined into pMEN20 or pMEN65 expression vectors are transformed into a plant for the purpose of modifying plant traits. The cloning vector may be introduced into a variety of cereal plants by means well-known in the art such

as, for example, direct DNA transfer or *Agrobacterium tumefaciens*-transformation. It is now routine to produce transgenic plants using (see Weissbach and Weissbach, (1989) *supra;* Gelvin et al., (1990) *supra*; Herrera-Estrella et al. (1983) *supra*; Bevan (1984) *supra*; and Klee (1985) *supra*). Methods for analysis of traits are routine in the art and examples are disclosed above.

Example X Transformation of Cereal Plants with an Expression Vector

Cereal plants such as corn, wheat, rice, sorghum or barley, may also be transformed with the present polynucleotide sequences in pMEN20 or pMEN65 expression vectors for the purpose of modifying plant traits. For example, pMEN020 may be modified to replace the NptII coding region with the BAR gene of *Streptomyces hygroscopicus* that confers resistance to phosphinothricin. The KpnI and BglII sites of the Bar gene are removed by site-directed mutagenesis with silent codon changes.

The cloning vector may be introduced into a variety of cereal plants by means well-known in the art such as, for example, direct DNA transfer or *Agrobacterium tumefaciens*-mediated transformation. It is now routine to produce transgenic plants of most cereal crops (Vasil, I., Plant Molec. Biol. 25: 925-937 (1994)) such as corn, wheat, rice, sorghum (Cassas, A. et al., Proc. Natl. Acad Sci USA 90: 11212-11216 (1993) and barley (Wan, Y. and Lemeaux, P. Plant Physiol. 104:37-48 (1994). DNA transfer methods such as the microprojectile can be used for corn (Fromm. et al. Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al. Plant Cell 2: 603-618 (1990); Ishida, Y., Nature Biotechnology 14:745-750 (1990)), wheat (Vasil, et al. Bio/Technology 10:667-674 (1992) ; Vasil et al., Bio/Technology 11:1553-1558 (1993); Weeks et al., Plant Physiol. 102:1077-1084 (1993)), rice (Christou Bio/Technology 9:957-962 (1991); Hiei et al. Plant J. 6:271-282 (1994); Aldemita and Hodges, Planta 199:612-617; Hiei et al., Plant Mol Biol. 35:205-18 (1997)). For most cereal plants, embryogenic cells derived from immature scutellum tissues are the preferred cellular targets for transformation (Hiei et al., Plant Mol Biol. 35:205-18 (1997); Vasil, Plant Molec. Biol. 25: 925-937 (1994)).

Vectors according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile

bombardment, with the A188XB73 genotype as the preferred genot al., Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al., Plant (1990)). After microprojectile bombardment the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm, et al., Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)).

The plasmids prepared as described above can also be used to produce transgenic wheat and rice plants (Christou, Bio/Technology 9:957-962 (1991); Hiei et al., Plant J. 6:271-282 (1994); Aldemita and Hodges, Planta 199:612-617 (1996); Hiei et al., Plant Mol Biol. 35:205-18 (1997)) that coordinately express genes of interest by following standard transformation protocols known to those skilled in the art for rice and wheat Vasil, et al. Bio/Technology 10:667-674 (1992) ; Vasil et al., Bio/Technology 11:1553-1558 (1993); Weeks et al., Plant Physiol. 102:1077-1084 (1993)), where the bar gene is used as the selectable marker.

All references, publications, patent documents, web pages, and other documents cited or mentioned herein are hereby incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to specific embodiments and examples, it should be understood that one of ordinary skill can make various modifications without departing from the spirit of the invention. The scope of the invention is not limited to the specific embodiments and examples provided.

We claim:

1. A transgenic plant comprising a recombinant polynucleotide having a nucleotide sequence selected from the group consisting of:
(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from those of, SEQ ID NOs: 26, 46, 176, 114, 142, 144, 82, 50, 72, 96, 18, 22, 24, 240, or a complementary nucleotide sequence thereof;
(b) a nucleotide sequence of SEQ ID NOs: 25, 45, 175, 113, 141, 143, 81, 49, 71, 95, 17, 21, 23, 239, or a complementary nucleotide sequence thereof; and
(c) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of one or more polynucleotides of: (a) or (b).

2. The transgenic plant of claim 1 wherein the transgenic plant possesses an altered trait as compared to another plant, or the transgenic plant exhibits an altered phenotype as compared to another plant, or the transgenic plant expresses an altered level of one or more genes associated with a plant trait as compared to another plant, wherein the other plant does not comprise the recombinant polynucleotide.

3. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is an enhanced tolerance to environmental conditions.

4. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is an improved tolerance to microbial, fungal or viral diseases.

5. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is an improved tolerance to pest infestations.

6. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is a decreased herbicide sensitivity.

7. The transgenic plant of claim 1 wherein the plant possesses ar
compared to another plant wherein the trait is an improved toleranc
or enhanced ability to take up heavy metals.

8. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is improved growth under poor photoconditions.

9. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is improved nutrient uptake.

10. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is reduced hormone sensitivity.

11. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:26.

12. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:46.

13. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:176.

14. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:114.

15. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:142.

16. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:144.

17. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:82.

18. The transgenic plant of claim 1, wherein the recombinant poly comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:50.

19. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:72.

20. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:96.

21. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:18.

22. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:22.

23. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:24.

24. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:240.

25. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:25.

26. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:45.

27. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:175.

28. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:113.

29. The transgenic plant of claim 1, wherein the recombinant polyı comprises a nucleotide sequence of SEQ ID NO:141.

30. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:143.

31. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:81.

32. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:49.

33. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:71.

34. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:95.

35. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:17.

36. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:21.

37. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:23.

38. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:239.

39. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said nucleotide sequence.

40. The transgenic plant of claim 1, wherein the plant is selected fr consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, mint and other labiates, rosaceous fruits, and vegetable brassicas.

41. The transgenic plant of claim 1 wherein the encoded polypeptide is expressed and regulates transcription of a gene.

42. A method of using the transgenic plant of claim 1 to grow a progeny plant from a parent plant, the method comprising crossing the transgenic plant with another plant, selecting seed, and growing the progeny plant from the seed.

43. An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID NOs:26, 82, 24, 240, or a complementary nucleotide sequence thereof;
(b) a nucleotide sequence of SEQ ID NOs:25, 81, 23, 239, or a complementary nucleotide sequence thereof; and
(c) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a) or (b).

44. The isolated or recombinant polynucleotide of claim 43, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:26.

45. The isolated or recombinant polynucleotide of claim 43, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:82.

46. The isolated or recombinant polynucleotide of claim 43, wher recombinant polynucleotide comprises a nucleotide sequence encoc of SEQ ID NO:24.

47. The isolated or recombinant polynucleotide of claim 43, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:240.

48. The isolated or recombinant polynucleotide of claim 43, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:26.

49. The isolated or recombinant polynucleotide of claim 43, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:81.

50. The isolated or recombinant polynucleotide of claim 43, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:23.

51. The isolated or recombinant polynucleotide of claim 43, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:239.

52. The isolated or recombinant polynucleotide of claim 43, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to the nucleotide sequence.

53. The isolated or recombinant polynucleotide of claim 43 wherein the encoded polypeptide is expressed and regulates transcription of a gene.

54. A vector comprising the isolated or recombinant polynucleotide of claim 43.

55. A host cell comprising the vector of claim 54.

56. A method of using the isolated or recombinant polynucleotide of claim 43 for producing a modified plant having a modified trait, the method comprising selecting a

polynucleotide that encodes a polypeptide, inserting the polynucleo expression vector, introducing the vector into a plant or a cell of a p overexpress the polypeptide, thereby producing a modified plant, and selecting for a modified trait.

57. The method of claim 54 wherein the modified plant possesses a modified trait as compared to another plant wherein the trait is an enhanced tolerance to environmental conditions.

58. The method of claim 54 wherein the modified plant possesses a modified as compared to another plant wherein the trait is an improved tolerance to microbial, fungal or viral diseases.

59. The method of claim 54 wherein the modified plant possesses a modified trait as compared to another plant wherein the trait is an improved tolerance to pest infestations.

60. The method of claim 54 wherein the modified plant possesses a modified trait as compared to another plant wherein the trait is a decreased herbicide sensitivity.

61. The method of claim 54 wherein the modified plant possesses a modified trait as compared to another plant wherein the trait is an improved tolerance of heavy metals or enhanced ability to take up heavy metals.

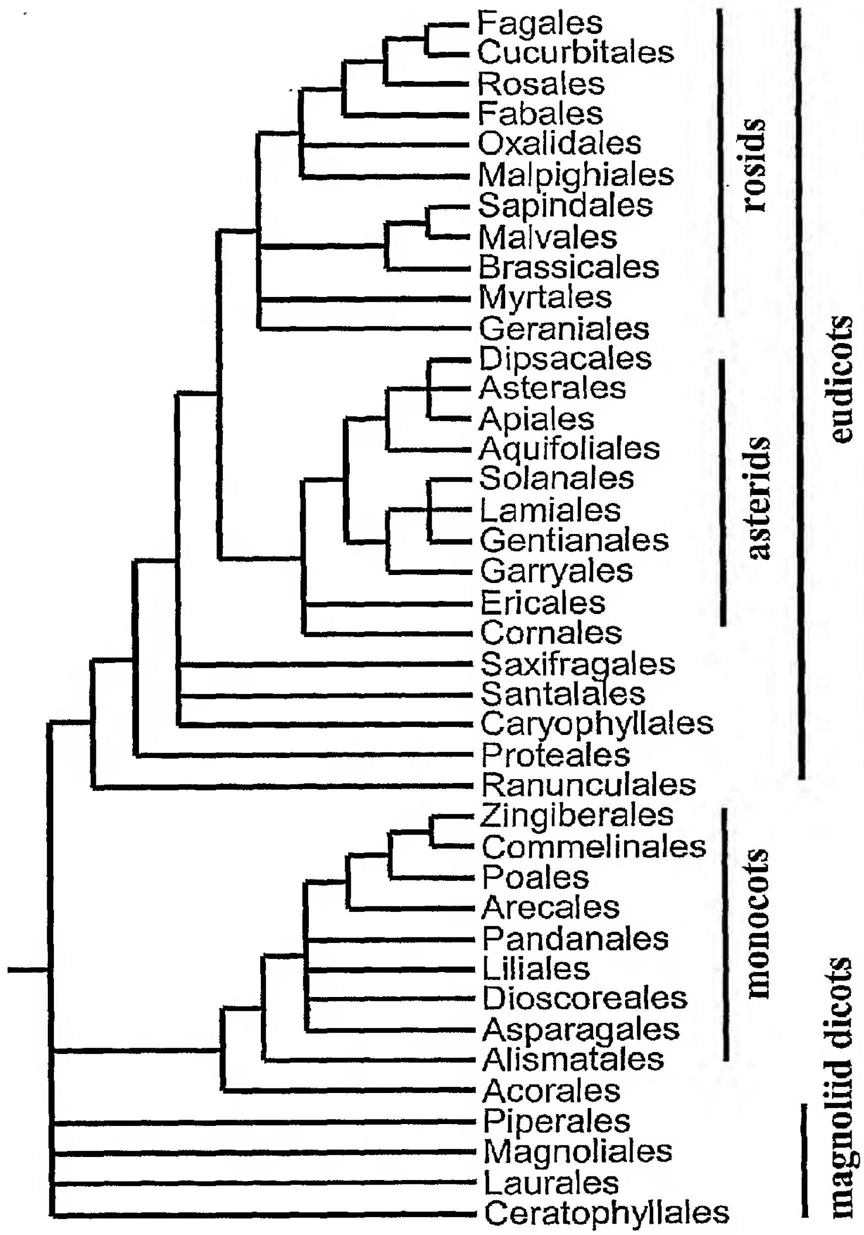
62. The method of claim 54 wherein the modified plant possesses a modified trait as compared to another plant wherein the trait is improved growth under poor photoconditions.

63. The method of claim 54 wherein the modified plant possesses a modified trait as compared to another plant wherein the trait is improved nutrient uptake.

64. The method of claim 54 wherein the modified plant possesses a modified trait as compared to another plant wherein the trait is reduced hormone sensitivity.

65. A modified plant produced by the method of claim 54.

66. A method of using the plant of claim 63 to grow a progeny plant from a parent plant, the method comprising crossing the transgenic plant with another plant, selecting seed, and growing the progeny plant from the seed.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asterids
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magnoliid dicots

Figure 1

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      Jiang, Cai-Zhong
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      Dubell, Arnold T.
      Ratcliffe, Oliver
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65 70 75

atc atc cac ctt caa gct ctt ttg gga aat aga tgg gca gct ata gca 590
Ile Ile His Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala
80 85 90

tca tat cta cct cag agg acc gac aat gat atc aag aac tac tgg aac 638
Ser Tyr Leu Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn
95 100 105

act cat ctt aaa aag aaa cta gtg atg atg aag ttt caa aat ggt atc 686
Thr His Leu Lys Lys Lys Leu Val Met Met Lys Phe Gln Asn Gly Ile
110 115 120 125

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atc aac gaa aac aaa acc aat ctg gca aca gat att tcg tct tgt aat     734
Ile Asn Glu Asn Lys Thr Asn Leu Ala Thr Asp Ile Ser Ser Cys Asn
                130                 135                 140

aat aac aac aat gga tgt aat cac aac aaa agg acc acc aac aaa ggc     782
Asn Asn Asn Asn Gly Cys Asn His Asn Lys Arg Thr Thr Asn Lys Gly
            145                 150                 155

caa tgg gag aaa aaa ctt caa aca gac atc aac atg gcc aaa caa gcc     830
Gln Trp Glu Lys Lys Leu Gln Thr Asp Ile Asn Met Ala Lys Gln Ala
        160                 165                 170

tta ttc caa gcc ttg tca ctt gac caa cca tct tca ttg atc cct ccc     878
Leu Phe Gln Ala Leu Ser Leu Asp Gln Pro Ser Ser Leu Ile Pro Pro
    175                 180                 185

gat cct gac tca cca aaa cct cat cat cat tct acc acc act tat gcc     926
Asp Pro Asp Ser Pro Lys Pro His His His Ser Thr Thr Thr Tyr Ala
190                 195                 200                 205

tca agc aca gat aac atc tct aaa tta ctc cag aac tgg aca agc tca     974
Ser Ser Thr Asp Asn Ile Ser Lys Leu Leu Gln Asn Trp Thr Ser Ser
                210                 215                 220

tca tcg tca aag cct aac act tca tca gtc tcc aac aac cgg agc tca     1022
Ser Ser Ser Lys Pro Asn Thr Ser Ser Val Ser Asn Asn Arg Ser Ser
            225                 230                 235

agc ccc ggt gaa gga gga ctt ttt gat cat cac tct ttg ttc tca tcg     1070
Ser Pro Gly Glu Gly Gly Leu Phe Asp His His Ser Leu Phe Ser Ser
        240                 245                 250

aat tca gaa tct gga tca gtt gat gag aag ctg aat ttg atg tcc gag     1118
Asn Ser Glu Ser Gly Ser Val Asp Glu Lys Leu Asn Leu Met Ser Glu
    255                 260                 265

aca agc atg ttc aaa ggt gag agc aag cca gac ata gac atg gaa gct     1166
Thr Ser Met Phe Lys Gly Glu Ser Lys Pro Asp Ile Asp Met Glu Ala
270                 275                 280                 285

aca cct act act act act act act act gat gat caa ggc tcg ttg tca     1214
Thr Pro Thr Thr Thr Thr Thr Thr Thr Asp Asp Gln Gly Ser Leu Ser
                290                 295                 300

ttg atc gag aaa tgg ttg ttt gat gat caa ggc ttg gtt cag tgt gat     1262
Leu Ile Glu Lys Trp Leu Phe Asp Asp Gln Gly Leu Val Gln Cys Asp
            305                 310                 315

gat agt caa gaa gat ctc atc gac gtg tct tta gag gag tta aaa taa     1310
Asp Ser Gln Glu Asp Leu Ile Asp Val Ser Leu Glu Glu Leu Lys  *
        320                 325                 330

tgataacaac agtcaagatt tgttctataa gaaaataaaa cgtatagaac aacgataaag 1370
ctagctaggt ttattaattt ttctttcttt tgtcttttct ctatgatctt tagttacatt 1430
ttattttact gtgtggcttg cttgtggtca agtcgatgaa gatcaaactg tgatatacta 1490
tttatatgta aagtactata aagttaagag tagttgaata aaaaaaaaaa aaaaaaa    1547
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<210> 6
<211> 332
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (13)...(115)
<223> Conserved domain

<400> 6
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 1               5                  10                  15
Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Gln His
            20                  25                  30
Gly Pro Gly Asn Trp Arg Ser Val Pro Ala Asn Thr Gly Leu Leu Arg
        35                  40                  45
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
    50                  55                  60
Ile Lys Arg Gly Asn Phe Thr Gln Pro Glu Glu Lys Met Ile Ile His
65                  70                  75                  80
Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
                85                  90                  95
Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
            100                 105                 110
Lys Lys Lys Leu Val Met Met Lys Phe Gln Asn Gly Ile Ile Asn Glu
        115                 120                 125
Asn Lys Thr Asn Leu Ala Thr Asp Ile Ser Ser Cys Asn Asn Asn Asn
    130                 135                 140
Asn Gly Cys Asn His Asn Lys Arg Thr Thr Asn Lys Gly Gln Trp Glu
145                 150                 155                 160
Lys Lys Leu Gln Thr Asp Ile Asn Met Ala Lys Gln Ala Leu Phe Gln
                165                 170                 175
Ala Leu Ser Leu Asp Gln Pro Ser Ser Leu Ile Pro Pro Asp Pro Asp
            180                 185                 190
Ser Pro Lys Pro His His His Ser Thr Thr Thr Tyr Ala Ser Ser Thr
        195                 200                 205
Asp Asn Ile Ser Lys Leu Leu Gln Asn Trp Thr Ser Ser Ser Ser Ser
    210                 215                 220
Lys Pro Asn Thr Ser Ser Val Ser Asn Asn Arg Ser Ser Ser Pro Gly
225                 230                 235                 240
Glu Gly Gly Leu Phe Asp His His Ser Leu Phe Ser Ser Asn Ser Glu
                245                 250                 255
Ser Gly Ser Val Asp Glu Lys Leu Asn Leu Met Ser Glu Thr Ser Met
            260                 265                 270
Phe Lys Gly Glu Ser Lys Pro Asp Ile Asp Met Glu Ala Thr Pro Thr
        275                 280                 285
Thr Thr Thr Thr Thr Thr Asp Asp Gln Gly Ser Leu Ser Leu Ile Glu
    290                 295                 300
Lys Trp Leu Phe Asp Asp Gln Gly Leu Val Gln Cys Asp Asp Ser Gln
305                 310                 315                 320
Glu Asp Leu Ile Asp Val Ser Leu Glu Glu Leu Lys
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<210> 7

<211> 1249
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (82)...(918)

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taatacgaag agaaaattca a atg ggt ctt gat gat tca tgc aac aca ggt 111
Met Gly Leu Asp Asp Ser Cys Asn Thr Gly
1 5 10

ctt gtt ctt ggt tta ggc ctc tca cca acg cct aat aat tac aat cat 159
Leu Val Leu Gly Leu Gly Leu Ser Pro Thr Pro Asn Asn Tyr Asn His
15 20 25

gcc atc aag aaa tct tcc tcc act gtg gac cat cgt ttc atc agg ctc 207
Ala Ile Lys Lys Ser Ser Ser Thr Val Asp His Arg Phe Ile Arg Leu
30 35 40

gat ccg tcg ttg act cta agc cta tcc ggt gag agc tac aag atc aag 255
Asp Pro Ser Leu Thr Leu Ser Leu Ser Gly Glu Ser Tyr Lys Ile Lys
45 50 55

act ggt gcc ggc gcc ggc gac caa att tgc cgg cag acc tcg tcc cac 303
Thr Gly Ala Gly Ala Gly Asp Gln Ile Cys Arg Gln Thr Ser Ser His
60 65 70

agc ggc atc tca tct ttc tcg agc gga agg gta aag aga gaa aga gaa 351
Ser Gly Ile Ser Ser Phe Ser Ser Gly Arg Val Lys Arg Glu Arg Glu
75 80 85 90

atc tcc ggc ggc gat gga gaa gaa gag gcg gag gag acg acg gag aga 399
Ile Ser Gly Gly Asp Gly Glu Glu Glu Ala Glu Glu Thr Thr Glu Arg
95 100 105

gtg gtg tgt tcg aga gtg agt gat gat cat gac gat gaa gaa ggt gtt 447
Val Val Cys Ser Arg Val Ser Asp Asp His Asp Asp Glu Glu Gly Val
110 115 120

agt gct cgt aaa aag ctt aga ctc act aaa caa caa tct gct ctt ctc 495
Ser Ala Arg Lys Lys Leu Arg Leu Thr Lys Gln Gln Ser Ala Leu Leu
125 130 135

gaa gat aac ttc aaa ctt cat agc acc ctt aat ccc aag caa aaa caa 543
Glu Asp Asn Phe Lys Leu His Ser Thr Leu Asn Pro Lys Gln Lys Gln
140 145 150

gct ctt gcg aga cag ctg aat cta agg cct aga caa gtt gaa gtg tgg 591
Ala Leu Ala Arg Gln Leu Asn Leu Arg Pro Arg Gln Val Glu Val Trp
155 160 165 170

ttc caa aac agg aga gct aga aca aaa cta aag caa aca gaa gtg gat 639
Phe Gln Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp
175 180 185

tgt gag ttt ttg aag aaa tgt tgc gag act tta acg gat gag aat aga 687
Cys Glu Phe Leu Lys Lys Cys Cys Glu Thr Leu Thr Asp Glu Asn Arg
190 195 200

agg ctt caa aaa gag ctt caa gac ctt aag gct tta aaa ttg tct caa 735
Arg Leu Gln Lys Glu Leu Gln Asp Leu Lys Ala Leu Lys Leu Ser Gln
205 210 215

ccg ttt tac atg cac atg ccg gcg gcg act ttg act atg tgc cct tct 783
Pro Phe Tyr Met His Met Pro Ala Ala Thr Leu Thr Met Cys Pro Ser
220 225 230

tgt gag aga ctc ggc ggt ggt ggt gtc gga gga gat acg acg gcg gtt 831
Cys Glu Arg Leu Gly Gly Gly Gly Val Gly Gly Asp Thr Thr Ala Val
235 240 245 250

gat gaa gaa acg gcg aaa gga gct ttc tcc atc gtc aca aag cct cgt 879
Asp Glu Glu Thr Ala Lys Gly Ala Phe Ser Ile Val Thr Lys Pro Arg
255 260 265

ttc tat aac cct ttc act aat cct tct gca gca tgt tag ttacttatta 928
Phe Tyr Asn Pro Phe Thr Asn Pro Ser Ala Ala Cys *
270 275

gttatttaat tctttttgtt ggtttttttt ttgtttctta aatcaaatta ggaattagtt 988
agaagataaa tcccagggaa aaaatattac gttgaaattg gggggaaatg gggtatagtc 1048
tttatagata agactcttca acgattccac tttatttttc ggtgggattg ttggttgatg 1108
aagaaaaaaa aatagtttgt aattacaggt ttaaatatgt agagaaaaaa tgacgaatat 1168
gtattatctt gttttttttt ccttcgaata tgtattacgg taatataaat ttgcttgtaa 1228
aaataataaa tatattattt g 1249

<210> 8
<211> 278
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (121)...(182)
<223> Conserved domain

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Met Gly Leu Asp Asp Ser Cys Asn Thr Gly Leu Val Leu Gly Leu Gly
1 5 10 15
Leu Ser Pro Thr Pro Asn Asn Tyr Asn His Ala Ile Lys Lys Ser Ser
20 25 30
Ser Thr Val Asp His Arg Phe Ile Arg Leu Asp Pro Ser Leu Thr Leu
35 40 45
Ser Leu Ser Gly Glu Ser Tyr Lys Ile Lys Thr Gly Ala Gly Ala Gly
50 55 60
Asp Gln Ile Cys Arg Gln Thr Ser Ser His Ser Gly Ile Ser Ser Phe
65 70 75 80
Ser Ser Gly Arg Val Lys Arg Glu Arg Glu Ile Ser Gly Gly Asp Gly
85 90 95
Glu Glu Glu Ala Glu Glu Thr Thr Glu Arg Val Val Cys Ser Arg Val
100 105 110

```
Ser Asp Asp His Asp Asp Glu Glu Gly Val Ser Ala Arg Lys Lys Leu
        115                 120                 125
Arg Leu Thr Lys Gln Gln Ser Ala Leu Leu Glu Asp Asn Phe Lys Leu
    130                 135                 140
His Ser Thr Leu Asn Pro Lys Gln Lys Gln Ala Leu Ala Arg Gln Leu
145                 150                 155                 160
Asn Leu Arg Pro Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg Ala
                165                 170                 175
Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Phe Leu Lys Lys
            180                 185                 190
Cys Cys Glu Thr Leu Thr Asp Glu Asn Arg Arg Leu Gln Lys Glu Leu
        195                 200                 205
Gln Asp Leu Lys Ala Leu Lys Leu Ser Gln Pro Phe Tyr Met His Met
    210                 215                 220
Pro Ala Ala Thr Leu Thr Met Cys Pro Ser Cys Glu Arg Leu Gly Gly
225                 230                 235                 240
Gly Gly Val Gly Gly Asp Thr Thr Ala Val Asp Glu Glu Thr Ala Lys
                245                 250                 255
Gly Ala Phe Ser Ile Val Thr Lys Pro Arg Phe Tyr Asn Pro Phe Thr
            260                 265                 270
Asn Pro Ser Ala Ala Cys
        275
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<210> 9
<211> 1087
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (104)...(952)

<400> 9

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caatccctca atataaaata acaagtagaa ttgatctgcc tatatataag attttgagac 60
gaaataagat ctaaaccaca agaaagaaag taaacataaa agt atg gga agg tca   115
                                                Met Gly Arg Ser
                                                 1

ccg tgc tgt gag aaa gct cac aca aac aaa gga gca tgg acg aaa gaa   163
Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala Trp Thr Lys Glu
 5                  10                  15                  20

gag gac gag agg ctc gtc gcc tac att aaa gct cat gga gaa ggc tgc   211
Glu Asp Glu Arg Leu Val Ala Tyr Ile Lys Ala His Gly Glu Gly Cys
                25                  30                  35

tgg aga tct ctc ccc aaa gcc gcc gga ctt ctt cgc tgt ggc aag agc   259
Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg Cys Gly Lys Ser
            40                  45                  50

tgc cgt ctc cgg tgg atc aac tat ctc cgg cct gac ctt aag cgt gga   307
Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly
        55                  60                  65

aac ttc acc gag gaa gaa gac gaa ctc atc atc aag ctc cat agc ctt   355
Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys Leu His Ser Leu
```

```
  70                           75                             80

ctt ggc aac aaa tgg tcg ctt att gcc ggg aga tta ccg gga aga aca    403
Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
 85                      90                       95                  100

gat aac gag ata aag aac tat tgg aac acg cat ata cga aga aag ctt    451
Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile Arg Arg Lys Leu
                105                      110                      115

ata aac aga ggg att gat cca acg agt cat aga cca atc caa gaa tca    499
Ile Asn Arg Gly Ile Asp Pro Thr Ser His Arg Pro Ile Gln Glu Ser
            120                      125                      130

tca gct tct caa gat tct aaa cct aca caa cta gaa cca gtt acg agt    547
Ser Ala Ser Gln Asp Ser Lys Pro Thr Gln Leu Glu Pro Val Thr Ser
        135                      140                      145

aat acc att aat atc tca ttc act tct gct cca aag gtc gaa acg ttc    595
Asn Thr Ile Asn Ile Ser Phe Thr Ser Ala Pro Lys Val Glu Thr Phe
    150                      155                      160

cat gaa agt ata agc ttt ccg gga aaa tca gag aaa atc tca atg ctt    643
His Glu Ser Ile Ser Phe Pro Gly Lys Ser Glu Lys Ile Ser Met Leu
165                      170                      175                      180

acg ttc aaa gaa gaa aaa gat gag tgc cca gtt caa gaa aag ttc cca    691
Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln Glu Lys Phe Pro
                185                      190                      195

gat ttg aat ctt gag ctc aga atc agt ctt cct gat gat gtt gat cgt    739
Asp Leu Asn Leu Glu Leu Arg Ile Ser Leu Pro Asp Asp Val Asp Arg
            200                      205                      210

ctt caa ggg cat gga aag tca aca acg cca cgt tgt ttc aag tgc agc    787
Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys Phe Lys Cys Ser
        215                      220                      225

tta ggg atg ata aac ggc atg gag tgc aga tgc gga aga atg aga tgc    835
Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly Arg Met Arg Cys
    230                      235                      240

gat gta gtc gga ggt agc agc aag ggg agt gac atg agc aat gga ttt    883
Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met Ser Asn Gly Phe
245                      250                      255                      260

gat ttt tta ggg ttg gca aag aaa gag acc act tct ctt ttg ggc ttt    931
Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser Leu Leu Gly Phe
                265                      270                      275

cga agc ttg gag atg aaa taa tattgtcaaa ttttaggcgt aactgtacaa       982
Arg Ser Leu Glu Met Lys  *
            280

aacttttgcc tagataattt gaaagtatat cttcaacttg tatgagaaat ttaactggtg 1042
aattataata tatagaattt gttttttaaa aaaaaaaaaa aaaaa                 1087
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<210> 10
<211> 282
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (13)...(116)
<223> Conserved domain

<400> 10
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Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1               5                  10                  15
Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ala Tyr Ile Lys Ala His
            20                  25                  30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
        35                  40                  45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
    50                  55                  60
Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65                  70                  75                  80
Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
                85                  90                  95
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
            100                 105                 110
Arg Arg Lys Leu Ile Asn Arg Gly Ile Asp Pro Thr Ser His Arg Pro
        115                 120                 125
Ile Gln Glu Ser Ser Ala Ser Gln Asp Ser Lys Pro Thr Gln Leu Glu
    130                 135                 140
Pro Val Thr Ser Asn Thr Ile Asn Ile Ser Phe Thr Ser Ala Pro Lys
145                 150                 155                 160
Val Glu Thr Phe His Glu Ser Ile Ser Phe Pro Gly Lys Ser Glu Lys
                165                 170                 175
Ile Ser Met Leu Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln
            180                 185                 190
Glu Lys Phe Pro Asp Leu Asn Leu Glu Leu Arg Ile Ser Leu Pro Asp
        195                 200                 205
Asp Val Asp Arg Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys
    210                 215                 220
Phe Lys Cys Ser Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly
225                 230                 235                 240
Arg Met Arg Cys Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met
                245                 250                 255
Ser Asn Gly Phe Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser
            260                 265                 270
Leu Leu Gly Phe Arg Ser Leu Glu Met Lys
        275                 280
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<210> 11
<211> 1747
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (503)...(1534)

<400> 11

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tgcaaaaaca ttttcttgtc tctcctctgc ccaaattttt tttctttcca ggaatatttc 60
ctagaaaaac ccaagcaaag ctttaacccc ttcctcctcc aaaagtagca tcttcctctt 120
tttctatttc tcctttcctc ttcttatctc tctctcgttt gtgaacgatt ccttaagaat 180
ataaccaaaa gccctttttct cctttcttca actttccggg aaaaatcttc acgcagcaag 240
gtttctctct cggctctcgc agtgtttttc gggccttttg ttctttctat aaaaaaaaaa 300
ttcgcgtcct ttaagaaaac tttttccacc tagagaagaa gaagagtatc actcttgttg 360
ttcaagtttc tctctttaat aaaaaatcca tctttattct ttgtcttctt tcctttttgc 420
tttccctaat ctctatgtta taaacacaca gagagaaaca aagtcacagt ctcgagtcaa 480
aaacagagaa tacgaaagaa aa atg gaa gcg gag aag aaa atg gtt cta ccg  532
                         Met Glu Ala Glu Lys Lys Met Val Leu Pro
                         1               5                   10

aga atc aaa ttc aca gag cac aaa acc aac acg aca aca atc gta tcg   580
Arg Ile Lys Phe Thr Glu His Lys Thr Asn Thr Thr Thr Ile Val Ser
                15                  20                  25

gag tta acc aac act cac caa acc agg att ctt cgt atc tca gtc act   628
Glu Leu Thr Asn Thr His Gln Thr Arg Ile Leu Arg Ile Ser Val Thr
            30                  35                  40

gac cca gac gct act gat tcc tcc agt gac gac gaa gaa gaa gaa cat   676
Asp Pro Asp Ala Thr Asp Ser Ser Ser Asp Asp Glu Glu Glu Glu His
        45                  50                  55

caa cgc ttt gtc tct aaa cgc cgt cgt gtt aag aag ttt gtc aac gaa   724
Gln Arg Phe Val Ser Lys Arg Arg Arg Val Lys Lys Phe Val Asn Glu
    60                  65                  70

gtc tat ctc gat tcc ggt gct gtt gtt act ggt agt tgt ggt caa atg   772
Val Tyr Leu Asp Ser Gly Ala Val Val Thr Gly Ser Cys Gly Gln Met
75                  80                  85                  90

gag tcg aag aag aga caa aag aga gcg gtt aaa tcg gag tct act gtt   820
Glu Ser Lys Lys Arg Gln Lys Arg Ala Val Lys Ser Glu Ser Thr Val
                95                  100                 105

tct ccg gtt gtt tca gcg acg acg act acg acg gga gag aag aag ttc   868
Ser Pro Val Val Ser Ala Thr Thr Thr Thr Thr Gly Glu Lys Lys Phe
            110                 115                 120

cga gga gtg aga cag cgt cca tgg gga aaa tgg gcg gcg gag ata aga   916
Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
        125                 130                 135

gat ccg ttg aaa cgt gta cgg ctc tgg tta ggt act tac aac acg gcg   964
Asp Pro Leu Lys Arg Val Arg Leu Trp Leu Gly Thr Tyr Asn Thr Ala
    140                 145                 150

gaa gaa gct gct atg gtt tac gat aac gcc gct att cag ctt cgt ggt   1012
Glu Glu Ala Ala Met Val Tyr Asp Asn Ala Ala Ile Gln Leu Arg Gly
155                 160                 165                 170

ccc gac gct ctg act aat ttc tca gtc act ccg aca aca gcg acg gag   1060
Pro Asp Ala Leu Thr Asn Phe Ser Val Thr Pro Thr Thr Ala Thr Glu
                175                 180                 185
```

```
aag aaa gcc cca cca ccg tct ccg gtg aag aag aag aag aag aaa aac    1108
Lys Lys Ala Pro Pro Pro Ser Pro Val Lys Lys Lys Lys Lys Lys Asn
            190                 195                 200

aac aaa agc aaa aaa tcc gtt act gct tct tcc tcc atc agc aga agc    1156
Asn Lys Ser Lys Lys Ser Val Thr Ala Ser Ser Ser Ile Ser Arg Ser
        205                 210                 215

agc agc aac gat tgt ctc tgc tct ccg gtg tct gtt ctc cga tct cct    1204
Ser Ser Asn Asp Cys Leu Cys Ser Pro Val Ser Val Leu Arg Ser Pro
    220                 225                 230

ttc gcc gtc gac gaa ttc tcc ggc att tct tca tca cca gtc gcg gcc    1252
Phe Ala Val Asp Glu Phe Ser Gly Ile Ser Ser Ser Pro Val Ala Ala
235                 240                 245                 250

gtt gta gtc aag gaa gag cca tcc atg aca acg gta tct gaa act ttc    1300
Val Val Val Lys Glu Glu Pro Ser Met Thr Thr Val Ser Glu Thr Phe
                255                 260                 265

tct gat ttc tcg gcg ccc ttg ttc tca gat gat gac gtg ttc gat ttc    1348
Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp Val Phe Asp Phe
            270                 275                 280

cgg agc tca gtg gtt ccc gac tat ctc ggc ggc gat tta ttt ggg gaa    1396
Arg Ser Ser Val Val Pro Asp Tyr Leu Gly Gly Asp Leu Phe Gly Glu
        285                 290                 295

gat cta ttc acg gcg gat atg tgt acg gat atg aac ttc gga ttc gat    1444
Asp Leu Phe Thr Ala Asp Met Cys Thr Asp Met Asn Phe Gly Phe Asp
    300                 305                 310

ttc gga tcc gga tta tcc agc tgg cac atg gag gac cat ttt caa gat    1492
Phe Gly Ser Gly Leu Ser Ser Trp His Met Glu Asp His Phe Gln Asp
315                 320                 325                 330

atc ggg gat cta ttc ggg tcg gat cct ctt tta gct gtt taa            1534
Ile Gly Asp Leu Phe Gly Ser Asp Pro Leu Leu Ala Val  *
                335                 340

taatatttta aataaataaa tagttatacc ggccgttact aaacggaacc ggagaaagtt 1594
ttgtataccg gtgacataaa atctcggtta tgttcgtaat ctttttttct ttgttatata 1654
taaaaatatg aatgaaactg aattaatgta agttaatggt gataattatt aacgttttaa 1714
gttttgaaaa aaaaaaaaaa aaaaaaaaaa aaa                              1747

<210> 12
<211> 343
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (119)...(186)
<223> Conserved domain

<400> 12
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His Lys Thr Asn Thr Thr Thr Ile Val Ser Glu Leu Thr Asn Thr His
            20                  25                  30
Gln Thr Arg Ile Leu Arg Ile Ser Val Thr Asp Pro Asp Ala Thr Asp
        35                  40                  45
Ser Ser Ser Asp Asp Glu Glu Glu Glu His Gln Arg Phe Val Ser Lys
    50                  55                  60
Arg Arg Arg Val Lys Lys Phe Val Asn Glu Val Tyr Leu Asp Ser Gly
65                  70                  75                  80
Ala Val Val Thr Gly Ser Cys Gly Gln Met Glu Ser Lys Lys Arg Gln
                85                  90                  95
Lys Arg Ala Val Lys Ser Glu Ser Thr Val Ser Pro Val Val Ser Ala
            100                 105                 110
Thr Thr Thr Thr Thr Gly Glu Lys Lys Phe Arg Gly Val Arg Gln Arg
        115                 120                 125
Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Leu Lys Arg Val
    130                 135                 140
Arg Leu Trp Leu Gly Thr Tyr Asn Thr Ala Glu Glu Ala Ala Met Val
145                 150                 155                 160
Tyr Asp Asn Ala Ala Ile Gln Leu Arg Gly Pro Asp Ala Leu Thr Asn
                165                 170                 175
Phe Ser Val Thr Pro Thr Thr Ala Thr Glu Lys Lys Ala Pro Pro Pro
            180                 185                 190
Ser Pro Val Lys Lys Lys Lys Lys Lys Asn Asn Lys Ser Lys Lys Ser
        195                 200                 205
Val Thr Ala Ser Ser Ser Ile Ser Arg Ser Ser Ser Asn Asp Cys Leu
    210                 215                 220
Cys Ser Pro Val Ser Val Leu Arg Ser Pro Phe Ala Val Asp Glu Phe
225                 230                 235                 240
Ser Gly Ile Ser Ser Ser Pro Val Ala Ala Val Val Val Lys Glu Glu
                245                 250                 255
Pro Ser Met Thr Thr Val Ser Glu Thr Phe Ser Asp Phe Ser Ala Pro
            260                 265                 270
Leu Phe Ser Asp Asp Asp Val Phe Asp Phe Arg Ser Ser Val Val Pro
        275                 280                 285
Asp Tyr Leu Gly Gly Asp Leu Phe Gly Glu Asp Leu Phe Thr Ala Asp
    290                 295                 300
Met Cys Thr Asp Met Asn Phe Gly Phe Asp Phe Gly Ser Gly Leu Ser
305                 310                 315                 320
Ser Trp His Met Glu Asp His Phe Gln Asp Ile Gly Asp Leu Phe Gly
                325                 330                 335
Ser Asp Pro Leu Leu Ala Val
            340
```

<210> 13
<211> 609
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(609)

<400> 13
atg gct gag aac aac aac aac aac ggc gac aac atg aac aac gac aac   48

```
Met Ala Glu Asn Asn Asn Asn Asn Gly Asp Asn Met Asn Asn Asp Asn
1               5                   10                  15

cac cag caa cca ccg tcg tac tcg cag ctg ccg ccg atg gca tca tcc      96
His Gln Gln Pro Pro Ser Tyr Ser Gln Leu Pro Pro Met Ala Ser Ser
            20                  25                  30

aac cct cag tta cgt aat tac tgg att gag cag atg gaa acc gtc tcg      144
Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
        35                  40                  45

gat ttc aaa aac cgt cag ctt cca ttg gct cga att aag aag atc atg      192
Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
    50                  55                  60

aag gct gat cca gat gtg cac atg gtc tcc gca gag gct ccg atc atc      240
Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
65                  70                  75                  80

ttc gca aag gct tgc gaa atg ttc atc gtt gat ctc acg atg cgg tcg      288
Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
                85                  90                  95

tgg ctc aaa gcc gag gag aac aaa cgc cac acg ctt cag aaa tcg gat      336
Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
            100                 105                 110

atc tcc aac gca gtg gct agc tct ttc acc tac gat ttc ctt ctt gat      384
Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
        115                 120                 125

gtt gtc cct aag gac gag tct atc gcc acc gct gat cct ggc ttt gtg      432
Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
    130                 135                 140

gct atg cca cat cct gac ggt gga gga gta ccg caa tat tat tat cca      480
Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
145                 150                 155                 160

ccg gga gtg gtg atg gga act cct atg gtt ggt agt gga atg tac gcg      528
Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
                165                 170                 175

cca tcg cag gcg tgg cca gca gcg gct ggt gac ggg gag gat gat gct      576
Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
            180                 185                 190

gag gat aat gga gga aac ggc ggc gga aat tga                          609
Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn  *
        195                 200

<210> 14
<211> 202
<212> PRT
<213> Arabidopsis thaliana
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<220>
<221> DOMAIN
<222> (70)...(133)
<223> Conserved domain

<400> 14
Met Ala Glu Asn Asn Asn Asn Asn Gly Asp Asn Met Asn Asn Asp Asn
1 5 10 15
His Gln Gln Pro Pro Ser Tyr Ser Gln Leu Pro Pro Met Ala Ser Ser
20 25 30
Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
35 40 45
Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
50 55 60
Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
65 70 75 80
Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
85 90 95
Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
100 105 110
Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
115 120 125
Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
130 135 140
Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
145 150 155 160
Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
165 170 175
Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
180 185 190
Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn
195 200

<210> 15
<211> 724
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (20)...(694)

<400> 15
catcttatcc aaagaaaaa atg aat cca ttt tac tct aca ttc cca gac tcg 52
Met Asn Pro Phe Tyr Ser Thr Phe Pro Asp Ser
1 5 10

ttt ctc tca atc tcc gat cat aga tct ccg gtt tca gac agt agt gag 100
Phe Leu Ser Ile Ser Asp His Arg Ser Pro Val Ser Asp Ser Ser Glu
15 20 25

tgt tca cca aag tta gct tca agt tgt cca aag aaa cga gct ggg agg 148
Cys Ser Pro Lys Leu Ala Ser Ser Cys Pro Lys Lys Arg Ala Gly Arg
30 35 40

aag aag ttt cgt gag aca cgt cat ccg att tac aga gga gtt cgt cag 196

```
Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln
     45                  50                  55

agg aat tct ggt aaa tgg gtt tgt gaa gtt aga gag cct aat aag aaa      244
Arg Asn Ser Gly Lys Trp Val Cys Glu Val Arg Glu Pro Asn Lys Lys
 60                  65                  70                  75

tct agg att tgg tta ggt act ttt ccg acg gtt gaa atg gct gct cgt      292
Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Val Glu Met Ala Ala Arg
                 80                  85                  90

gct cat gat gtt gct gct tta gct ctt cgt ggt cgc tct gct tgt ctc      340
Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys Leu
             95                 100                 105

aat ttc gct gat tct gct tgg cgg ctt cgt att cct gag act act tgt      388
Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Thr Thr Cys
        110                 115                 120

cct aag gag att cag aaa gct gcg tct gaa gct gca atg gcg ttt cag      436
Pro Lys Glu Ile Gln Lys Ala Ala Ser Glu Ala Ala Met Ala Phe Gln
    125                 130                 135

aat gag act acg acg gag gga tct aaa act gcg gcg gag gca gag gag      484
Asn Glu Thr Thr Thr Glu Gly Ser Lys Thr Ala Ala Glu Ala Glu Glu
140                 145                 150                 155

gcg gca ggg gag ggg gtg agg gag ggg gag agg agg gcg gag gag cag      532
Ala Ala Gly Glu Gly Val Arg Glu Gly Glu Arg Arg Ala Glu Glu Gln
                160                 165                 170

aat ggt ggt gtg ttt tat atg gat gat gag gcg ctt ttg ggg atg ccc      580
Asn Gly Gly Val Phe Tyr Met Asp Asp Glu Ala Leu Leu Gly Met Pro
            175                 180                 185

aac ttt ttt gag aat atg gcg gag ggg atg ctt ttg ccg ccg ccg gaa      628
Asn Phe Phe Glu Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Glu
        190                 195                 200

gtt ggc tgg aat cat aac gac ttt gac gga gtg ggt gac gtg tca ctc      676
Val Gly Trp Asn His Asn Asp Phe Asp Gly Val Gly Asp Val Ser Leu
    205                 210                 215

tgg agt ttt gac gag taa tttttggct ctttttctgg ataataagtt              724
Trp Ser Phe Asp Glu  *
220
```

<210> 16
<211> 224
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (51)...(118)

<223> Conserved domain

<400> 16
Met Asn Pro Phe Tyr Ser Thr Phe Pro Asp Ser Phe Leu Ser Ile Ser
1 5 10 15
Asp His Arg Ser Pro Val Ser Asp Ser Ser Glu Cys Ser Pro Lys Leu
20 25 30
Ala Ser Ser Cys Pro Lys Lys Arg Ala Gly Arg Lys Lys Phe Arg Glu
35 40 45
Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys
50 55 60
Trp Val Cys Glu Val Arg Glu Pro Asn Lys Lys Ser Arg Ile Trp Leu
65 70 75 80
Gly Thr Phe Pro Thr Val Glu Met Ala Ala Arg Ala His Asp Val Ala
85 90 95
Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser
100 105 110
Ala Trp Arg Leu Arg Ile Pro Glu Thr Thr Cys Pro Lys Glu Ile Gln
115 120 125
Lys Ala Ala Ser Glu Ala Ala Met Ala Phe Gln Asn Glu Thr Thr Thr
130 135 140
Glu Gly Ser Lys Thr Ala Ala Glu Ala Glu Glu Ala Ala Gly Glu Gly
145 150 155 160
Val Arg Glu Gly Glu Arg Arg Ala Glu Glu Gln Asn Gly Gly Val Phe
165 170 175
Tyr Met Asp Asp Glu Ala Leu Leu Gly Met Pro Asn Phe Phe Glu Asn
180 185 190
Met Ala Glu Gly Met Leu Leu Pro Pro Pro Glu Val Gly Trp Asn His
195 200 205
Asn Asp Phe Asp Gly Val Gly Asp Val Ser Leu Trp Ser Phe Asp Glu
210 215 220

<210> 17
<211> 653
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (38)...(607)

<400> 17
caaatcagaa aatatagagt ttgaaggaaa ctaaaag atg gta cat tcg agg aag 55
Met Val His Ser Arg Lys
1 5

ttc cga ggt gtc cgc cag cga caa tgg ggt tct tgg gtc tct gag att 103
Phe Arg Gly Val Arg Gln Arg Gln Trp Gly Ser Trp Val Ser Glu Ile
10 15 20

cgc cat cct cta ttg aag aga aga gtg tgg ctt gga act ttc gaa acg 151
Arg His Pro Leu Leu Lys Arg Arg Val Trp Leu Gly Thr Phe Glu Thr
25 30 35

gca gaa gcg gct gca aga gca tac gac caa gcg gct ctt cta atg aac 199
Ala Glu Ala Ala Ala Arg Ala Tyr Asp Gln Ala Ala Leu Leu Met Asn

```
    40                    45                    50

ggc caa aac gct aag acc aat ttc cct gtc gta aaa tca gag gaa ggc    247
Gly Gln Asn Ala Lys Thr Asn Phe Pro Val Val Lys Ser Glu Glu Gly
 55                 60                  65                  70

tcc gat cac gtt aaa gat gtt aac tct ccg ttg atg tca cca aag tca    295
Ser Asp His Val Lys Asp Val Asn Ser Pro Leu Met Ser Pro Lys Ser
                75                  80                  85

tta tct gag ctt ttg aac gct aag cta agg aag agc tgc aaa gac cta    343
Leu Ser Glu Leu Leu Asn Ala Lys Leu Arg Lys Ser Cys Lys Asp Leu
            90                  95                 100

acg cct tct ttg acg tgt ctc cgt ctt gat act gac agt tcc cac att    391
Thr Pro Ser Leu Thr Cys Leu Arg Leu Asp Thr Asp Ser Ser His Ile
        105                 110                 115

gga gtt tgg cag aaa cgg gcc ggg tcg aaa aca agt ccg act tgg gtc    439
Gly Val Trp Gln Lys Arg Ala Gly Ser Lys Thr Ser Pro Thr Trp Val
    120                 125                 130

atg cgc ctc gaa ctt ggg aac gta gtc aac gaa agt gcg gtt gac tta    487
Met Arg Leu Glu Leu Gly Asn Val Val Asn Glu Ser Ala Val Asp Leu
135                 140                 145                 150

ggg ttg act acg atg aac aaa caa aac gtt gag aaa gaa gaa gaa gaa    535
Gly Leu Thr Thr Met Asn Lys Gln Asn Val Glu Lys Glu Glu Glu Glu
                155                 160                 165

gaa gaa gct att att agt gat gag gat cag tta gct atg gag atg atc    583
Glu Glu Ala Ile Ile Ser Asp Glu Asp Gln Leu Ala Met Glu Met Ile
            170                 175                 180

gag gag ttg ctg aat tgg agt tga cttttgactt taacttgttg caagtccaca  637
Glu Glu Leu Leu Asn Trp Ser  *
        185

aggggtaagg gttttc                                                  653

<210> 18
<211> 768
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (58)...(657)

<400> 18
attactcatc atcaagttcc tactttctct ctgacaaaca tcacagagta agtaaga atg 60
                                                               Met
                                                                 1

gta cag acg aag aag ttc aga ggt gtc agg caa cgc cat tgg ggt tct    108
Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly Ser
                5                  10                  15
```

```
tgg gtc gct gag att cgt cat cct ctc ttg aaa cgg agg att tgg cta     156
Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp Leu
         20                  25                  30

ggg acg ttc gag acc gca gag gag gca gca aga gca tac gac gag gcc     204
Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu Ala
     35                  40                  45

gcc gtt tta atg agc ggc cgc aac gcc aaa acc aac ttt ccc ctc aac     252
Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu Asn
 50                  55                  60                  65

aac aac aac acc gga gaa act tcc gag ggc aaa acc gat att tca gct     300
Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser Ala
                 70                  75                  80

tcg tcc aca atg tca tcc tca aca tca tct tca tcg ctc tct tcc atc     348
Ser Ser Thr Met Ser Ser Ser Thr Ser Ser Ser Ser Leu Ser Ser Ile
             85                  90                  95

ctc agc gcc aaa ctg agg aaa tgc tgc aag tct cct tcc cca tcc ctc     396
Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser Leu
        100                 105                 110

acc tgc ctc cgt ctt gac aca gcc agc tcc cat atc ggc gtc tgg cag     444
Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp Gln
    115                 120                 125

aaa cgg gcc ggt tca aag tct gac tcc agc tgg gtc atg acg gtg gag     492
Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val Glu
130                 135                 140                 145

cta ggt ccc gca agc tcc tcc caa gag act act agt aaa gct tca caa     540
Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser Gln
                150                 155                 160

gac gct att ctt gct ccg acc act gaa gtt gaa att ggt ggc agc aga     588
Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser Arg
            165                 170                 175

gaa gaa gta ttg gat gag gaa gaa aag gtt gct ttg caa atg ata gag     636
Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile Glu
        180                 185                 190

gag ctt ctc aat aca aac taa atcttatttg cttatatata tgtacctatt        687
Glu Leu Leu Asn Thr Asn  *
    195

ttcattgctg atttacagcc aaaataatca attataccgt gtattttata gatgttttat 747
attaaaaggt tgttagatat a                                           768

<210> 19
<211> 189
<212> PRT
<213> Arabidopsis thaliana
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<220>
<221> DOMAIN
<222> (4)...(71)
<223> Conserved domain

<400> 19
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Met Val His Ser Arg Lys Phe Arg Gly Val Arg Gln Arg Gln Trp Gly
 1               5                  10                  15
Ser Trp Val Ser Glu Ile Arg His Pro Leu Leu Lys Arg Arg Val Trp
            20                  25                  30
Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Gln
        35                  40                  45
Ala Ala Leu Leu Met Asn Gly Gln Asn Ala Lys Thr Asn Phe Pro Val
    50                  55                  60
Val Lys Ser Glu Glu Gly Ser Asp His Val Lys Asp Val Asn Ser Pro
65                  70                  75                  80
Leu Met Ser Pro Lys Ser Leu Ser Glu Leu Leu Asn Ala Lys Leu Arg
                85                  90                  95
Lys Ser Cys Lys Asp Leu Thr Pro Ser Leu Thr Cys Leu Arg Leu Asp
            100                 105                 110
Thr Asp Ser Ser His Ile Gly Val Trp Gln Lys Arg Ala Gly Ser Lys
        115                 120                 125
Thr Ser Pro Thr Trp Val Met Arg Leu Glu Leu Gly Asn Val Val Asn
    130                 135                 140
Glu Ser Ala Val Asp Leu Gly Leu Thr Thr Met Asn Lys Gln Asn Val
145                 150                 155                 160
Glu Lys Glu Glu Glu Glu Glu Glu Ala Ile Ile Ser Asp Glu Asp Gln
                165                 170                 175
Leu Ala Met Glu Met Ile Glu Glu Leu Leu Asn Trp Ser
            180                 185
```

<210> 20
<211> 199
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (4)...(71)
<223> Conserved domain

<400> 20
```
Met Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly
 1               5                  10                  15
Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp
            20                  25                  30
Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu
        35                  40                  45
Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu
    50                  55                  60
Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser
65                  70                  75                  80
Ala Ser Ser Thr Met Ser Ser Ser Thr Ser Ser Ser Ser Leu Ser Ser
                85                  90                  95
Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser
            100                 105                 110
```

Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp
115 120 125
Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val
130 135 140
Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser
145 150 155 160
Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser
165 170 175
Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile
180 185 190
Glu Glu Leu Leu Asn Thr Asn
195

<210> 21
<211> 1011
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (213)...(833)

<400> 21
aaagttattg atagtttctg ttacttatta atttttaagg ttatgtgtat tattaccaat 60
tggaggacta tatagtcgca agtctcaacc ctataaaaga aaacattcgt cgatcatctt 120
cccgcctcga gtatctctct ctctctctct cttctctgtt ttctttattg attgcataga 180
caaaaataca cacatacaca acagaaagaa ag atg gag acg acg atg aag aag 233
Met Glu Thr Thr Met Lys Lys
1 5

aaa ggg aga gtg aaa gcg aca ata acg tca cag aaa gaa gaa gaa gga 281
Lys Gly Arg Val Lys Ala Thr Ile Thr Ser Gln Lys Glu Glu Glu Gly
10 15 20

aca gtg aga aaa gga cct tgg act atg gaa gaa gat ttc atc ctc ttt 329
Thr Val Arg Lys Gly Pro Trp Thr Met Glu Glu Asp Phe Ile Leu Phe
25 30 35

aat tac atc ctt aat cat ggt gaa ggt ctt tgg aac tct gtc gcc aaa 377
Asn Tyr Ile Leu Asn His Gly Glu Gly Leu Trp Asn Ser Val Ala Lys
40 45 50 55

gcc tct ggt cta aaa cgt act gga aaa agt tgt cgg ctc cgg tgg ctg 425
Ala Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu
60 65 70

aac tat ctc cga cca gat gtg cgg cga ggg aac ata acc gaa gaa gaa 473
Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Glu Glu Glu
75 80 85

cag ctt ttg atc att cag ctt cat gct aag ctt gga aac agg tgg tcg 521
Gln Leu Leu Ile Ile Gln Leu His Ala Lys Leu Gly Asn Arg Trp Ser
90 95 100

aag att gcg aag cat ctt ccg gga aga acg gac aac gag ata aag aac 569
Lys Ile Ala Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn

```
    105                 110                 115

ttc tgg agg aca aag att cag aga cac atg aaa gtg tca tcg gaa aat    617
Phe Trp Arg Thr Lys Ile Gln Arg His Met Lys Val Ser Ser Glu Asn
120                 125                 130                 135

atg atg aat cat caa cat cat tgt tcg gga aac tca cag agc tcg ggg    665
Met Met Asn His Gln His His Cys Ser Gly Asn Ser Gln Ser Ser Gly
                140                 145                 150

atg acg acg caa ggc agc tcc ggc aaa gcc ata gac acg gct gag agc    713
Met Thr Thr Gln Gly Ser Ser Gly Lys Ala Ile Asp Thr Ala Glu Ser
            155                 160                 165

ttc tct cag gcg aag acg acg acg ttt aat gtg gtg gaa caa cag tca    761
Phe Ser Gln Ala Lys Thr Thr Thr Phe Asn Val Val Glu Gln Gln Ser
        170                 175                 180

aac gag aat tac tgg aac gtt gaa gat ctg tgg ccc gtc cac ttg ctt    809
Asn Glu Asn Tyr Trp Asn Val Glu Asp Leu Trp Pro Val His Leu Leu
    185                 190                 195

aat ggt gac cac cat gtg att taa gatatatata tagacctcct atacatttat   863
Asn Gly Asp His His Val Ile  *
200                 205

atgccccagc tgggtttttt tgtatggtac gttatttggt ttttctattg ctgaaatgtc 923
gttgcattta atttacatac gaaaagtgca ttaaatcatt aaatcttcaa tacatatgga 983
ggtggtgttt gagtaaaaaa aaaaaaaa                                    1011

<210> 22
<211> 206
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (26)...(130)
<223> Conserved domain

<400> 22
Met Glu Thr Thr Met Lys Lys Lys Gly Arg Val Lys Ala Thr Ile Thr
 1               5                  10                  15
Ser Gln Lys Glu Glu Glu Gly Thr Val Arg Lys Gly Pro Trp Thr Met
            20                  25                  30
Glu Glu Asp Phe Ile Leu Phe Asn Tyr Ile Leu Asn His Gly Glu Gly
        35                  40                  45
Leu Trp Asn Ser Val Ala Lys Ala Ser Gly Leu Lys Arg Thr Gly Lys
    50                  55                  60
Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg
65                  70                  75                  80
Gly Asn Ile Thr Glu Glu Glu Gln Leu Leu Ile Ile Gln Leu His Ala
                85                  90                  95
Lys Leu Gly Asn Arg Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg
            100                 105                 110
Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr Lys Ile Gln Arg His
        115                 120                 125
```

```
Met Lys Val Ser Ser Glu Asn Met Met Asn His Gln His His Cys Ser
    130                 135                 140
Gly Asn Ser Gln Ser Ser Gly Met Thr Thr Gln Gly Ser Ser Gly Lys
145                 150                 155                 160
Ala Ile Asp Thr Ala Glu Ser Phe Ser Gln Ala Lys Thr Thr Thr Phe
                165                 170                 175
Asn Val Val Glu Gln Gln Ser Asn Glu Asn Tyr Trp Asn Val Glu Asp
            180                 185                 190
Leu Trp Pro Val His Leu Leu Asn Gly Asp His His Val Ile
        195                 200                 205
```

<210> 23
<211> 1072
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (87)...(977)

<400> 23

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aaaagataac gtagccatta acttttatgc attaactcct tcatttcttt ttgtgctcgt 60
ttggttgaga gagagagagg ctatat atg atg ttc caa caa gat tac cct cat  113
                             Met Met Phe Gln Gln Asp Tyr Pro His
                              1               5

ggc ttt tca ctc gtg gaa aca tcc tta agt tac gaa atg ttg gat tac   161
Gly Phe Ser Leu Val Glu Thr Ser Leu Ser Tyr Glu Met Leu Asp Tyr
 10                 15                  20                  25

ttt caa aac atc gtc gtt tcg aac tct gaa gac gtg gcg tca cag caa   209
Phe Gln Asn Ile Val Val Ser Asn Ser Glu Asp Val Ala Ser Gln Gln
                30                  35                  40

aat tcc att tcg tcc tct tct tat tca tca gcg aca ctc tcc tgc tcc   257
Asn Ser Ile Ser Ser Ser Ser Tyr Ser Ser Ala Thr Leu Ser Cys Ser
            45                  50                  55

ata aca gag caa aaa tct cac tta act gaa aag tta tct cct cta cga   305
Ile Thr Glu Gln Lys Ser His Leu Thr Glu Lys Leu Ser Pro Leu Arg
        60                  65                  70

gaa aga tat ggt tgc ggt gac ttt ctg tcg cgg aag agg aga agg aga   353
Glu Arg Tyr Gly Cys Gly Asp Phe Leu Ser Arg Lys Arg Arg Arg Arg
    75                  80                  85

agt gaa aaa acg att gta gat aaa gag aat caa agg atg aat cac att   401
Ser Glu Lys Thr Ile Val Asp Lys Glu Asn Gln Arg Met Asn His Ile
 90                 95                  100                 105

gcc gtc gag cgt aac cgg aga aaa cag atg aat cat ttt ctg tct atc   449
Ala Val Glu Arg Asn Arg Arg Lys Gln Met Asn His Phe Leu Ser Ile
                110                 115                 120

ctc aag tct atg atg cct ctc tct tat tct caa cct aat gac caa gca   497
Leu Lys Ser Met Met Pro Leu Ser Tyr Ser Gln Pro Asn Asp Gln Ala
```

```
            125                 130                 135

tca atc ata gaa ggg acc att agc tat ctg aag aag cta gaa caa cgt    545
Ser Ile Ile Glu Gly Thr Ile Ser Tyr Leu Lys Lys Leu Glu Gln Arg
        140                 145                 150

ctc caa tct ctc gaa gcc caa tta aaa gct act aaa ctc aat caa tca    593
Leu Gln Ser Leu Glu Ala Gln Leu Lys Ala Thr Lys Leu Asn Gln Ser
    155                 160                 165

cca aat ata ttt tcc gac ttc ttc atg ttc cct caa tac tcc acc gcc    641
Pro Asn Ile Phe Ser Asp Phe Phe Met Phe Pro Gln Tyr Ser Thr Ala
170                 175                 180                 185

act gcc act gcc acc gcc act gcc tcc tca tcc tcc tcg agc cac cac    689
Thr Ala Thr Ala Thr Ala Thr Ala Ser Ser Ser Ser Ser Ser His His
                190                 195                 200

cat cac aag cga cta gag gtg gtt gct gac gtg gag gtt aca atg gta    737
His His Lys Arg Leu Glu Val Val Ala Asp Val Glu Val Thr Met Val
            205                 210                 215

gaa aga cat gcc aac att aaa gtg tta acg aag aca cag cca aga ttg    785
Glu Arg His Ala Asn Ile Lys Val Leu Thr Lys Thr Gln Pro Arg Leu
        220                 225                 230

ctc ttc aag att atc aat gag ttt aac tct tta ggt tta agt act ctt    833
Leu Phe Lys Ile Ile Asn Glu Phe Asn Ser Leu Gly Leu Ser Thr Leu
    235                 240                 245

cat ctc aac ctc aca act tcc aaa gac atg tct ctc ttc act ttt agc    881
His Leu Asn Leu Thr Thr Ser Lys Asp Met Ser Leu Phe Thr Phe Ser
250                 255                 260                 265

gtc aag gta gag gca gat tgt caa ttg acg cct tct ggt aat gag gtc    929
Val Lys Val Glu Ala Asp Cys Gln Leu Thr Pro Ser Gly Asn Glu Val
                270                 275                 280

gca aat acg gtg cat gaa gtc gtt aga aga gtt cac aag gaa cgt tga    977
Ala Asn Thr Val His Glu Val Val Arg Arg Val His Lys Glu Arg  *
            285                 290                 295

attttgttta catactagct aactttgaaa ttctatttta ttgtataaac aatctcttat 1037
gtgtgtaatt tacatatata caattaatta acatt                            1072

&lt;210&gt; 24
&lt;211&gt; 296
&lt;212&gt; PRT
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; DOMAIN
&lt;222&gt; (92)...(161)
&lt;223&gt; Conserved domain

&lt;400&gt; 24
Met Met Phe Gln Gln Asp Tyr Pro His Gly Phe Ser Leu Val Glu Thr
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1 5 10 15
Ser Leu Ser Tyr Glu Met Leu Asp Tyr Phe Gln Asn Ile Val Val Ser
20 25 30
Asn Ser Glu Asp Val Ala Ser Gln Gln Asn Ser Ile Ser Ser Ser Ser
35 40 45
Tyr Ser Ser Ala Thr Leu Ser Cys Ser Ile Thr Glu Gln Lys Ser His
50 55 60
Leu Thr Glu Lys Leu Ser Pro Leu Arg Glu Arg Tyr Gly Cys Gly Asp
65 70 75 80
Phe Leu Ser Arg Lys Arg Arg Arg Arg Ser Glu Lys Thr Ile Val Asp
85 90 95
Lys Glu Asn Gln Arg Met Asn His Ile Ala Val Glu Arg Asn Arg Arg
100 105 110
Lys Gln Met Asn His Phe Leu Ser Ile Leu Lys Ser Met Met Pro Leu
115 120 125
Ser Tyr Ser Gln Pro Asn Asp Gln Ala Ser Ile Ile Glu Gly Thr Ile
130 135 140
Ser Tyr Leu Lys Lys Leu Glu Gln Arg Leu Gln Ser Leu Glu Ala Gln
145 150 155 160
Leu Lys Ala Thr Lys Leu Asn Gln Ser Pro Asn Ile Phe Ser Asp Phe
165 170 175
Phe Met Phe Pro Gln Tyr Ser Thr Ala Thr Ala Thr Ala Thr Ala Thr
180 185 190
Ala Ser Ser Ser Ser Ser Ser His His His His Lys Arg Leu Glu Val
195 200 205
Val Ala Asp Val Glu Val Thr Met Val Glu Arg His Ala Asn Ile Lys
210 215 220
Val Leu Thr Lys Thr Gln Pro Arg Leu Leu Phe Lys Ile Ile Asn Glu
225 230 235 240
Phe Asn Ser Leu Gly Leu Ser Thr Leu His Leu Asn Leu Thr Thr Ser
245 250 255
Lys Asp Met Ser Leu Phe Thr Phe Ser Val Lys Val Glu Ala Asp Cys
260 265 270
Gln Leu Thr Pro Ser Gly Asn Glu Val Ala Asn Thr Val His Glu Val
275 280 285
Val Arg Arg Val His Lys Glu Arg
290 295

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<211> 2209
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (186)...(1793)

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ctttgaatgt gactcaggat agagagaggg cgagacagat aaagagagct tgaggaagga 60
tttaagcaga tctgcaagaa acactctctc agtgtttact ttttttccgt agaatcaaac 120
cggcggcgac agtgacggcg gcgaaaagcg gcggtgttgg ccgcaaaaac gatgcaaaac 180
cagct atg gtc att acc gct aac gat tta tca aaa tgg gaa aat ttt cct 230
Met Val Ile Thr Ala Asn Asp Leu Ser Lys Trp Glu Asn Phe Pro
1 5 10 15

aaa gga ctt aag gtt ctt ctt ctc ctc aac ggc tgt gac agc gac gga 278

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Lys Gly Leu Lys Val Leu Leu Leu Leu Asn Gly Cys Asp Ser Asp Gly
                20                  25                  30

gat ggc tcc tca gcc gcc gag act cga tca gag ctc gaa tca atg gac    326
Asp Gly Ser Ser Ala Ala Glu Thr Arg Ser Glu Leu Glu Ser Met Asp
            35                  40                  45

tat atc gtt act aca ttc acc gat gaa act gaa gca ctc tct gcg gtt    374
Tyr Ile Val Thr Thr Phe Thr Asp Glu Thr Glu Ala Leu Ser Ala Val
        50                  55                  60

gtc aag aac ccg gag agc ttc cac att gcc atc gtc gag gtg aat atg    422
Val Lys Asn Pro Glu Ser Phe His Ile Ala Ile Val Glu Val Asn Met
    65                  70                  75

agc gct gag agt gag agt ttc aag ttt ctt gag gct gcc aaa gac gtt    470
Ser Ala Glu Ser Glu Ser Phe Lys Phe Leu Glu Ala Ala Lys Asp Val
80                  85                  90                  95

ctt cct act ata atg att tca acc gat cat tgc atc act act aca atg    518
Leu Pro Thr Ile Met Ile Ser Thr Asp His Cys Ile Thr Thr Thr Met
                100                 105                 110

aaa tgc ata gcg ctt ggt gca gtt gag ttc cta caa aaa ccg ctc tca    566
Lys Cys Ile Ala Leu Gly Ala Val Glu Phe Leu Gln Lys Pro Leu Ser
            115                 120                 125

ccg gag aaa tta aag aac att tgg cag cat gtt gtt cat aag gca ttc    614
Pro Glu Lys Leu Lys Asn Ile Trp Gln His Val Val His Lys Ala Phe
        130                 135                 140

aat gat ggt gga agt aat gtt tcg ata tca ctt aag cca gtg aaa gaa    662
Asn Asp Gly Gly Ser Asn Val Ser Ile Ser Leu Lys Pro Val Lys Glu
    145                 150                 155

tcc gtt gtc tcg atg ctt cat ctt gag acc gac atg aca atc gag gag    710
Ser Val Val Ser Met Leu His Leu Glu Thr Asp Met Thr Ile Glu Glu
160                 165                 170                 175

aaa gat cca gcg cca tca aca ccg caa ttg aaa caa gat tca cgg tta    758
Lys Asp Pro Ala Pro Ser Thr Pro Gln Leu Lys Gln Asp Ser Arg Leu
                180                 185                 190

cta gac ggt gat tgc caa gag aac ata aat ttc tcg atg gaa aat gta    806
Leu Asp Gly Asp Cys Gln Glu Asn Ile Asn Phe Ser Met Glu Asn Val
            195                 200                 205

aat tcc tcg acc gag aaa gat aac atg gaa gat cat caa gac atc ggt    854
Asn Ser Ser Thr Glu Lys Asp Asn Met Glu Asp His Gln Asp Ile Gly
        210                 215                 220

gaa tct aaa tca gtc gac act aca aac cgc aaa tta gat gac gac aaa    902
Glu Ser Lys Ser Val Asp Thr Thr Asn Arg Lys Leu Asp Asp Asp Lys
    225                 230                 235

gtg gtt gtc aaa gaa gag aga gga gac agt gaa aaa gaa gaa gaa ggt    950
Val Val Val Lys Glu Glu Arg Gly Asp Ser Glu Lys Glu Glu Glu Gly
```

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240                 245                 250                 255

gaa acc gga gat ctc ata agc gag aag aca gat tca gtt gat att cat    998
Glu Thr Gly Asp Leu Ile Ser Glu Lys Thr Asp Ser Val Asp Ile His
                260                 265                 270

aag aaa gaa gat gag act aaa ccg att aat aaa tca tcc ggg atc aag   1046
Lys Lys Glu Asp Glu Thr Lys Pro Ile Asn Lys Ser Ser Gly Ile Lys
            275                 280                 285

aac gtg tct ggt aac aaa act agt cga aag aag gtg gat tgg aca cca   1094
Asn Val Ser Gly Asn Lys Thr Ser Arg Lys Lys Val Asp Trp Thr Pro
        290                 295                 300

gag ctg cac aag aag ttt gtg caa gca gtt gag caa ctc ggc gtt gat   1142
Glu Leu His Lys Lys Phe Val Gln Ala Val Glu Gln Leu Gly Val Asp
    305                 310                 315

caa gcg ata ccc tcg cgg att ctt gag ttg atg aaa gta ggc acc tta   1190
Gln Ala Ile Pro Ser Arg Ile Leu Glu Leu Met Lys Val Gly Thr Leu
320                 325                 330                 335

aca aga cac aat gta gct agt cac ctt cag aaa ttt cgg cag cat agg   1238
Thr Arg His Asn Val Ala Ser His Leu Gln Lys Phe Arg Gln His Arg
                340                 345                 350

aag aat att ctt cca aag gat gat cat aac cat aga tgg ata caa tct   1286
Lys Asn Ile Leu Pro Lys Asp Asp His Asn His Arg Trp Ile Gln Ser
            355                 360                 365

aga gag aac cat aga cca aat caa cgt aat tat aac gtt ttt caa cag   1334
Arg Glu Asn His Arg Pro Asn Gln Arg Asn Tyr Asn Val Phe Gln Gln
        370                 375                 380

caa cac cgt ccc gtg atg gct tat ccc gtt tgg ggt ctt ccc ggt gtt   1382
Gln His Arg Pro Val Met Ala Tyr Pro Val Trp Gly Leu Pro Gly Val
    385                 390                 395

tat ccg cca gga gcg att cca cct ttg tgg cca ccg ccg ctg cag tcc   1430
Tyr Pro Pro Gly Ala Ile Pro Pro Leu Trp Pro Pro Pro Leu Gln Ser
400                 405                 410                 415

att ggt caa cca cct ccg tgg cat tgg aaa cca cct tat cca acg gtg   1478
Ile Gly Gln Pro Pro Pro Trp His Trp Lys Pro Pro Tyr Pro Thr Val
                420                 425                 430

agc ggt aat gca tgg ggt tgt ccg gtt gga ccg cct gtg acc gga tca   1526
Ser Gly Asn Ala Trp Gly Cys Pro Val Gly Pro Pro Val Thr Gly Ser
            435                 440                 445

tat att act cct tcg aat act acc gcc ggc gga ttt caa tat ccc aac   1574
Tyr Ile Thr Pro Ser Asn Thr Thr Ala Gly Gly Phe Gln Tyr Pro Asn
        450                 455                 460

gga gct gaa acc ggc ttc aaa ata atg ccg gcg agt cag ccg gac gag   1622
Gly Ala Glu Thr Gly Phe Lys Ile Met Pro Ala Ser Gln Pro Asp Glu
    465                 470                 475
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gaa atg tta gat caa gtg gtt aaa gaa gcg ata agc aaa ccg tgg ctg 1670
Glu Met Leu Asp Gln Val Val Lys Glu Ala Ile Ser Lys Pro Trp Leu
480 485 490 495

ccg cta ccg ctc ggg cta aaa ccg ccg tcc gcg gag agc gtt ttg gct 1718
Pro Leu Pro Leu Gly Leu Lys Pro Pro Ser Ala Glu Ser Val Leu Ala
500 505 510

gag cta acg cgt caa ggc atc tca gcc gtc cct tct tct tct tgt cta 1766
Glu Leu Thr Arg Gln Gly Ile Ser Ala Val Pro Ser Ser Ser Cys Leu
515 520 525

atc aac ggc tct cat cgt ctc cgc tga cgtgtccatg atgaaacaga 1813
Ile Asn Gly Ser His Arg Leu Arg *
530 535

acccgcagat atgatgacgt catgcgtggc gtacttgtcc gtgtctgacg atccgaagcg 1873
ggaactgatt cggatcctga gagttgtttt ttaattgttg tttttaattt tttgttgtca 1933
taaaaacatt tgtctctatt ggtattatta aagaagatcg gacggtggag atagaggcaa 1993
cgatgttagt ctgaggacca caagtggact ctgcggctgt aagtagatct cggacacggg 2053
attttgacaa gtcggaatct gacgtgtgtg cgtactcgct tttgtgggtt gtcgagaatt 2113
taatagttga cactgtttta ggtggatatg agatatgatg atgataataa taaaaaggta 2173
caactcaaag attccgtgat gaaaaaaaaa aaaaaa 2209

<210> 26
<211> 535
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (301)...(349)
<223> Conserved domain

<400> 26
Met Val Ile Thr Ala Asn Asp Leu Ser Lys Trp Glu Asn Phe Pro Lys
1 5 10 15
Gly Leu Lys Val Leu Leu Leu Leu Asn Gly Cys Asp Ser Asp Gly Asp
20 25 30
Gly Ser Ser Ala Ala Glu Thr Arg Ser Glu Leu Glu Ser Met Asp Tyr
35 40 45
Ile Val Thr Thr Phe Thr Asp Glu Thr Glu Ala Leu Ser Ala Val Val
50 55 60
Lys Asn Pro Glu Ser Phe His Ile Ala Ile Val Glu Val Asn Met Ser
65 70 75 80
Ala Glu Ser Glu Ser Phe Lys Phe Leu Glu Ala Ala Lys Asp Val Leu
85 90 95
Pro Thr Ile Met Ile Ser Thr Asp His Cys Ile Thr Thr Thr Met Lys
100 105 110
Cys Ile Ala Leu Gly Ala Val Glu Phe Leu Gln Lys Pro Leu Ser Pro
115 120 125
Glu Lys Leu Lys Asn Ile Trp Gln His Val Val His Lys Ala Phe Asn
130 135 140
Asp Gly Gly Ser Asn Val Ser Ile Ser Leu Lys Pro Val Lys Glu Ser
145 150 155 160
Val Val Ser Met Leu His Leu Glu Thr Asp Met Thr Ile Glu Glu Lys

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                    165                     170                     175
Asp Pro Ala Pro Ser Thr Pro Gln Leu Lys Gln Asp Ser Arg Leu Leu
            180                     185                     190
Asp Gly Asp Cys Gln Glu Asn Ile Asn Phe Ser Met Glu Asn Val Asn
        195                     200                     205
Ser Ser Thr Glu Lys Asp Asn Met Glu Asp His Gln Asp Ile Gly Glu
    210                     215                     220
Ser Lys Ser Val Asp Thr Thr Asn Arg Lys Leu Asp Asp Asp Lys Val
225                     230                     235                     240
Val Val Lys Glu Glu Arg Gly Asp Ser Glu Lys Glu Glu Glu Gly Glu
                245                     250                     255
Thr Gly Asp Leu Ile Ser Glu Lys Thr Asp Ser Val Asp Ile His Lys
            260                     265                     270
Lys Glu Asp Glu Thr Lys Pro Ile Asn Lys Ser Ser Gly Ile Lys Asn
        275                     280                     285
Val Ser Gly Asn Lys Thr Ser Arg Lys Lys Val Asp Trp Thr Pro Glu
    290                     295                     300
Leu His Lys Lys Phe Val Gln Ala Val Glu Gln Leu Gly Val Asp Gln
305                     310                     315                     320
Ala Ile Pro Ser Arg Ile Leu Glu Leu Met Lys Val Gly Thr Leu Thr
                325                     330                     335
Arg His Asn Val Ala Ser His Leu Gln Lys Phe Arg Gln His Arg Lys
            340                     345                     350
Asn Ile Leu Pro Lys Asp Asp His Asn His Arg Trp Ile Gln Ser Arg
        355                     360                     365
Glu Asn His Arg Pro Asn Gln Arg Asn Tyr Asn Val Phe Gln Gln Gln
    370                     375                     380
His Arg Pro Val Met Ala Tyr Pro Val Trp Gly Leu Pro Gly Val Tyr
385                     390                     395                     400
Pro Pro Gly Ala Ile Pro Pro Leu Trp Pro Pro Pro Leu Gln Ser Ile
                405                     410                     415
Gly Gln Pro Pro Pro Trp His Trp Lys Pro Pro Tyr Pro Thr Val Ser
            420                     425                     430
Gly Asn Ala Trp Gly Cys Pro Val Gly Pro Pro Val Thr Gly Ser Tyr
        435                     440                     445
Ile Thr Pro Ser Asn Thr Thr Ala Gly Gly Phe Gln Tyr Pro Asn Gly
    450                     455                     460
Ala Glu Thr Gly Phe Lys Ile Met Pro Ala Ser Gln Pro Asp Glu Glu
465                     470                     475                     480
Met Leu Asp Gln Val Val Lys Glu Ala Ile Ser Lys Pro Trp Leu Pro
                485                     490                     495
Leu Pro Leu Gly Leu Lys Pro Pro Ser Ala Glu Ser Val Leu Ala Glu
            500                     505                     510
Leu Thr Arg Gln Gly Ile Ser Ala Val Pro Ser Ser Ser Cys Leu Ile
        515                     520                     525
Asn Gly Ser His Arg Leu Arg
    530                     535
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<210> 27
<211> 890
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (108)...(806)

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<400> 27
cattcaaaaa catcatatat atacacaaac acactttgat acaacaaaaa aaaacagaac 60
acaaacaaaa acacattgta acattagttt aagcattaag cttcttt atg tcg aat   116
                                                    Met Ser Asn
                                                    1

aat aat aat tct ccg acc acc gtg aat caa gaa acg acg acg tct cgt   164
Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr Thr Ser Arg
    5                   10                  15

gaa gtc tca atc aca ttg cct act gat caa tct cct caa acc tca cca   212
Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln Thr Ser Pro
20                  25                  30                  35

gga tca tct tct tct cct tca ccg aga cct tcc ggt gga tca ccg gcg   260
Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly Ser Pro Ala
                40                  45                  50

aga aga acg gcg act gga tta tcc ggc aag cac tct att ttc agg ggg   308
Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile Phe Arg Gly
            55                  60                  65

att cga cta cgt aac gga aaa tgg gta tcg gag att aga gag cca cgt   356
Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg
        70                  75                  80

aaa acg aca aga att tgg ctc ggg act tat ccg gta ccg gag atg gct   404
Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro Glu Met Ala
    85                  90                  95

gcc gcc gct tac gac gtg gct gcg tta gct tta aaa gga ccc gac gcc   452
Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Pro Asp Ala
100                 105                 110                 115

gtt ttg aat ttt cct ggt tta gct ttg act tac gtg gct ccg gtt tca   500
Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala Pro Val Ser
                120                 125                 130

aac tct gct gcg gat ata aga gcg gct gct agt aga gca gcg gag atg   548
Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala Ala Glu Met
            135                 140                 145

aag caa ccg gat cag ggt ggg gat gag aag gta ttg gaa ccg gtt caa   596
Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val Gln
        150                 155                 160

ccc ggc aaa gag gaa gaa tta gaa gaa gtg tcg tgt aac tcg tgt tcg   644
Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn Ser Cys Ser
    165                 170                 175

ttg gag ttt atg gat gag gaa gcg atg ttg aat atg ccg act ttg ttg   692
Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu Leu
180                 185                 190                 195

acg gag atg gct gaa ggg atg ttg atg agt cca ccg aga atg atg ata   740
Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met Ile
```

```
                200                 205                 210

cat ccg acg atg gaa gat gat tcg ccg gag aat cat gaa gga gat aat      788
His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp Asn
            215                 220                 225

ctt tgg agt tat aaa tga atccattgaa gctgctctct tttttattgt             836
Leu Trp Ser Tyr Lys  *
        230

tttccggtcg aatgagattt tcccccttttt ttttttctt tttgggtcgc tgtt          890

<210> 28
<211> 232
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (62)...(128)
<223> Conserved domain

<400> 28
Met Ser Asn Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr
 1               5                  10                  15
Thr Ser Arg Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln
            20                  25                  30
Thr Ser Pro Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly
        35                  40                  45
Ser Pro Ala Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile
    50                  55                  60
Phe Arg Gly Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg
65                  70                  75                  80
Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro
                85                  90                  95
Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly
            100                 105                 110
Pro Asp Ala Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala
        115                 120                 125
Pro Val Ser Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala
    130                 135                 140
Ala Glu Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu
145                 150                 155                 160
Pro Val Gln Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn
                165                 170                 175
Ser Cys Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro
            180                 185                 190
Thr Leu Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg
        195                 200                 205
Met Met Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu
    210                 215                 220
Gly Asp Asn Leu Trp Ser Tyr Lys
225                 230


<210> 29
<211> 720
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<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(720)

<400> 29
atg ggg aat aga aga gca cca tgc tgt gac aaa agc caa gtg aag aga 48
Met Gly Asn Arg Arg Ala Pro Cys Cys Asp Lys Ser Gln Val Lys Arg
1 5 10 15

ggg cca tgg agt gat gaa gaa agt gaa aga ctc aga tct ttt atc ctc 96
Gly Pro Trp Ser Asp Glu Glu Ser Glu Arg Leu Arg Ser Phe Ile Leu
20 25 30

aaa aat ggt cat caa aat tgg cga tct ctt ccc aaa ctc gct gga ttg 144
Lys Asn Gly His Gln Asn Trp Arg Ser Leu Pro Lys Leu Ala Gly Leu
35 40 45

atg aga tgc gga aag agt tgt cgt cta aga tgg ata aac tat ctg aga 192
Met Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg
50 55 60

cca ggt ctc aaa cga ggc aac ttc acc aag gag gag gaa gat acc att 240
Pro Gly Leu Lys Arg Gly Asn Phe Thr Lys Glu Glu Glu Asp Thr Ile
65 70 75 80

atc cac ctt cac caa gct tat gga aac aag tgg tct aag atc gca tcc 288
Ile His Leu His Gln Ala Tyr Gly Asn Lys Trp Ser Lys Ile Ala Ser
85 90 95

aac ttc ccg gga agg aca gac aac gag atc aag aat gta tgg aac act 336
Asn Phe Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp Asn Thr
100 105 110

cat ctc aag aag cgg ttg gtg aag agg agc att tca tca tca tca tcc 384
His Leu Lys Lys Arg Leu Val Lys Arg Ser Ile Ser Ser Ser Ser Ser
115 120 125

gat gtt acc aat cat tca gtg tct tct acc tct tct tcc tct tcc tca 432
Asp Val Thr Asn His Ser Val Ser Ser Thr Ser Ser Ser Ser Ser Ser
130 135 140

atc tcg tca gtc ttg cag gac gtt att att aag agt gag agg cct aac 480
Ile Ser Ser Val Leu Gln Asp Val Ile Ile Lys Ser Glu Arg Pro Asn
145 150 155 160

cag gaa gag gag ttt ggg gaa atc ttg gtg gag caa atg gca tgt gga 528
Gln Glu Glu Glu Phe Gly Glu Ile Leu Val Glu Gln Met Ala Cys Gly
165 170 175

ttt gag gtg gat gca cca caa tca cta gaa tgt ctc ttt gac gat agc 576
Phe Glu Val Asp Ala Pro Gln Ser Leu Glu Cys Leu Phe Asp Asp Ser
180 185 190

cag gtt cct cct cct ata tct aaa cca gac tca cta caa acc cat ggg 624

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Gln Val Pro Pro Pro Ile Ser Lys Pro Asp Ser Leu Gln Thr His Gly
        195                 200                 205

aag tca tca gat cac gaa ttt tgg agc cga ctg att gaa cca ggg ttc     672
Lys Ser Ser Asp His Glu Phe Trp Ser Arg Leu Ile Glu Pro Gly Phe
    210                 215                 220

gat gat tac aat gag tgg ctc att ttc ttg gat aac caa act tgc tag     720
Asp Asp Tyr Asn Glu Trp Leu Ile Phe Leu Asp Asn Gln Thr Cys  *
225                 230                 235


<210> 30
<211> 239
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (15)...(118)
<223> Conserved domain

<400> 30
Met Gly Asn Arg Arg Ala Pro Cys Cys Asp Lys Ser Gln Val Lys Arg
 1               5                  10                  15
Gly Pro Trp Ser Asp Glu Glu Ser Glu Arg Leu Arg Ser Phe Ile Leu
            20                  25                  30
Lys Asn Gly His Gln Asn Trp Arg Ser Leu Pro Lys Leu Ala Gly Leu
        35                  40                  45
Met Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg
    50                  55                  60
Pro Gly Leu Lys Arg Gly Asn Phe Thr Lys Glu Glu Glu Asp Thr Ile
65                  70                  75                  80
Ile His Leu His Gln Ala Tyr Gly Asn Lys Trp Ser Lys Ile Ala Ser
                85                  90                  95
Asn Phe Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp Asn Thr
            100                 105                 110
His Leu Lys Lys Arg Leu Val Lys Arg Ser Ile Ser Ser Ser Ser Ser
        115                 120                 125
Asp Val Thr Asn His Ser Val Ser Ser Thr Ser Ser Ser Ser Ser Ser
    130                 135                 140
Ile Ser Ser Val Leu Gln Asp Val Ile Ile Lys Ser Glu Arg Pro Asn
145                 150                 155                 160
Gln Glu Glu Glu Phe Gly Glu Ile Leu Val Glu Gln Met Ala Cys Gly
                165                 170                 175
Phe Glu Val Asp Ala Pro Gln Ser Leu Glu Cys Leu Phe Asp Asp Ser
            180                 185                 190
Gln Val Pro Pro Pro Ile Ser Lys Pro Asp Ser Leu Gln Thr His Gly
        195                 200                 205
Lys Ser Ser Asp His Glu Phe Trp Ser Arg Leu Ile Glu Pro Gly Phe
    210                 215                 220
Asp Asp Tyr Asn Glu Trp Leu Ile Phe Leu Asp Asn Gln Thr Cys
225                 230                 235


<210> 31
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<211> 1144
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (25)...(1104)

<400> 31
cgtcgacctc ccaacactaa ctcc atg ttt ata acg gaa aaa caa gtg tgg     51
                           Met Phe Ile Thr Glu Lys Gln Val Trp
                            1               5

atg gat gag atc gtc gca aga aga gct tct tct tct tgg gac ttc cct     99
Met Asp Glu Ile Val Ala Arg Arg Ala Ser Ser Ser Trp Asp Phe Pro
 10                  15                  20                  25

ttc aac gac att aat att cat cag cat cat cat cgt cac tgc aac aca    147
Phe Asn Asp Ile Asn Ile His Gln His His His Arg His Cys Asn Thr
                30                  35                  40

agt cat gag ttt gaa atc ttg aag agt cct ctt gga gat gta gcg gtt    195
Ser His Glu Phe Glu Ile Leu Lys Ser Pro Leu Gly Asp Val Ala Val
            45                  50                  55

cac gaa gaa gag agt aat aat aat aac cct aat ttc agt aac agc gag    243
His Glu Glu Glu Ser Asn Asn Asn Asn Pro Asn Phe Ser Asn Ser Glu
        60                  65                  70

agt ggt aag aag gag aca aca gat agt ggt cag tct tgg tcc tcg tcg    291
Ser Gly Lys Lys Glu Thr Thr Asp Ser Gly Gln Ser Trp Ser Ser Ser
    75                  80                  85

tct tca aaa cca tcg gtc ttg ggg aga gga cat tgg aga cca gct gaa    339
Ser Ser Lys Pro Ser Val Leu Gly Arg Gly His Trp Arg Pro Ala Glu
 90                  95                 100                 105

gat gtt aaa ctc aaa gag ctt gtc tcc att tac ggc cca caa aac tgg    387
Asp Val Lys Leu Lys Glu Leu Val Ser Ile Tyr Gly Pro Gln Asn Trp
                110                 115                 120

aac ctc ata gct gaa aag ctt caa gga aga tct ggg aag agc tgt aga    435
Asn Leu Ile Ala Glu Lys Leu Gln Gly Arg Ser Gly Lys Ser Cys Arg
            125                 130                 135

cta cga tgg ttt aac caa ttg gac ccg agg ata aac cga aga gct ttc    483
Leu Arg Trp Phe Asn Gln Leu Asp Pro Arg Ile Asn Arg Arg Ala Phe
        140                 145                 150

aca gaa gaa gaa gag gag agg ctg atg caa gca cat agg ctt tat ggt    531
Thr Glu Glu Glu Glu Glu Arg Leu Met Gln Ala His Arg Leu Tyr Gly
    155                 160                 165

aac aaa tgg gca atg att gcg agg ctt ttc cct ggt aga act gat aat    579
Asn Lys Trp Ala Met Ile Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn
170                 175                 180                 185
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tca gtg aag aac cat tgg cat gtt gtc atg gct cgt aag tat aga gaa    627
Ser Val Lys Asn His Trp His Val Val Met Ala Arg Lys Tyr Arg Glu
                190                 195                 200

cac tct tct gct tac cgt agg aga aag ctt atg agt aat aat cca ctt    675
His Ser Ser Ala Tyr Arg Arg Arg Lys Leu Met Ser Asn Asn Pro Leu
            205                 210                 215

aaa cct cac ctc acc aat aat cat cat cct aac cct aac cct aat tac    723
Lys Pro His Leu Thr Asn Asn His His Pro Asn Pro Asn Pro Asn Tyr
        220                 225                 230

cac tct ttt atc tcc act aat cat tac ttc gct cag cct ttc ccc gag    771
His Ser Phe Ile Ser Thr Asn His Tyr Phe Ala Gln Pro Phe Pro Glu
    235                 240                 245

ttt aat ttg act cat cac ctg gtt aat aat gcc cct atc acg agt gac    819
Phe Asn Leu Thr His His Leu Val Asn Asn Ala Pro Ile Thr Ser Asp
250                 255                 260                 265

cat aac cag ctt gtg ttg cct ttc cat tgc ttt caa ggt tat gag aac    867
His Asn Gln Leu Val Leu Pro Phe His Cys Phe Gln Gly Tyr Glu Asn
                270                 275                 280

aat gaa cct ccg atg gtt gtg agt atg ttt ggc aac caa atg atg gtc    915
Asn Glu Pro Pro Met Val Val Ser Met Phe Gly Asn Gln Met Met Val
            285                 290                 295

ggc gat aac gtt ggt gcc acg tca gac gcg tta tgc aat att ccg cac    963
Gly Asp Asn Val Gly Ala Thr Ser Asp Ala Leu Cys Asn Ile Pro His
        300                 305                 310

att gac cct agt aac caa gag aaa ccg gag cca aat gat gca atg cat    1011
Ile Asp Pro Ser Asn Gln Glu Lys Pro Glu Pro Asn Asp Ala Met His
    315                 320                 325

tgg atc gga atg gac gcg gta gat gag gag gtg ttc gaa aag gct aag    1059
Trp Ile Gly Met Asp Ala Val Asp Glu Glu Val Phe Glu Lys Ala Lys
330                 335                 340                 345

cag caa cca cat ttt ttc gat ttt ctt ggc ttg ggg acg gcg tga        1104
Gln Gln Pro His Phe Phe Asp Phe Leu Gly Leu Gly Thr Ala  *
                350                 355

atgttgaaca aattggtgtt aatcagataa cgacagtggc                       1144
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<210> 32
<211> 359
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (90)...(210)
<223> Conserved domain

<400> 32

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 1               5                  10                  15
Arg Ala Ser Ser Ser Trp Asp Phe Pro Phe Asn Asp Ile Asn Ile His
            20                  25                  30
Gln His His His Arg His Cys Asn Thr Ser His Glu Phe Glu Ile Leu
        35                  40                  45
Lys Ser Pro Leu Gly Asp Val Ala Val His Glu Glu Glu Ser Asn Asn
    50                  55                  60
Asn Asn Pro Asn Phe Ser Asn Ser Glu Ser Gly Lys Lys Glu Thr Thr
65                  70                  75                  80
Asp Ser Gly Gln Ser Trp Ser Ser Ser Ser Ser Lys Pro Ser Val Leu
                85                  90                  95
Gly Arg Gly His Trp Arg Pro Ala Glu Asp Val Lys Leu Lys Glu Leu
            100                 105                 110
Val Ser Ile Tyr Gly Pro Gln Asn Trp Asn Leu Ile Ala Glu Lys Leu
        115                 120                 125
Gln Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe Asn Gln Leu
    130                 135                 140
Asp Pro Arg Ile Asn Arg Arg Ala Phe Thr Glu Glu Glu Glu Glu Arg
145                 150                 155                 160
Leu Met Gln Ala His Arg Leu Tyr Gly Asn Lys Trp Ala Met Ile Ala
                165                 170                 175
Arg Leu Phe Pro Gly Arg Thr Asp Asn Ser Val Lys Asn His Trp His
            180                 185                 190
Val Val Met Ala Arg Lys Tyr Arg Glu His Ser Ser Ala Tyr Arg Arg
        195                 200                 205
Arg Lys Leu Met Ser Asn Asn Pro Leu Lys Pro His Leu Thr Asn Asn
    210                 215                 220
His His Pro Asn Pro Asn Pro Asn Tyr His Ser Phe Ile Ser Thr Asn
225                 230                 235                 240
His Tyr Phe Ala Gln Pro Phe Pro Glu Phe Asn Leu Thr His His Leu
                245                 250                 255
Val Asn Asn Ala Pro Ile Thr Ser Asp His Asn Gln Leu Val Leu Pro
            260                 265                 270
Phe His Cys Phe Gln Gly Tyr Glu Asn Asn Glu Pro Pro Met Val Val
        275                 280                 285
Ser Met Phe Gly Asn Gln Met Met Val Gly Asp Asn Val Gly Ala Thr
    290                 295                 300
Ser Asp Ala Leu Cys Asn Ile Pro His Ile Asp Pro Ser Asn Gln Glu
305                 310                 315                 320
Lys Pro Glu Pro Asn Asp Ala Met His Trp Ile Gly Met Asp Ala Val
                325                 330                 335
Asp Glu Glu Val Phe Glu Lys Ala Lys Gln Gln Pro His Phe Phe Asp
            340                 345                 350
Phe Leu Gly Leu Gly Thr Ala
        355
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<210> 33
<211> 1009
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (177)...(866)

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gagaacaaga agagtccagg gccaatgagc ctgagggtat caaatcagtg attgatgaca 120
tctacatttt tgaagacgac cctgtggttg ataggttcaa taggtttggc acggag atg 179
Met
1

tct gcc atg gtc tcg gcc ttg aca cag gtg gtt tct gct cgc tct cag 227
Ser Ala Met Val Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser Gln
5 10 15

act gag gct gaa ggt gct cac tct cag act gag gct gaa ggt gct cac 275
Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala His
20 25 30

tct tct tcc tct tcg gct gga cat aaa aga gga tgg ctt gga atc gat 323
Ser Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile Asp
35 40 45

tct gct cct att ccc tca tca ttt gct cgt gta gac tct tca cat aat 371
Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His Asn
50 55 60 65

ccg atc gaa gaa tcc atg agc aag gca ttt cca gag gaa gca agg gag 419
Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg Glu
70 75 80

aaa aaa agg agg tac aga gga gta agg cag aga cca tgg ggc aaa tgg 467
Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp
85 90 95

gca gct gag ata cgt gat cca cat aga gcc gct agg gtt tgg ctc ggg 515
Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu Gly
100 105 110

acg ttt gat aca gcg gag gcc gcg gct aga gcc tac gac gag gct gca 563
Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala Ala
115 120 125

ctc cgg ttc cgt gga aat aaa gca aag cta aat ttc cca gag gat gta 611
Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp Val
130 135 140 145

agg att ctt cct cct ccc cct cct ctt ctt cgt tca cca gct gac acg 659
Arg Ile Leu Pro Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp Thr
150 155 160

gtg gcg aat aaa gca gaa gag gat ctg ata aat tat tgg agt tat aca 707
Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr Thr
165 170 175

aag ttg ttg caa agt tca ggc caa cgg tca ttt ctc gag cga gga caa 755
Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly Gln
180 185 190

gaa gag agt agt aac ata ttt gaa cat tca cca atg gaa caa cct ctg 803
Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro Leu

```
    195                 200                 205

cct cct tca agt tct ggt cca agt tcc tct aat ttt cct gca cct tct   851
Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro Ser
210                 215                 220                 225

cta cct aat aca tag tttcactttt attaaagctc tacaaataca attaaataca   906
Leu Pro Asn Thr  *


tagctaaatg aaaatgattt tcttgtctgt ataccttctt aagtgctaaa caatatattg 966
tactctttgt tttccttaac taaaaaaaaa aaaaaaaaaa aaa                   1009
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<210> 34
<211> 229
<212> PRT
<213> Arabidopsis thaliana

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Met Ser Ala Met Val Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser
 1               5                  10                  15
Gln Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala
            20                  25                  30
His Ser Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile
        35                  40                  45
Asp Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His
    50                  55                  60
Asn Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg
65                  70                  75                  80
Glu Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys
                85                  90                  95
Trp Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu
            100                 105                 110
Gly Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala
        115                 120                 125
Ala Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp
    130                 135                 140
Val Arg Ile Leu Pro Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp
145                 150                 155                 160
Thr Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr
                165                 170                 175
Thr Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly
            180                 185                 190
Gln Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro
        195                 200                 205
Leu Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro
    210                 215                 220
Ser Leu Pro Asn Thr
225
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<210> 35
<211> 1997
<212> DNA
<213> Arabidopsis thaliana

<220>

<221> CDS
<222> (69)...(1907)

<400> 35
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aacttcaaca tacacataat ctctcactta aaaatatctc tctctctctc tctacaaaat 60
caattcca atg ttg gtg gga aag ata agt gga tat gaa gat aat act cgc  110
         Met Leu Val Gly Lys Ile Ser Gly Tyr Glu Asp Asn Thr Arg
          1               5                  10

tct ttg gag cga gaa aca tct gaa atc act tct ctt ctc agc caa ttt   158
Ser Leu Glu Arg Glu Thr Ser Glu Ile Thr Ser Leu Leu Ser Gln Phe
 15                  20                  25                  30

ccg ggg aat act aat gtc ctt gtt gtt gac acc aat ttc acc act cta   206
Pro Gly Asn Thr Asn Val Leu Val Val Asp Thr Asn Phe Thr Thr Leu
                 35                  40                  45

ctc aac atg aaa caa atc atg aaa caa tac gct tat caa gtg tct att   254
Leu Asn Met Lys Gln Ile Met Lys Gln Tyr Ala Tyr Gln Val Ser Ile
             50                  55                  60

gag aca gat gca gaa aaa gct ctt gcg ttt ttg aca agc tgc aaa cat   302
Glu Thr Asp Ala Glu Lys Ala Leu Ala Phe Leu Thr Ser Cys Lys His
         65                  70                  75

gaa atc aat att gtg att tgg gat ttt cat atg cct gga att gat gga   350
Glu Ile Asn Ile Val Ile Trp Asp Phe His Met Pro Gly Ile Asp Gly
     80                  85                  90

ctt caa gct ctc aag agc att act tca aag ttg gat tta cct gta gtg   398
Leu Gln Ala Leu Lys Ser Ile Thr Ser Lys Leu Asp Leu Pro Val Val
 95                 100                 105                 110

att atg tct gat gat aat caa acg gaa tct gtg atg aaa gca aca ttt   446
Ile Met Ser Asp Asp Asn Gln Thr Glu Ser Val Met Lys Ala Thr Phe
                115                 120                 125

tac ggt gct tgt gac tat gtt gtg aaa ccg gtt aaa gaa gag gta atg   494
Tyr Gly Ala Cys Asp Tyr Val Val Lys Pro Val Lys Glu Glu Val Met
            130                 135                 140

gcc aat ata tgg caa cac att gta cgg aag agg ctg atc ttt aaa ccg   542
Ala Asn Ile Trp Gln His Ile Val Arg Lys Arg Leu Ile Phe Lys Pro
        145                 150                 155

gat gtt gct cca ccg gtt caa tca gat ccg gct cgc tct gac cgt tta   590
Asp Val Ala Pro Pro Val Gln Ser Asp Pro Ala Arg Ser Asp Arg Leu
    160                 165                 170

gac caa gtc aaa gct gat ttc aag atc gta gaa gat gaa cca ata atc   638
Asp Gln Val Lys Ala Asp Phe Lys Ile Val Glu Asp Glu Pro Ile Ile
175                 180                 185                 190

aat gag aca ccg ctg atc aca tgg acc gaa gaa att caa ccg gtt cag   686
Asn Glu Thr Pro Leu Ile Thr Trp Thr Glu Glu Ile Gln Pro Val Gln
                195                 200                 205
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tca gat ctg gtt caa gcc aac aag ttc gac caa gtg aat ggc tat tcc 734
Ser Asp Leu Val Gln Ala Asn Lys Phe Asp Gln Val Asn Gly Tyr Ser
210 215 220

cca atc atg aac caa gat aac atg ttc aac aaa gca cca cct aaa ccg 782
Pro Ile Met Asn Gln Asp Asn Met Phe Asn Lys Ala Pro Pro Lys Pro
225 230 235

cga atg acg tgg aca gaa gtt att caa ccg gtt caa tca aat ctg gtt 830
Arg Met Thr Trp Thr Glu Val Ile Gln Pro Val Gln Ser Asn Leu Val
240 245 250

caa aca aaa gag ttc ggc caa ctc aat gac tat tcc caa atc atg aac 878
Gln Thr Lys Glu Phe Gly Gln Leu Asn Asp Tyr Ser Gln Ile Met Asn
255 260 265 270

caa gat agc atg tac aac aaa gca gca acc aaa cca caa ttg acg tgg 926
Gln Asp Ser Met Tyr Asn Lys Ala Ala Thr Lys Pro Gln Leu Thr Trp
275 280 285

acc gaa gaa att caa ccg gtt caa tca ggt ctg gtt caa gcc aac gag 974
Thr Glu Glu Ile Gln Pro Val Gln Ser Gly Leu Val Gln Ala Asn Glu
290 295 300

ttc agc aaa gtg aat gga tat tcc caa agc atg aac caa gat agc atg 1022
Phe Ser Lys Val Asn Gly Tyr Ser Gln Ser Met Asn Gln Asp Ser Met
305 310 315

ttc aac aaa tca gca acc aac ccg cga ttg aca tgg aac gaa tta ctt 1070
Phe Asn Lys Ser Ala Thr Asn Pro Arg Leu Thr Trp Asn Glu Leu Leu
320 325 330

caa ccg gtt caa tca gat ctg gtt caa tcc aat gag ttt agc caa ttc 1118
Gln Pro Val Gln Ser Asp Leu Val Gln Ser Asn Glu Phe Ser Gln Phe
335 340 345 350

agt gac tat tct caa atc atg aac gaa gat aac atg ttc aac aaa gca 1166
Ser Asp Tyr Ser Gln Ile Met Asn Glu Asp Asn Met Phe Asn Lys Ala
355 360 365

gca aag aaa ccg cgg atg aca tgg agt gaa gta ttt caa ccg gtt caa 1214
Ala Lys Lys Pro Arg Met Thr Trp Ser Glu Val Phe Gln Pro Val Gln
370 375 380

tca cat ctg gtt ccg act gac ggt tta gac cga gac cac ttt gat tcc 1262
Ser His Leu Val Pro Thr Asp Gly Leu Asp Arg Asp His Phe Asp Ser
385 390 395

ata acc ata aac gga ggt aac ggc ata caa aac atg gaa aag aaa caa 1310
Ile Thr Ile Asn Gly Gly Asn Gly Ile Gln Asn Met Glu Lys Lys Gln
400 405 410

gga aaa aaa cca cgg aag ccg cgg atg acg tgg acc gaa gag ctt cac 1358
Gly Lys Lys Pro Arg Lys Pro Arg Met Thr Trp Thr Glu Glu Leu His
415 420 425 430

caa aaa ttt ctg gaa gcc atc gaa ata att ggt ggt atc gaa aaa gct 1406

```
Gln Lys Phe Leu Glu Ala Ile Glu Ile Ile Gly Gly Ile Glu Lys Ala
                435                 440                 445

aac cca aag gta ctt gtc gaa tgc ttg caa gaa atg agg ata gaa gga     1454
Asn Pro Lys Val Leu Val Glu Cys Leu Gln Glu Met Arg Ile Glu Gly
            450                 455                 460

att act aga agc aat gtg gca agt cat ctt cag aaa cac cgt atc aat     1502
Ile Thr Arg Ser Asn Val Ala Ser His Leu Gln Lys His Arg Ile Asn
        465                 470                 475

ctt gaa gaa aac caa att cct caa caa aca caa ggg aat ggt tgg gcc     1550
Leu Glu Glu Asn Gln Ile Pro Gln Gln Thr Gln Gly Asn Gly Trp Ala
    480                 485                 490

act gcg tat ggt aca cta gct ccc tct ctc caa ggt tca gac aat gtc     1598
Thr Ala Tyr Gly Thr Leu Ala Pro Ser Leu Gln Gly Ser Asp Asn Val
495                 500                 505                 510

aac aca aca ata cca tcg tac ctt atg aat ggt cca gcc act ttg aac     1646
Asn Thr Thr Ile Pro Ser Tyr Leu Met Asn Gly Pro Ala Thr Leu Asn
                515                 520                 525

caa atc cag cag aat caa tat caa aat ggt ttc ttg aca atg aac aac     1694
Gln Ile Gln Gln Asn Gln Tyr Gln Asn Gly Phe Leu Thr Met Asn Asn
            530                 535                 540

aac cag atc ata acc aat cct ccg cct cct ttg ccc tat ttg gac cat     1742
Asn Gln Ile Ile Thr Asn Pro Pro Pro Pro Leu Pro Tyr Leu Asp His
        545                 550                 555

cat cac caa cag caa cat cag tct tct cct caa ttt aat tac ctg atg     1790
His His Gln Gln Gln His Gln Ser Ser Pro Gln Phe Asn Tyr Leu Met
    560                 565                 570

aac aat gaa gaa ctt ctt caa gcc tct ggc ctc tct gcg aca gat ctt     1838
Asn Asn Glu Glu Leu Leu Gln Ala Ser Gly Leu Ser Ala Thr Asp Leu
575                 580                 585                 590

gaa ctc act tat cca agt tta cca tat gat cca caa gag tat cta atc     1886
Glu Leu Thr Tyr Pro Ser Leu Pro Tyr Asp Pro Gln Glu Tyr Leu Ile
                595                 600                 605

aat ggc tac aat tat aat tag tcatatagcc cttctcttta cttaaggcag        1937
Asn Gly Tyr Asn Tyr Asn  *
            610

tctatgtatg acaaataata tgcgacttcc cttgtgagtc acaatattgt ttcattattc 1997
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<210> 36
<211> 612
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
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<222> (425)...(478)
<223> Conserved domain

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Glu Arg Glu Thr Ser Glu Ile Thr Ser Leu Leu Ser Gln Phe Pro Gly
20 25 30
Asn Thr Asn Val Leu Val Val Asp Thr Asn Phe Thr Thr Leu Leu Asn
35 40 45
Met Lys Gln Ile Met Lys Gln Tyr Ala Tyr Gln Val Ser Ile Glu Thr
50 55 60
Asp Ala Glu Lys Ala Leu Ala Phe Leu Thr Ser Cys Lys His Glu Ile
65 70 75 80
Asn Ile Val Ile Trp Asp Phe His Met Pro Gly Ile Asp Gly Leu Gln
85 90 95
Ala Leu Lys Ser Ile Thr Ser Lys Leu Asp Leu Pro Val Val Ile Met
100 105 110
Ser Asp Asp Asn Gln Thr Glu Ser Val Met Lys Ala Thr Phe Tyr Gly
115 120 125
Ala Cys Asp Tyr Val Val Lys Pro Val Lys Glu Glu Val Met Ala Asn
130 135 140
Ile Trp Gln His Ile Val Arg Lys Arg Leu Ile Phe Lys Pro Asp Val
145 150 155 160
Ala Pro Pro Val Gln Ser Asp Pro Ala Arg Ser Asp Arg Leu Asp Gln
165 170 175
Val Lys Ala Asp Phe Lys Ile Val Glu Asp Glu Pro Ile Ile Asn Glu
180 185 190
Thr Pro Leu Ile Thr Trp Thr Glu Glu Ile Gln Pro Val Gln Ser Asp
195 200 205
Leu Val Gln Ala Asn Lys Phe Asp Gln Val Asn Gly Tyr Ser Pro Ile
210 215 220
Met Asn Gln Asp Asn Met Phe Asn Lys Ala Pro Pro Lys Pro Arg Met
225 230 235 240
Thr Trp Thr Glu Val Ile Gln Pro Val Gln Ser Asn Leu Val Gln Thr
245 250 255
Lys Glu Phe Gly Gln Leu Asn Asp Tyr Ser Gln Ile Met Asn Gln Asp
260 265 270
Ser Met Tyr Asn Lys Ala Ala Thr Lys Pro Gln Leu Thr Trp Thr Glu
275 280 285
Glu Ile Gln Pro Val Gln Ser Gly Leu Val Gln Ala Asn Glu Phe Ser
290 295 300
Lys Val Asn Gly Tyr Ser Gln Ser Met Asn Gln Asp Ser Met Phe Asn
305 310 315 320
Lys Ser Ala Thr Asn Pro Arg Leu Thr Trp Asn Glu Leu Leu Gln Pro
325 330 335
Val Gln Ser Asp Leu Val Gln Ser Asn Glu Phe Ser Gln Phe Ser Asp
340 345 350
Tyr Ser Gln Ile Met Asn Glu Asp Asn Met Phe Asn Lys Ala Ala Lys
355 360 365
Lys Pro Arg Met Thr Trp Ser Glu Val Phe Gln Pro Val Gln Ser His
370 375 380
Leu Val Pro Thr Asp Gly Leu Asp Arg Asp His Phe Asp Ser Ile Thr
385 390 395 400
Ile Asn Gly Gly Asn Gly Ile Gln Asn Met Glu Lys Lys Gln Gly Lys
405 410 415
Lys Pro Arg Lys Pro Arg Met Thr Trp Thr Glu Glu Leu His Gln Lys

```
            420                     425                     430
Phe Leu Glu Ala Ile Glu Ile Ile Gly Gly Ile Glu Lys Ala Asn Pro
        435                     440                     445
Lys Val Leu Val Glu Cys Leu Gln Glu Met Arg Ile Glu Gly Ile Thr
    450                     455                     460
Arg Ser Asn Val Ala Ser His Leu Gln Lys His Arg Ile Asn Leu Glu
465                     470                     475                     480
Glu Asn Gln Ile Pro Gln Gln Thr Gln Gly Asn Gly Trp Ala Thr Ala
                485                     490                     495
Tyr Gly Thr Leu Ala Pro Ser Leu Gln Gly Ser Asp Asn Val Asn Thr
            500                     505                     510
Thr Ile Pro Ser Tyr Leu Met Asn Gly Pro Ala Thr Leu Asn Gln Ile
        515                     520                     525
Gln Gln Asn Gln Tyr Gln Asn Gly Phe Leu Thr Met Asn Asn Asn Gln
    530                     535                     540
Ile Ile Thr Asn Pro Pro Pro Pro Leu Pro Tyr Leu Asp His His His
545                     550                     555                     560
Gln Gln Gln His Gln Ser Ser Pro Gln Phe Asn Tyr Leu Met Asn Asn
                565                     570                     575
Glu Glu Leu Leu Gln Ala Ser Gly Leu Ser Ala Thr Asp Leu Glu Leu
            580                     585                     590
Thr Tyr Pro Ser Leu Pro Tyr Asp Pro Gln Glu Tyr Leu Ile Asn Gly
        595                     600                     605
Tyr Asn Tyr Asn
    610


<210> 37
<211> 759
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (16)...(477)

<400> 37
gtttgtcttt tatca atg gaa aga gaa caa gaa gag tct acg atg aga aag   51
                 Met Glu Arg Glu Gln Glu Glu Ser Thr Met Arg Lys
                  1               5                  10

aga agg cag cca cct caa gaa gaa gtg cct aac cac gtg gct aca agg    99
Arg Arg Gln Pro Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg
        15                  20                  25

aag ccg tac aga ggg ata cgg agg agg aag tgg ggc aag tgg gtg gct   147
Lys Pro Tyr Arg Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala
    30                  35                  40

gag att cgt gag cct aac aaa cgc tca cgg ctt tgg ctt ggc tct tac   195
Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr
45                  50                  55                  60

aca acc gat atc gcc gcc gct aga gcc tac gac gtg gcc gtc ttc tac   243
Thr Thr Asp Ile Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr
                65                  70                  75
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```
ctc cgt ggc ccc tcc gca cgt ctc aac ttc cct gat ctt ctc ttg caa    291
Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu Gln
            80                  85                  90

gaa gag gac cat ctc tca gcc gcc acc acc gct gac atg ccc gca gct    339
Glu Glu Asp His Leu Ser Ala Ala Thr Thr Ala Asp Met Pro Ala Ala
        95                  100                 105

ctt ata agg gaa aaa gcg gcg gag gtc ggc gcc aga gtc gac gct ctt    387
Leu Ile Arg Glu Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Leu
    110                 115                 120

cta gct tct gcc gct cct tcg atg gct cac tcc act ccg ccg gta ata    435
Leu Ala Ser Ala Ala Pro Ser Met Ala His Ser Thr Pro Pro Val Ile
125                 130                 135                 140

aaa ccc gac ttg aat caa ata ccc gaa tcc gga gat ata tag            477
Lys Pro Asp Leu Asn Gln Ile Pro Glu Ser Gly Asp Ile  *
                145                 150

tcaatttata tacatgtagt ttgttttgtt tgattagaag attacattta catacaagat 537
acacatagat actggaaaat ataggtatgt atacattcat aaattatctt atgtatcaaa 597
gaattttata gattctgatt agctttttgt ttttgttttt gataagaact ctgattagtt 657
gtccggagac aaaaccggct aagagcaatc catgagaagc tagcgagtgt tttttagttc 717
aagttgtaat ataaatgcat attaattctt tagtaatttt gt                    759

<210> 38
<211> 153
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (28)...(95)
<223> Conserved domain

<400> 38
Met Glu Arg Glu Gln Glu Glu Ser Thr Met Arg Lys Arg Arg Gln Pro
 1               5                  10                  15
Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg Lys Pro Tyr Arg
            20                  25                  30
Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
        35                  40                  45
Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr Thr Thr Asp Ile
    50                  55                  60
Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr Leu Arg Gly Pro
65                  70                  75                  80
Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu Gln Glu Glu Asp His
                85                  90                  95
Leu Ser Ala Ala Thr Thr Ala Asp Met Pro Ala Ala Leu Ile Arg Glu
            100                 105                 110
Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Leu Leu Ala Ser Ala
        115                 120                 125
Ala Pro Ser Met Ala His Ser Thr Pro Pro Val Ile Lys Pro Asp Leu
    130                 135                 140
Asn Gln Ile Pro Glu Ser Gly Asp Ile
145                 150
```

<210> 39
<211> 992
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (41)...(760)

<400> 39
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ctctgctggt atcattggag tctagggttt tgttattgac atg cgt ggt gtg tca     55
                                            Met Arg Gly Val Ser
                                             1               5

gaa ttg gag gtg ggg aag agt aat ctt ccg gcg gag agt gag ctg gaa     103
Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala Glu Ser Glu Leu Glu
                10                  15                  20

ttg gga tta ggg ctc agc ctc ggt ggt ggc gcg tgg aaa gag cgt ggg     151
Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala Trp Lys Glu Arg Gly
            25                  30                  35

agg att ctt act gct aag gat ttt cct tcc gtt ggg tct aaa cgc tct     199
Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ser
        40                  45                  50

gct gaa tct tcc tct cac caa gga gct tct cct cct cgt tca agt caa     247
Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro Pro Arg Ser Ser Gln
    55                  60                  65

gtg gta gga tgg cca cca att ggg tta cac agg atg aac agt ttg gtt     295
Val Val Gly Trp Pro Pro Ile Gly Leu His Arg Met Asn Ser Leu Val
70                  75                  80                  85

aat aac caa gct atg aag gca gca aga gcg gaa gaa gga gac ggg gag     343
Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu Glu Gly Asp Gly Glu
                90                  95                  100

aag aaa gtt gtg aag aat gat gag ctc aaa gat gtg tca atg aag gtg     391
Lys Lys Val Val Lys Asn Asp Glu Leu Lys Asp Val Ser Met Lys Val
            105                 110                 115

aat ccg aaa gtt cag ggc tta ggg ttt gtt aag gtg aat atg gat gga     439
Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys Val Asn Met Asp Gly
        120                 125                 130

gtt ggt ata ggc aga aaa gtg gat atg aga gct cat tcg tct tac gaa     487
Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala His Ser Ser Tyr Glu
    135                 140                 145

aac ttg gct cag acg ctt gag gaa atg ttc ttt gga atg aca ggt act     535
Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe Gly Met Thr Gly Thr
150                 155                 160                 165

act tgt cga gaa aag gtt aaa cct tta agg ctt tta gat gga tca tca     583
```

```
Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser
                170                 175                 180

gac ttt gta ctc act tat gaa gat aag gaa ggg gat tgg atg ctt gtt    631
Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val
            185                 190                 195

gga gat gtt cca tgg aga atg ttt atc aac tcg gtg aaa agg ctt cgg    679
Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg
        200                 205                 210

atc atg gga acc tca gaa gct agt gga cta gct cca aga cgt caa gag    727
Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala Pro Arg Arg Gln Glu
    215                 220                 225

cag aag gat aga caa aga aac aac cct gtt tag cttcccttcc aaagctggca 780
Gln Lys Asp Arg Gln Arg Asn Asn Pro Val  *
230                 235

ttgtttatgt attgtttgag gtttgcaatt tactcgatac tttttgaaga aagtattttg 840
gagaatatgg ataaaagcat gcagaagctt agatatgatt tgaatccggt tttcggatat 900
ggttttgctt aggtcattca attcgtagtt ttccagtttg tttcttcttt ggctgtgtac 960
caattatcta tgttctgtga gagaaagctc tt                               992

<210> 40
<211> 239
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (20)...(28)
<223> Conserved domain

<221> DOMAIN
<222> (71)...(82)
<223> Conserved domain

<221> DOMAIN
<222> (126)...(142)
<223> Conserved domain

<221> DOMAIN
<222> (187)...(224)
<223> Conserved domain

<400> 40
Met Arg Gly Val Ser Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala
 1               5                  10                  15
Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala
            20                  25                  30
Trp Lys Glu Arg Gly Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val
        35                  40                  45
Gly Ser Lys Arg Ser Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro
    50                  55                  60
Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Leu His Arg
65                  70                  75                  80
```

```
Met Asn Ser Leu Val Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu
                85                  90                  95
Glu Gly Asp Gly Glu Lys Lys Val Val Lys Asn Asp Glu Leu Lys Asp
            100                 105                 110
Val Ser Met Lys Val Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys
        115                 120                 125
Val Asn Met Asp Gly Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala
    130                 135                 140
His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe
145                 150                 155                 160
Gly Met Thr Gly Thr Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu
                165                 170                 175
Leu Asp Gly Ser Ser Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly
            180                 185                 190
Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser
        195                 200                 205
Val Lys Arg Leu Arg Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala
    210                 215                 220
Pro Arg Arg Gln Glu Gln Lys Asp Arg Gln Arg Asn Asn Pro Val
225                 230                 235
```

```
<210> 41
<211> 228
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(228)

<400> 41
atg gat aac cat cgc agg act aag caa ccc aag acc aac tcc atc gtt      48
Met Asp Asn His Arg Arg Thr Lys Gln Pro Lys Thr Asn Ser Ile Val
 1               5                  10                  15

act tct tct tct gaa gaa gtg agt agt ctt gag tgg gaa gtt gtg aac      96
Thr Ser Ser Ser Glu Glu Val Ser Ser Leu Glu Trp Glu Val Val Asn
            20                  25                  30

atg agt caa gaa gaa gaa gat ttg gtc tct cga atg cat aag ctt gtc      144
Met Ser Gln Glu Glu Glu Asp Leu Val Ser Arg Met His Lys Leu Val
        35                  40                  45

ggt gac agg tgg gaa ctg ata gct ggg agg atc cca gga aga acc gct      192
Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
    50                  55                  60

gga gaa att gag agg ttt tgg gtc atg aaa aat tga                      228
Gly Glu Ile Glu Arg Phe Trp Val Met Lys Asn  *
 65                 70                  75

<210> 42
<211> 75
<212> PRT
<213> Arabidopsis thaliana
```

<220>
<221> DOMAIN
<222> (27)...(63)
<223> Conserved domain

<400> 42
Met Asp Asn His Arg Arg Thr Lys Gln Pro Lys Thr Asn Ser Ile Val
1 5 10 15
Thr Ser Ser Ser Glu Glu Val Ser Ser Leu Glu Trp Glu Val Val Asn
20 25 30
Met Ser Gln Glu Glu Glu Asp Leu Val Ser Arg Met His Lys Leu Val
35 40 45
Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
50 55 60
Gly Glu Ile Glu Arg Phe Trp Val Met Lys Asn
65 70 75

<210> 43
<211> 1221
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (162)...(1013)

<400> 43
atttctcttc cacaaagagt cctaacttcg agttgaaaca aacaccattt ctcatctcta 60
tctcagaaag aacaaaccat ttcgtgttct ttctttctct attctcataa ggaaatataa 120
ttcctgaaac tgttgagttc ttgtgaaagg aaataaaaaa c atg atg atg ggc aaa 176
Met Met Met Gly Lys
1 5

gaa gat cta ggt ttg agc cta agc tta ggg ttt tca caa aat cac aat 224
Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser Gln Asn His Asn
10 15 20

cct ctt cag atg aat ctg aat cct aac tct tca tta tca aac aat ctc 272
Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser Leu Ser Asn Asn Leu
25 30 35

cag aga ctc cca tgg aac caa aca ttc gat cct aca tca gat ctt cgc 320
Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro Thr Ser Asp Leu Arg
40 45 50

aag ata gac gtg aac agt ttt cca tca acg gtt aac tgc gag gaa gac 368
Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val Asn Cys Glu Glu Asp
55 60 65

aca gga gtt tcg tca cca aac agt acg atc tca agc acc att agc ggg 416
Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser Ser Thr Ile Ser Gly
70 75 80 85

aag aga agt gag aga gaa gga atc tcc gga acc ggc gtt ggc tcc ggc 464
Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr Gly Val Gly Ser Gly

```
                90                  95                  100

gac gat cac gac gag atc act ccg gat cga ggg tac tca cgt gga acc     512
Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly Tyr Ser Arg Gly Thr
            105                 110                 115

tca gat gaa gaa gaa gac ggg ggc gaa acg tcg agg aag aag ctc agg     560
Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser Arg Lys Lys Leu Arg
        120                 125                 130

tta tca aaa gat cag tct gct ttt ctc gaa gag act ttc aaa gaa cac     608
Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu Thr Phe Lys Glu His
    135                 140                 145

aac act ctc aat ccc aaa cag aag cta gct ttg gct aag aag ctg aac     656
Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu Ala Lys Lys Leu Asn
150                 155                 160                 165

ttg acg gca aga caa gtg gaa gtg tgg ttc caa aac aga aga gct aga     704
Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg Ala Arg
                170                 175                 180

acc aag tta aag caa acg gag gta gat tgc gaa tac ttg aaa cgg tgc     752
Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Tyr Leu Lys Arg Cys
            185                 190                 195

gta gag aag cta acg gaa gag aac cgg aga ctt cag aaa gag gct atg     800
Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu Gln Lys Glu Ala Met
        200                 205                 210

gag ctt cga act ctc aag ctg tct cca caa ttc tac ggt cag atg act     848
Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe Tyr Gly Gln Met Thr
    215                 220                 225

cca cca act aca ctc atc atg tgt cct tcg tgc gag cgt gta gct ggt     896
Pro Pro Thr Thr Leu Ile Met Cys Pro Ser Cys Glu Arg Val Ala Gly
230                 235                 240                 245

cca tca tca tcg aac cat cac cac aat cac agg ccg gtt tcg att aac     944
Pro Ser Ser Ser Asn His His His Asn His Arg Pro Val Ser Ile Asn
                250                 255                 260

ccg tgg att gct tgt gct ggt cag gtg gct cat ggg ctg aat ttt gaa     992
Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His Gly Leu Asn Phe Glu
            265                 270                 275

gcc ttg cgt cca cga tcg taa tttttagtgg tgggggaagg gtgttttggg       1043
Ala Leu Arg Pro Arg Ser  *
        280

tttttttcatt atcgttatat agtctatctg tgtggggtca ttgtaatttt ggatgattgg 1103
ccttctcatg aactagtcat atgtatgatg caaccttaaa aatatttcaa gtagcaaaac 1163
ttaattacaa acttgctata ttaaccaaaa attatgaaaa aaaaaaaaaa aaaaaaaa   1221
```

<210> 44
<211> 283
<212> PRT

<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (126)...(186)
<223> Conserved domain

<400> 44
Met Met Met Gly Lys Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe
1 5 10 15
Ser Gln Asn His Asn Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser
20 25 30
Leu Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro
35 40 45
Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val
50 55 60
Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser
65 70 75 80
Ser Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr
85 90 95
Gly Val Gly Ser Gly Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly
100 105 110
Tyr Ser Arg Gly Thr Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser
115 120 125
Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu
130 135 140
Thr Phe Lys Glu His Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu
145 150 155 160
Ala Lys Lys Leu Asn Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln
165 170 175
Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu
180 185 190
Tyr Leu Lys Arg Cys Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu
195 200 205
Gln Lys Glu Ala Met Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe
210 215 220
Tyr Gly Gln Met Thr Pro Pro Thr Thr Leu Ile Met Cys Pro Ser Cys
225 230 235 240
Glu Arg Val Ala Gly Pro Ser Ser Ser Asn His His His Asn His Arg
245 250 255
Pro Val Ser Ile Asn Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His
260 265 270
Gly Leu Asn Phe Glu Ala Leu Arg Pro Arg Ser
275 280

<210> 45
<211> 696
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (77)...(496)

<400> 45
aatccataga tctcttatta aataacagtg ctgaccaagc tcttacaaag caaaccaatc 60

```
tagaacacca aagtta atg gag agc tca aac agg agc agc aac aac caa tca 112
                  Met Glu Ser Ser Asn Arg Ser Ser Asn Asn Gln Ser
                   1               5                   10

caa gat gac aag caa gct cgt ttc cgg gga gtt cga aga agg cct tgg   160
Gln Asp Asp Lys Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp
        15                  20                  25

gga aag ttt gca gca gag att cga gac ccg tcg aga aac ggt gcc cgt   208
Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg
    30                  35                  40

ctt tgg ctc ggg aca ttt gag acc gct gag gag gca gca agg gct tat   256
Leu Trp Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr
45                  50                  55                  60

gac cga gca gcc ttt aac ctt agg ggt cat ctc gct ata ctc aac ttc   304
Asp Arg Ala Ala Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe
                65                  70                  75

cct aat gag tat tat cca cgt atg gac gac tac tcg ctt cgc cct cct   352
Pro Asn Glu Tyr Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro
            80                  85                  90

tat gct tct tct tct tcg tcg tcg tca tcg ggt tca act tct act aat   400
Tyr Ala Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn
        95                  100                 105

gtg agt cga caa aac caa aga gaa gtt ttc gag ttt gag tat ttg gac   448
Val Ser Arg Gln Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp
    110                 115                 120

gat aag gtt ctt gaa gaa ctt ctt gat tca gaa gaa agg aag aga taa   496
Asp Lys Val Leu Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg  *
125                 130                 135

tcacgattag ttttgttttg atattttatg tggcactgtt gtggctacct acgtgcatta 556
tgtgcatgta taggtcgctt gattagtact ttataacatg catgccacga ccataaattg 616
taagagaaga cgtactttgc gttttcatga aatatgaatg ttagatggtt tgagtacaaa 676
aaaaaaaaaa aaaaaaaaaa                                             696

&lt;210&gt; 46
&lt;211&gt; 139
&lt;212&gt; PRT
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; DOMAIN
&lt;222&gt; (17)...(85)
&lt;223&gt; Conserved domain

&lt;400&gt; 46
Met Glu Ser Ser Asn Arg Ser Ser Asn Asn Gln Ser Gln Asp Asp Lys
 1               5                   10                  15
Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
            20                  25                  30
Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg Leu Trp Leu Gly
```

```
        35                  40                  45
Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala
    50                  55                  60
Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe Pro Asn Glu Tyr
65                  70                  75                  80
Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro Tyr Ala Ser Ser
                85                  90                  95
Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn Val Ser Arg Gln
            100                 105                 110
Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp Asp Lys Val Leu
        115                 120                 125
Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg
    130                 135
```

```
<210> 47
<211> 1562
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (160)...(1335)

<400> 47
tctttctttc ttcctctttg tctctgtttc ttgtttctct ctctctctct ctacagagtt 60
ttctttccct cgaagaaaaa gaatattttt aaatttaatt ttctctgcgt ttataagctt 120
taagtttcag aggaggagga tttagaagga gggttttgt atg tgt gtc tta aaa    174
                                         Met Cys Val Leu Lys
                                         1               5

gtg gca aat cag gaa gat aac gtt ggc aaa aaa gcc gag tct att aga   222
Val Ala Asn Gln Glu Asp Asn Val Gly Lys Lys Ala Glu Ser Ile Arg
                10                  15                  20

gac gat gat cat cgg acg tta tct gaa atc gat caa tgg ctt tac tta   270
Asp Asp Asp His Arg Thr Leu Ser Glu Ile Asp Gln Trp Leu Tyr Leu
            25                  30                  35

ttc gca gcc gaa gac gac cac cac cgt cat agc ttc cct acg cag cag   318
Phe Ala Ala Glu Asp Asp His His Arg His Ser Phe Pro Thr Gln Gln
        40                  45                  50

ccg cct cca tcg tcg tcg tcc tca tct ctt atc tca ggt ttc agt aga   366
Pro Pro Pro Ser Ser Ser Ser Ser Ser Leu Ile Ser Gly Phe Ser Arg
    55                  60                  65

gag atg gag atg tct gct att gtc tct gct ttg act cac gtt gtt gct   414
Glu Met Glu Met Ser Ala Ile Val Ser Ala Leu Thr His Val Val Ala
70                  75                  80                  85

gga aat gtt cct cag cat caa caa gga ggc ggt gaa ggt agc gga gaa   462
Gly Asn Val Pro Gln His Gln Gln Gly Gly Gly Glu Gly Ser Gly Glu
                90                  95                  100

ggg act tcg aat tcg tct tct tcc tcg ggg cag aaa agg agg aga gag   510
Gly Thr Ser Asn Ser Ser Ser Ser Ser Gly Gln Lys Arg Arg Arg Glu
```

105 110 115

gtg gag gaa ggt ggc gcc aaa gcg gtt aag gca gct aat act ttg acg 558
Val Glu Glu Gly Gly Ala Lys Ala Val Lys Ala Ala Asn Thr Leu Thr
120 125 130

gtt gat caa tat ttc tcc ggt ggt agc tct act tct aaa gtg aga gaa 606
Val Asp Gln Tyr Phe Ser Gly Gly Ser Ser Thr Ser Lys Val Arg Glu
135 140 145

gct tcg agt aac atg tca ggt ccg ggc cca aca tac gag tat aca act 654
Ala Ser Ser Asn Met Ser Gly Pro Gly Pro Thr Tyr Glu Tyr Thr Thr
150 155 160 165

acg gca act gct agt agc gaa acg tcg tcg ttt agt ggg gac caa cct 702
Thr Ala Thr Ala Ser Ser Glu Thr Ser Ser Phe Ser Gly Asp Gln Pro
170 175 180

cgg cga aga tac aga gga gtt aga caa aga cca tgg gga aag tgg gcg 750
Arg Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala
185 190 195

gct gag att cga gat cca ttt aaa gca gct aga gtt tgg ctc ggt acg 798
Ala Glu Ile Arg Asp Pro Phe Lys Ala Ala Arg Val Trp Leu Gly Thr
200 205 210

ttc gac aat gct gaa tca gca gca aga gct tac gac gaa gct gca ctt 846
Phe Asp Asn Ala Glu Ser Ala Ala Arg Ala Tyr Asp Glu Ala Ala Leu
215 220 225

cgg ttt aga ggc aac aaa gcc aaa ctc aac ttc cct gaa aac gtc aaa 894
Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asn Val Lys
230 235 240 245

ctc gtt aga cct gct tca acc gaa gca caa cct gtg cac caa acc gct 942
Leu Val Arg Pro Ala Ser Thr Glu Ala Gln Pro Val His Gln Thr Ala
250 255 260

gct caa aga ccg acc cag tca agg aac tcg ggt tca acg act acc ctt 990
Ala Gln Arg Pro Thr Gln Ser Arg Asn Ser Gly Ser Thr Thr Thr Leu
265 270 275

ttg ccc ata aga cct gct tcg aat caa agc gtt cat tcg cag ccg ttg 1038
Leu Pro Ile Arg Pro Ala Ser Asn Gln Ser Val His Ser Gln Pro Leu
280 285 290

atg caa tca tac aac ttg agt tac tct gaa atg gct cgt caa caa caa 1086
Met Gln Ser Tyr Asn Leu Ser Tyr Ser Glu Met Ala Arg Gln Gln Gln
295 300 305

cag ttt cag caa cat cat caa caa tct ttg gat tta tac gat caa atg 1134
Gln Phe Gln Gln His His Gln Gln Ser Leu Asp Leu Tyr Asp Gln Met
310 315 320 325

tcg ttt ccg ttg cgt ttc ggt cac act gga ggt tca atg atg caa tct 1182
Ser Phe Pro Leu Arg Phe Gly His Thr Gly Gly Ser Met Met Gln Ser
330 335 340

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acg tcg tca tca tca tct cat tct cgt cct ctg ttt tcc ccg gct gct    1230
Thr Ser Ser Ser Ser Ser His Ser Arg Pro Leu Phe Ser Pro Ala Ala
            345                 350                 355

gtt cag ccg cca cca gaa tca gct agc gaa acc ggt tat ctc cag gat    1278
Val Gln Pro Pro Pro Glu Ser Ala Ser Glu Thr Gly Tyr Leu Gln Asp
        360                 365                 370

ata caa tgg cca tca gac aag act agt aat aac tac aat aat agt cca    1326
Ile Gln Trp Pro Ser Asp Lys Thr Ser Asn Asn Tyr Asn Asn Ser Pro
    375                 380                 385

tcc tcc tga tgacttgctt cattttattt gtttcactat agagtaatag            1375
Ser Ser  *
390

aaaacaggaa aatgattata tgttatagag ttatttttcc aaatattata gggtttaggt 1435
tgtttgtatt gttctgcttt catcctctca tgcttttttt cttaatttat tatatttttg 1495
cattataatt tcgtttcatt gtaacaaaca ttaaaaagac cacatggaga aaggaaaaaa 1555
aagagag                                                            1562

&lt;210&gt; 48
&lt;211&gt; 391
&lt;212&gt; PRT
&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48
Met Cys Val Leu Lys Val Ala Asn Gln Glu Asp Asn Val Gly Lys Lys
1               5                   10                  15
Ala Glu Ser Ile Arg Asp Asp Asp His Arg Thr Leu Ser Glu Ile Asp
            20                  25                  30
Gln Trp Leu Tyr Leu Phe Ala Ala Glu Asp Asp His His Arg His Ser
        35                  40                  45
Phe Pro Thr Gln Gln Pro Pro Pro Ser Ser Ser Ser Ser Ser Leu Ile
    50                  55                  60
Ser Gly Phe Ser Arg Glu Met Glu Met Ser Ala Ile Val Ser Ala Leu
65                  70                  75                  80
Thr His Val Val Ala Gly Asn Val Pro Gln His Gln Gln Gly Gly Gly
                85                  90                  95
Glu Gly Ser Gly Glu Gly Thr Ser Asn Ser Ser Ser Ser Ser Gly Gln
            100                 105                 110
Lys Arg Arg Arg Glu Val Glu Glu Gly Gly Ala Lys Ala Val Lys Ala
        115                 120                 125
Ala Asn Thr Leu Thr Val Asp Gln Tyr Phe Ser Gly Gly Ser Ser Thr
    130                 135                 140
Ser Lys Val Arg Glu Ala Ser Ser Asn Met Ser Gly Pro Gly Pro Thr
145                 150                 155                 160
Tyr Glu Tyr Thr Thr Thr Ala Thr Ala Ser Ser Glu Thr Ser Ser Phe
                165                 170                 175
Ser Gly Asp Gln Pro Arg Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro
            180                 185                 190
Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Phe Lys Ala Ala Arg
        195                 200                 205
Val Trp Leu Gly Thr Phe Asp Asn Ala Glu Ser Ala Ala Arg Ala Tyr
    210                 215                 220
Asp Glu Ala Ala Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe
```

```
225                 230                 235                 240
Pro Glu Asn Val Lys Leu Val Arg Pro Ala Ser Thr Glu Ala Gln Pro
                245                 250                 255
Val His Gln Thr Ala Ala Gln Arg Pro Thr Gln Ser Arg Asn Ser Gly
            260                 265                 270
Ser Thr Thr Thr Leu Leu Pro Ile Arg Pro Ala Ser Asn Gln Ser Val
        275                 280                 285
His Ser Gln Pro Leu Met Gln Ser Tyr Asn Leu Ser Tyr Ser Glu Met
    290                 295                 300
Ala Arg Gln Gln Gln Gln Phe Gln Gln His His Gln Gln Ser Leu Asp
305                 310                 315                 320
Leu Tyr Asp Gln Met Ser Phe Pro Leu Arg Phe Gly His Thr Gly Gly
                325                 330                 335
Ser Met Met Gln Ser Thr Ser Ser Ser Ser Ser His Ser Arg Pro Leu
            340                 345                 350
Phe Ser Pro Ala Ala Val Gln Pro Pro Pro Glu Ser Ala Ser Glu Thr
        355                 360                 365
Gly Tyr Leu Gln Asp Ile Gln Trp Pro Ser Asp Lys Thr Ser Asn Asn
    370                 375                 380
Tyr Asn Asn Ser Pro Ser Ser
385                 390


<210> 49
<211> 1605
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (90)...(1547)

<400> 49
tctcacctat tgtaaaaatc accagtttcg tatataaaac cctaattttc tcaaaattcc 60
caaatattga cttggaatca aaaatccga atg gat gtg agc aaa gta acc aca    113
                                Met Asp Val Ser Lys Val Thr Thr
                                 1               5

agc gac ggc gga gga gat tca atg gag act aag cca tct cct caa cct    161
Ser Asp Gly Gly Gly Asp Ser Met Glu Thr Lys Pro Ser Pro Gln Pro
     10                  15                  20

cag cct gcg gcg att cta agt tca aac gcg cct cct ccg ttt ctg agc    209
Gln Pro Ala Ala Ile Leu Ser Ser Asn Ala Pro Pro Pro Phe Leu Ser
 25                  30                  35                  40

aag acc tat gat atg gtt gat gat cac aat aca gat tcg att gtc tct    257
Lys Thr Tyr Asp Met Val Asp Asp His Asn Thr Asp Ser Ile Val Ser
                 45                  50                  55

tgg agt gct aat aac aac agt ttt atc gtt tgg aaa cca ccg gag ttc    305
Trp Ser Ala Asn Asn Asn Ser Phe Ile Val Trp Lys Pro Pro Glu Phe
             60                  65                  70

gct cgc gat ctt ctt cct aag aac ttt aag cat aat aat ttc tcc agc    353
Ala Arg Asp Leu Leu Pro Lys Asn Phe Lys His Asn Asn Phe Ser Ser
         75                  80                  85
```

```
ttc gtt aga cag ctt aat acc tat ggt ttc agg aag gtt gac cca gat     401
Phe Val Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Val Asp Pro Asp
     90                  95                 100

aga tgg gaa ttt gcg aat gaa ggt ttt tta aga ggt cag aag cac ttg     449
Arg Trp Glu Phe Ala Asn Glu Gly Phe Leu Arg Gly Gln Lys His Leu
105                 110                 115                 120

cta caa tca ata act agg cga aaa cct gcc cat gga cag gga cag gga     497
Leu Gln Ser Ile Thr Arg Arg Lys Pro Ala His Gly Gln Gly Gln Gly
                125                 130                 135

cat cag cga tct cag cac tcg aat gga cag aac tca tct gtt agc gca     545
His Gln Arg Ser Gln His Ser Asn Gly Gln Asn Ser Ser Val Ser Ala
            140                 145                 150

tgt gtt gaa gtt ggc aaa ttt ggt ctc gaa gaa gaa gtt gaa agg ctt     593
Cys Val Glu Val Gly Lys Phe Gly Leu Glu Glu Glu Val Glu Arg Leu
        155                 160                 165

aaa aga gat aag aac gtc ctt atg caa gaa ctc gtc aga tta aga cag     641
Lys Arg Asp Lys Asn Val Leu Met Gln Glu Leu Val Arg Leu Arg Gln
    170                 175                 180

cag caa cag tcc act gat aac caa ctt caa acg atg gtt cag cgt ctc     689
Gln Gln Gln Ser Thr Asp Asn Gln Leu Gln Thr Met Val Gln Arg Leu
185                 190                 195                 200

cag ggc atg gag aat cgg caa caa caa tta atg tca ttc ctt gca aag     737
Gln Gly Met Glu Asn Arg Gln Gln Gln Leu Met Ser Phe Leu Ala Lys
                205                 210                 215

gca gta caa agc cct cat ttt cta tct caa ttc tta cag cag cag aat     785
Ala Val Gln Ser Pro His Phe Leu Ser Gln Phe Leu Gln Gln Gln Asn
            220                 225                 230

cag caa aac gag agt aat agg cgc atc agt gat acc agt aag aag cgg     833
Gln Gln Asn Glu Ser Asn Arg Arg Ile Ser Asp Thr Ser Lys Lys Arg
        235                 240                 245

aga ttc aag cga gac ggc att gtc cgt aat aat gat tct gct act cct     881
Arg Phe Lys Arg Asp Gly Ile Val Arg Asn Asn Asp Ser Ala Thr Pro
    250                 255                 260

gat gga cag ata gtg aag tat caa cct cca atg cac gag caa gcc aaa     929
Asp Gly Gln Ile Val Lys Tyr Gln Pro Pro Met His Glu Gln Ala Lys
265                 270                 275                 280

gca atg ttt aaa cag ctt atg aag atg gaa cct tac aaa acc ggc gat     977
Ala Met Phe Lys Gln Leu Met Lys Met Glu Pro Tyr Lys Thr Gly Asp
                285                 290                 295

gat ggt ttc ctt cta ggt aat ggt acg tct act acc gag gga aca gag    1025
Asp Gly Phe Leu Leu Gly Asn Gly Thr Ser Thr Thr Glu Gly Thr Glu
            300                 305                 310
```

```
atg gag act tca tca aac caa gta tcg ggt ata act ctt aag gaa atg    1073
Met Glu Thr Ser Ser Asn Gln Val Ser Gly Ile Thr Leu Lys Glu Met
        315                 320                 325

cct aca gct tct gag ata cag tca tca tca cca att gaa aca act cct    1121
Pro Thr Ala Ser Glu Ile Gln Ser Ser Ser Pro Ile Glu Thr Thr Pro
    330                 335                 340

gaa aat gtt tcg gca gca tca gaa gca acc gag aac tgt att cct tca    1169
Glu Asn Val Ser Ala Ala Ser Glu Ala Thr Glu Asn Cys Ile Pro Ser
345                 350                 355                 360

cct gat gat cta act ctt ccc gac ttc act cat atg cta ccg gaa aat    1217
Pro Asp Asp Leu Thr Leu Pro Asp Phe Thr His Met Leu Pro Glu Asn
                365                 370                 375

aat tca gag aag cct cca gag agt ttc atg gaa cca aac ctg gga ggt    1265
Asn Ser Glu Lys Pro Pro Glu Ser Phe Met Glu Pro Asn Leu Gly Gly
            380                 385                 390

tct agt cca tta cta gat cca gat ctg ttg atc gat gat tct ttg tcc    1313
Ser Ser Pro Leu Leu Asp Pro Asp Leu Leu Ile Asp Asp Ser Leu Ser
        395                 400                 405

ttc gac att gac gac ttt cca atg gat tct gat ata gac cct gtt gat    1361
Phe Asp Ile Asp Asp Phe Pro Met Asp Ser Asp Ile Asp Pro Val Asp
    410                 415                 420

tac ggt tta ctc gaa cgc tta ctc atg tca agc ccg gtt cca gat aat    1409
Tyr Gly Leu Leu Glu Arg Leu Leu Met Ser Ser Pro Val Pro Asp Asn
425                 430                 435                 440

atg gat tca aca cca gtg gac aat gaa aca gag cag gaa caa aat gga    1457
Met Asp Ser Thr Pro Val Asp Asn Glu Thr Glu Gln Glu Gln Asn Gly
                445                 450                 455

tgg gac aaa act aag cat atg gat aat ctg act caa cag atg ggt ctc    1505
Trp Asp Lys Thr Lys His Met Asp Asn Leu Thr Gln Gln Met Gly Leu
            460                 465                 470

ctc tct cct gaa acc tta gat ctc tca agg caa aat cct tga            1547
Leu Ser Pro Glu Thr Leu Asp Leu Ser Arg Gln Asn Pro  *
        475                 480                 485

ttttgggagt ttttaaagtc ttttgaggta acacagtccc tgagagcagc atattcat    1605
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<210> 50
<211> 485
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (32)...(130)
<223> Conserved domain

<400> 50

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Met Asp Val Ser Lys Val Thr Thr Ser Asp Gly Gly Gly Asp Ser Met
1               5                   10                  15
Glu Thr Lys Pro Ser Pro Gln Pro Gln Pro Ala Ala Ile Leu Ser Ser
            20                  25                  30
Asn Ala Pro Pro Pro Phe Leu Ser Lys Thr Tyr Asp Met Val Asp Asp
        35                  40                  45
His Asn Thr Asp Ser Ile Val Ser Trp Ser Ala Asn Asn Asn Ser Phe
    50                  55                  60
Ile Val Trp Lys Pro Pro Glu Phe Ala Arg Asp Leu Leu Pro Lys Asn
65                  70                  75                  80
Phe Lys His Asn Asn Phe Ser Ser Phe Val Arg Gln Leu Asn Thr Tyr
                85                  90                  95
Gly Phe Arg Lys Val Asp Pro Asp Arg Trp Glu Phe Ala Asn Glu Gly
            100                 105                 110
Phe Leu Arg Gly Gln Lys His Leu Leu Gln Ser Ile Thr Arg Arg Lys
        115                 120                 125
Pro Ala His Gly Gln Gly Gln Gly His Gln Arg Ser Gln His Ser Asn
    130                 135                 140
Gly Gln Asn Ser Ser Val Ser Ala Cys Val Glu Val Gly Lys Phe Gly
145                 150                 155                 160
Leu Glu Glu Glu Val Glu Arg Leu Lys Arg Asp Lys Asn Val Leu Met
                165                 170                 175
Gln Glu Leu Val Arg Leu Arg Gln Gln Gln Gln Ser Thr Asp Asn Gln
            180                 185                 190
Leu Gln Thr Met Val Gln Arg Leu Gln Gly Met Glu Asn Arg Gln Gln
        195                 200                 205
Gln Leu Met Ser Phe Leu Ala Lys Ala Val Gln Ser Pro His Phe Leu
    210                 215                 220
Ser Gln Phe Leu Gln Gln Gln Asn Gln Gln Asn Glu Ser Asn Arg Arg
225                 230                 235                 240
Ile Ser Asp Thr Ser Lys Lys Arg Arg Phe Lys Arg Asp Gly Ile Val
                245                 250                 255
Arg Asn Asn Asp Ser Ala Thr Pro Asp Gly Gln Ile Val Lys Tyr Gln
            260                 265                 270
Pro Pro Met His Glu Gln Ala Lys Ala Met Phe Lys Gln Leu Met Lys
        275                 280                 285
Met Glu Pro Tyr Lys Thr Gly Asp Asp Gly Phe Leu Leu Gly Asn Gly
    290                 295                 300
Thr Ser Thr Thr Glu Gly Thr Glu Met Glu Thr Ser Ser Asn Gln Val
305                 310                 315                 320
Ser Gly Ile Thr Leu Lys Glu Met Pro Thr Ala Ser Glu Ile Gln Ser
                325                 330                 335
Ser Ser Pro Ile Glu Thr Thr Pro Glu Asn Val Ser Ala Ala Ser Glu
            340                 345                 350
Ala Thr Glu Asn Cys Ile Pro Ser Pro Asp Asp Leu Thr Leu Pro Asp
        355                 360                 365
Phe Thr His Met Leu Pro Glu Asn Asn Ser Glu Lys Pro Pro Glu Ser
    370                 375                 380
Phe Met Glu Pro Asn Leu Gly Gly Ser Ser Pro Leu Leu Asp Pro Asp
385                 390                 395                 400
Leu Leu Ile Asp Asp Ser Leu Ser Phe Asp Ile Asp Asp Phe Pro Met
                405                 410                 415
Asp Ser Asp Ile Asp Pro Val Asp Tyr Gly Leu Leu Glu Arg Leu Leu
            420                 425                 430
Met Ser Ser Pro Val Pro Asp Asn Met Asp Ser Thr Pro Val Asp Asn
        435                 440                 445
Glu Thr Glu Gln Glu Gln Asn Gly Trp Asp Lys Thr Lys His Met Asp
```

```
    450                     455                     460
Asn Leu Thr Gln Gln Met Gly Leu Leu Ser Pro Glu Thr Leu Asp Leu
465                 470                     475                 480
Ser Arg Gln Asn Pro
                485
```

<210> 51
<211> 584
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (157)...(441)

<400> 51

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ctctctctct cactcttttc ttttccgaga acccaacaaa aaaaaagcta ctattaatcc 60
ttcccctcgt gaggaaatca tttcttcttg tttctcgaga tttattctct ttctctctct 120
ctttctctgt gtgtttcgtg tcttcagatt agttcg atg ttt cgt tca gac aag   174
                                        Met Phe Arg Ser Asp Lys
                                         1               5

gcg gaa aaa atg gat aaa cga cga cgg aga cag agc aaa gcc aag gct   222
Ala Glu Lys Met Asp Lys Arg Arg Arg Arg Gln Ser Lys Ala Lys Ala
            10                  15                  20

tct tgt tcc gaa gag gtg agt agt atc gaa tgg gaa gct gtg aag atg   270
Ser Cys Ser Glu Glu Val Ser Ser Ile Glu Trp Glu Ala Val Lys Met
        25                  30                  35

tca gaa gaa gaa gaa gat ctc att tct cgg atg tat aaa ctc gtt ggc   318
Ser Glu Glu Glu Glu Asp Leu Ile Ser Arg Met Tyr Lys Leu Val Gly
    40                  45                  50

gac agg tgg gag ttg atc gcc gga agg atc ccg gga cgg acg ccg gag   366
Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Pro Glu
 55                  60                  65                  70

gag ata gag aga tat tgg ctt atg aaa cac ggc gtc gtt ttt gcc aac   414
Glu Ile Glu Arg Tyr Trp Leu Met Lys His Gly Val Val Phe Ala Asn
                75                  80                  85

aga cga aga gac ttt ttt agg aaa tga tttttttgt ttggattaaa         461
Arg Arg Arg Asp Phe Phe Arg Lys  *
            90

agaaaatttt cctctcctta attcacaaga caagaaaaaa aggaaatgta cctgtccttg 521
aattactatt ttggaatgta taattatcta tatatataag aagaaaaaat tgcttaggaa 581
ttt                                                               584
```

<210> 52
<211> 94
<212> PRT
<213> Arabidopsis thaliana

<220>

<221> DOMAIN
<222> (39)...(76)
<223> Conserved domain

<400> 52
Met Phe Arg Ser Asp Lys Ala Glu Lys Met Asp Lys Arg Arg Arg Arg
1 5 10 15
Gln Ser Lys Ala Lys Ala Ser Cys Ser Glu Glu Val Ser Ser Ile Glu
20 25 30
Trp Glu Ala Val Lys Met Ser Glu Glu Glu Glu Asp Leu Ile Ser Arg
35 40 45
Met Tyr Lys Leu Val Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile
50 55 60
Pro Gly Arg Thr Pro Glu Glu Ile Glu Arg Tyr Trp Leu Met Lys His
65 70 75 80
Gly Val Val Phe Ala Asn Arg Arg Arg Asp Phe Phe Arg Lys
85 90

<210> 53
<211> 407
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (10)...(348)

<400> 53
ccagtagtt atg gat aat acc aac cgt ctt cgt ctt cgt cgc ggt ccc agt 51
Met Asp Asn Thr Asn Arg Leu Arg Leu Arg Arg Gly Pro Ser
1 5 10

ctt agg caa act aag ttc act cga tcc cga tat gac tct gaa gaa gtg 99
Leu Arg Gln Thr Lys Phe Thr Arg Ser Arg Tyr Asp Ser Glu Glu Val
15 20 25 30

agt agc atc gaa tgg gag ttt atc agt atg acc gaa caa gaa gaa gat 147
Ser Ser Ile Glu Trp Glu Phe Ile Ser Met Thr Glu Gln Glu Glu Asp
35 40 45

ctc atc tct cga atg tac aga ctt gtc ggt aat agg tgg gat tta ata 195
Leu Ile Ser Arg Met Tyr Arg Leu Val Gly Asn Arg Trp Asp Leu Ile
50 55 60

gca gga aga gtc gta gga aga aag gca aat gag att gag aga tac tgg 243
Ala Gly Arg Val Val Gly Arg Lys Ala Asn Glu Ile Glu Arg Tyr Trp
65 70 75

att atg aga aac tct gac tat ttt tct cac aaa cga cga cgt ctt aat 291
Ile Met Arg Asn Ser Asp Tyr Phe Ser His Lys Arg Arg Arg Leu Asn
80 85 90

aat tct ccc ttt ttt tct act tct cct ctt aat ctc caa gaa aat cta 339
Asn Ser Pro Phe Phe Ser Thr Ser Pro Leu Asn Leu Gln Glu Asn Leu
95 100 105 110

```
aaa ttg taa agaaatcaaa ataaaagctt tcaatcataa aagtagaaca           388
Lys Leu  *

aatcttgaat gtcttctca                                              407

<210> 54
<211> 112
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (28)...(78)
<223> Conserved domain

<400> 54
Met Asp Asn Thr Asn Arg Leu Arg Leu Arg Arg Gly Pro Ser Leu Arg
 1               5                  10                  15
Gln Thr Lys Phe Thr Arg Ser Arg Tyr Asp Ser Glu Glu Val Ser Ser
            20                  25                  30
Ile Glu Trp Glu Phe Ile Ser Met Thr Glu Gln Glu Glu Asp Leu Ile
        35                  40                  45
Ser Arg Met Tyr Arg Leu Val Gly Asn Arg Trp Asp Leu Ile Ala Gly
    50                  55                  60
Arg Val Val Gly Arg Lys Ala Asn Glu Ile Glu Arg Tyr Trp Ile Met
65                  70                  75                  80
Arg Asn Ser Asp Tyr Phe Ser His Lys Arg Arg Arg Leu Asn Asn Ser
                85                  90                  95
Pro Phe Phe Ser Thr Ser Pro Leu Asn Leu Gln Glu Asn Leu Lys Leu
            100                 105                 110


<210> 55
<211> 2405
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (381)...(2213)

<400> 55
aagccacaca atctcttttc ttctctctct ctctgttata tctcttctgt ttaattcttt 60
tattcttctt cgtctatctt ctcctataat ctcttctctc tccctcttca cctaaagaat 120
aagaagaaaa ataattcaca tctttatgca aactactttc ttgtagggtt ttaggagcta 180
tctctattgt cttggttctg atacaaagtt ttgtaatttt catggtatga gaagatttgc 240
ctttctattt tgtttattgg ttctttttaa ctttttcttg gagatgggtt cttgtagatc 300
ttaatgaaac ttctgttttt gtcccaaaaa gagtttcttt ttttcttctc ttctttttgg 360
gttttcaatt cttgagagac atg gca aga gat cag ttc tat ggt cac aat aac 413
                      Met Ala Arg Asp Gln Phe Tyr Gly His Asn Asn
                       1               5                  10

cat cat cat caa gag caa caa cat caa atg att aat cag atc caa ggg   461
His His His Gln Glu Gln Gln His Gln Met Ile Asn Gln Ile Gln Gly
            15                  20                  25
```

```
ttt gat gag aca aac caa aac cca acc gat cat cat cat tac aat cat    509
Phe Asp Glu Thr Asn Gln Asn Pro Thr Asp His His His Tyr Asn His
        30                  35                  40

cag atc ttt ggc tca aac tcc aac atg ggt atg atg ata gac ttc tct    557
Gln Ile Phe Gly Ser Asn Ser Asn Met Gly Met Met Ile Asp Phe Ser
    45                  50                  55

aag caa caa cag att agg atg aca agt ggt tcg gat cat cat cat cat    605
Lys Gln Gln Gln Ile Arg Met Thr Ser Gly Ser Asp His His His His
60                  65                  70                  75

cat cat cag aca agt ggt ggt act gat cag aat cag ctt ctg gaa gat    653
His His Gln Thr Ser Gly Gly Thr Asp Gln Asn Gln Leu Leu Glu Asp
                80                  85                  90

tct tca tct gcc atg aga cta tgc aat gtt aat aat gat ttc cca agt    701
Ser Ser Ser Ala Met Arg Leu Cys Asn Val Asn Asn Asp Phe Pro Ser
            95                  100                 105

gaa gta aat gat gag aga cca cca caa aga cca agc caa ggt ctt tcc    749
Glu Val Asn Asp Glu Arg Pro Pro Gln Arg Pro Ser Gln Gly Leu Ser
        110                 115                 120

ctt tct ctc tcc tct tca aat cct aca agc atc agt ctc caa tct ttc    797
Leu Ser Leu Ser Ser Ser Asn Pro Thr Ser Ile Ser Leu Gln Ser Phe
    125                 130                 135

gaa ctc aga ccc caa caa caa caa caa ggg tat tcc ggt aat aaa tca    845
Glu Leu Arg Pro Gln Gln Gln Gln Gln Gly Tyr Ser Gly Asn Lys Ser
140                 145                 150                 155

aca caa cat cag aat ctc caa cac acg cag atg atg atg atg atg atg    893
Thr Gln His Gln Asn Leu Gln His Thr Gln Met Met Met Met Met Met
                160                 165                 170

aat agt cac cac caa aac aac aac aat aac aat cat cag cat cat aat    941
Asn Ser His His Gln Asn Asn Asn Asn Asn Asn His Gln His His Asn
            175                 180                 185

cat cat cag ttt cag att ggg agt tcc aag tat ttg agt cca gct caa    989
His His Gln Phe Gln Ile Gly Ser Ser Lys Tyr Leu Ser Pro Ala Gln
        190                 195                 200

gag cta ctg agt gag ttt tgc agt ctt gga gta aag gaa agc gat gaa    1037
Glu Leu Leu Ser Glu Phe Cys Ser Leu Gly Val Lys Glu Ser Asp Glu
    205                 210                 215

gaa gtg atg atg atg aag cat aag aag aag caa aag ggt aaa caa caa    1085
Glu Val Met Met Met Lys His Lys Lys Lys Gln Lys Gly Lys Gln Gln
220                 225                 230                 235

gaa gag tgg gac aca agt cac cac agc aac aat gat caa cat gac caa    1133
Glu Glu Trp Asp Thr Ser His His Ser Asn Asn Asp Gln His Asp Gln
                240                 245                 250

tct gcg act act tct tca aag aaa cat gtt cca cca ctt cac tct ctt    1181
```

Ser Ala Thr Thr Ser Ser Lys Lys His Val Pro Pro Leu His Ser Leu
255 260 265

gag ttc atg gaa ctt cag aaa aga aaa gcc aag ttg ctc tcc atg ctc 1229
Glu Phe Met Glu Leu Gln Lys Arg Lys Ala Lys Leu Leu Ser Met Leu
270 275 280

gaa gag ctt aaa aga aga tat gga cat tac cga gag caa atg aga gtt 1277
Glu Glu Leu Lys Arg Arg Tyr Gly His Tyr Arg Glu Gln Met Arg Val
285 290 295

gcg gcg gca gcc ttt gaa gcg gcg gtt gga cta gga ggg gca gag ata 1325
Ala Ala Ala Ala Phe Glu Ala Ala Val Gly Leu Gly Gly Ala Glu Ile
300 305 310 315

tac act gcg tta gcg tca agg gca atg tca aga cac ttt cgg tgt tta 1373
Tyr Thr Ala Leu Ala Ser Arg Ala Met Ser Arg His Phe Arg Cys Leu
320 325 330

aaa gac gga ctt gtg gga cag att caa gca aca agt caa gct ttg gga 1421
Lys Asp Gly Leu Val Gly Gln Ile Gln Ala Thr Ser Gln Ala Leu Gly
335 340 345

gag aga gaa gag gat aat cgt gcg gtt tct att gca gca cgt gga gaa 1469
Glu Arg Glu Glu Asp Asn Arg Ala Val Ser Ile Ala Ala Arg Gly Glu
350 355 360

act cca cgg ttg aga ttg ctc gat caa gct ttg cgg caa cag aaa tcg 1517
Thr Pro Arg Leu Arg Leu Leu Asp Gln Ala Leu Arg Gln Gln Lys Ser
365 370 375

tat cgc caa atg act ctt gtt gac gct cat cct tgg cgt cca caa cgc 1565
Tyr Arg Gln Met Thr Leu Val Asp Ala His Pro Trp Arg Pro Gln Arg
380 385 390 395

ggc ttg cct gaa cgc gca gtc aca acg ttg aga gct tgg ctc ttt gaa 1613
Gly Leu Pro Glu Arg Ala Val Thr Thr Leu Arg Ala Trp Leu Phe Glu
400 405 410

cac ttt ctt cac cca tat ccg agc gat gtt gat aag cat ata ttg gcc 1661
His Phe Leu His Pro Tyr Pro Ser Asp Val Asp Lys His Ile Leu Ala
415 420 425

cga caa act ggt tta tca aga agt cag gta tca aat tgg ttt att aat 1709
Arg Gln Thr Gly Leu Ser Arg Ser Gln Val Ser Asn Trp Phe Ile Asn
430 435 440

gca aga gtt agg cta tgg aaa cca atg att gaa gaa atg tac tgt gaa 1757
Ala Arg Val Arg Leu Trp Lys Pro Met Ile Glu Glu Met Tyr Cys Glu
445 450 455

gaa aca aga agt gaa caa atg gag att aca aac ccg atg atg atc gat 1805
Glu Thr Arg Ser Glu Gln Met Glu Ile Thr Asn Pro Met Met Ile Asp
460 465 470 475

act aaa ccg gac ccg gac cag ttg atc cgt gtc gaa ccg gaa tct tta 1853
Thr Lys Pro Asp Pro Asp Gln Leu Ile Arg Val Glu Pro Glu Ser Leu

```
                480                   485                   490

tcc tca ata gtg aca aac cct aca tcc aaa tcc ggt cac aac tca acc    1901
Ser Ser Ile Val Thr Asn Pro Thr Ser Lys Ser Gly His Asn Ser Thr
            495                 500                 505

cat gga acg atg tcg tta ggg tca acg ttt gac ttt tcc ttg tac ggt    1949
His Gly Thr Met Ser Leu Gly Ser Thr Phe Asp Phe Ser Leu Tyr Gly
        510                 515                 520

aac caa gct gtg aca tac gct ggt gaa gga ggg cca cgt ggt gac gtt    1997
Asn Gln Ala Val Thr Tyr Ala Gly Glu Gly Gly Pro Arg Gly Asp Val
    525                 530                 535

tcc ttg acg ctt ggg tta caa cgt aac gat ggt aac ggt ggt gtg agt    2045
Ser Leu Thr Leu Gly Leu Gln Arg Asn Asp Gly Asn Gly Gly Val Ser
540                 545                 550                 555

tta gcg ttg tct cca gtg acg gct caa ggt ggc caa ctt ttc tac ggt    2093
Leu Ala Leu Ser Pro Val Thr Ala Gln Gly Gly Gln Leu Phe Tyr Gly
                560                 565                 570

aga gac cac att gaa gaa gga ccg gtt caa tat tca gcg tcg atg tta    2141
Arg Asp His Ile Glu Glu Gly Pro Val Gln Tyr Ser Ala Ser Met Leu
            575                 580                 585

gat gat gat caa gtt cag aat ttg cct tat agg aat ttg atg gga gct    2189
Asp Asp Asp Gln Val Gln Asn Leu Pro Tyr Arg Asn Leu Met Gly Ala
        590                 595                 600

caa tta ctt cat gat att gtt tga gattaaaaga ttaggaccaa agttatcgat   2243
Gln Leu Leu His Asp Ile Val  *
    605                 610

acatattttc caaaaccgat tcggttatgt aacggtttag ttagataaaa accaaattag 2303
atatttatat ataccgttgt ctgattggat tggaggattg gtggacaagg agatattatt 2363
aatgtatgag ttagttggtt cgtcaaaaaa aaaaaaaaaa aa                     2405

<210> 56
<211> 610
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (392)...(452)
<223> Conserved domain

<400> 56
Met Ala Arg Asp Gln Phe Tyr Gly His Asn Asn His His His Gln Glu
 1               5                  10                  15
Gln Gln His Gln Met Ile Asn Gln Ile Gln Gly Phe Asp Glu Thr Asn
            20                  25                  30
Gln Asn Pro Thr Asp His His His Tyr Asn His Gln Ile Phe Gly Ser
        35                  40                  45
Asn Ser Asn Met Gly Met Met Ile Asp Phe Ser Lys Gln Gln Gln Ile
    50                  55                  60
```

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Arg Met Thr Ser Gly Ser Asp His His His His His His Gln Thr Ser
65                  70                  75                  80
Gly Gly Thr Asp Gln Asn Gln Leu Leu Glu Asp Ser Ser Ser Ala Met
                85                  90                  95
Arg Leu Cys Asn Val Asn Asn Asp Phe Pro Ser Glu Val Asn Asp Glu
            100                 105                 110
Arg Pro Pro Gln Arg Pro Ser Gln Gly Leu Ser Leu Ser Leu Ser Ser
        115                 120                 125
Ser Asn Pro Thr Ser Ile Ser Leu Gln Ser Phe Glu Leu Arg Pro Gln
    130                 135                 140
Gln Gln Gln Gln Gly Tyr Ser Gly Asn Lys Ser Thr Gln His Gln Asn
145                 150                 155                 160
Leu Gln His Thr Gln Met Met Met Met Met Met Asn Ser His His Gln
                165                 170                 175
Asn Asn Asn Asn Asn Asn His Gln His His Asn His His Gln Phe Gln
            180                 185                 190
Ile Gly Ser Ser Lys Tyr Leu Ser Pro Ala Gln Glu Leu Leu Ser Glu
        195                 200                 205
Phe Cys Ser Leu Gly Val Lys Glu Ser Asp Glu Glu Val Met Met Met
    210                 215                 220
Lys His Lys Lys Lys Gln Lys Gly Lys Gln Gln Glu Glu Trp Asp Thr
225                 230                 235                 240
Ser His His Ser Asn Asn Asp Gln His Asp Gln Ser Ala Thr Thr Ser
                245                 250                 255
Ser Lys Lys His Val Pro Pro Leu His Ser Leu Glu Phe Met Glu Leu
            260                 265                 270
Gln Lys Arg Lys Ala Lys Leu Leu Ser Met Leu Glu Glu Leu Lys Arg
        275                 280                 285
Arg Tyr Gly His Tyr Arg Glu Gln Met Arg Val Ala Ala Ala Ala Phe
    290                 295                 300
Glu Ala Ala Val Gly Leu Gly Gly Ala Glu Ile Tyr Thr Ala Leu Ala
305                 310                 315                 320
Ser Arg Ala Met Ser Arg His Phe Arg Cys Leu Lys Asp Gly Leu Val
                325                 330                 335
Gly Gln Ile Gln Ala Thr Ser Gln Ala Leu Gly Glu Arg Glu Glu Asp
            340                 345                 350
Asn Arg Ala Val Ser Ile Ala Ala Arg Gly Glu Thr Pro Arg Leu Arg
        355                 360                 365
Leu Leu Asp Gln Ala Leu Arg Gln Gln Lys Ser Tyr Arg Gln Met Thr
    370                 375                 380
Leu Val Asp Ala His Pro Trp Arg Pro Gln Arg Gly Leu Pro Glu Arg
385                 390                 395                 400
Ala Val Thr Thr Leu Arg Ala Trp Leu Phe Glu His Phe Leu His Pro
                405                 410                 415
Tyr Pro Ser Asp Val Asp Lys His Ile Leu Ala Arg Gln Thr Gly Leu
            420                 425                 430
Ser Arg Ser Gln Val Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Leu
        435                 440                 445
Trp Lys Pro Met Ile Glu Glu Met Tyr Cys Glu Glu Thr Arg Ser Glu
    450                 455                 460
Gln Met Glu Ile Thr Asn Pro Met Met Ile Asp Thr Lys Pro Asp Pro
465                 470                 475                 480
Asp Gln Leu Ile Arg Val Glu Pro Glu Ser Leu Ser Ser Ile Val Thr
                485                 490                 495
Asn Pro Thr Ser Lys Ser Gly His Asn Ser Thr His Gly Thr Met Ser
            500                 505                 510
Leu Gly Ser Thr Phe Asp Phe Ser Leu Tyr Gly Asn Gln Ala Val Thr
```

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        515                 520                 525
Tyr Ala Gly Glu Gly Gly Pro Arg Gly Asp Val Ser Leu Thr Leu Gly
    530                 535                 540
Leu Gln Arg Asn Asp Gly Asn Gly Gly Val Ser Leu Ala Leu Ser Pro
545                 550                 555                 560
Val Thr Ala Gln Gly Gly Gln Leu Phe Tyr Gly Arg Asp His Ile Glu
                565                 570                 575
Glu Gly Pro Val Gln Tyr Ser Ala Ser Met Leu Asp Asp Asp Gln Val
            580                 585                 590
Gln Asn Leu Pro Tyr Arg Asn Leu Met Gly Ala Gln Leu Leu His Asp
        595                 600                 605
Ile Val
    610


<210> 57
<211> 890
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (55)...(738)

<400> 57
gcaaccttca aactaaaact cgagagacaa gaaatcctca gaatctttaa ctta atg    57
                                                            Met
                                                             1

gcg ctc gag gct ctt aca tca cca aga tta gct tct ccg att cct cct   105
Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro Pro
            5                   10                  15

ttg ttc gaa gat tct tca gtc ttc cat gga gtc gag cac tgg aca aag   153
Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr Lys
        20                  25                  30

ggt aag cga tct aag aga tca aga tcc gat ttc cac cac caa aac ctc   201
Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn Leu
    35                  40                  45

act gag gaa gag tat cta gct ttt tgc ctc atg ctt ctc gct cgc gac   249
Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp
50                  55                  60                  65

aac cgt cag cct cct cct cct ccg gcg gtg gag aag ttg agc tac aag   297
Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr Lys
                70                  75                  80

tgt agc gtc tgc gac aag acg ttc tct tct tac caa gct ctc ggt ggt   345
Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly
            85                  90                  95

cac aag gca agc cac cgt aag aac tta tca cag act ctc tcc ggc gga   393
His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly Gly
        100                 105                 110
```

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gga gat gat cat tca acc tcg tcg gcg aca acc aca tcc gcc gtg act     441
Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val Thr
    115                 120                 125

act gga agt ggg aaa tca cac gtt tgc acc atc tgt aac aag tct ttt     489
Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser Phe
130                 135                 140                 145

cct tcc ggt caa gct ctc ggc gga cac aag cgg tgc cac tac gaa gga     537
Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly
                150                 155                 160

aac aac aac atc aac act agt agc gtg tcc aac tcc gaa ggt gcg ggg     585
Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala Gly
            165                 170                 175

tcc act agc cac gtt agc agt agc cac cgt ggg ttt gac ctc aac atc     633
Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn Ile
        180                 185                 190

cct ccg atc cct gaa ttc tcg atg gtc aac gga gac gac gaa gtc atg     681
Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val Met
    195                 200                 205

agc cct atg ccg gcg aag aag cct cgg ttt gac ttt ccg gtc aaa ctt     729
Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys Leu
210                 215                 220                 225

caa ctt taa ggaaatttac ttagacgata agatttcgtt tgtatactgt             778
Gln Leu  *


tgagagttgt gtaggaattt gttgactgta cataccaaat tggactttga ctgattccaa 838
ttcttcttgt tctttcattt taaaaattat taaaccgatt ctttaccaca aa           890

<210> 58
<211> 227
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (82)...(102)
<223> Conserved domain

<221> DOMAIN
<222> (136)...(154)
<223> Conserved domain

<400> 58
Met Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro
 1               5                  10                  15
Pro Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr
            20                  25                  30
Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn
        35                  40                  45
Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
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    50                  55                  60
Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
65                  70                  75                  80
Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
                85                  90                  95
Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly
            100                 105                 110
Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val
        115                 120                 125
Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser
    130                 135                 140
Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu
145                 150                 155                 160
Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala
                165                 170                 175
Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn
            180                 185                 190
Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val
        195                 200                 205
Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys
    210                 215                 220
Leu Gln Leu
225


<210> 59
<211> 1413
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (86)...(1168)

<400> 59
aatttgtttt tttttctttt gtgggttcaa ttcgaattgt tttccctgag actcaagtta 60
ctgtgtcatt actctgcatt gagca atg ggt agc aac gaa gaa gga aac ccc    112
                            Met Gly Ser Asn Glu Glu Gly Asn Pro
                             1               5

act aac aac tct gat aag cca tcg caa gct gct gct cct gag cag agt    160
Thr Asn Asn Ser Asp Lys Pro Ser Gln Ala Ala Ala Pro Glu Gln Ser
 10                  15                  20                  25

aat gtt cat gtg tat cat cat gac tgg gct gct atg cag gca tat tat    208
Asn Val His Val Tyr His His Asp Trp Ala Ala Met Gln Ala Tyr Tyr
                 30                  35                  40

ggg cct aga gtt ggt ata cct caa tat tac aac tca aat ttg gcg cct    256
Gly Pro Arg Val Gly Ile Pro Gln Tyr Tyr Asn Ser Asn Leu Ala Pro
             45                  50                  55

ggt cat gct cca ccg cct tat atg tgg gcg tct cca tcg cca atg atg    304
Gly His Ala Pro Pro Pro Tyr Met Trp Ala Ser Pro Ser Pro Met Met
         60                  65                  70

gct cct tat gga gca cca tat cca cca ttt tgc cct cct ggt gga gtt    352
```

```
Ala Pro Tyr Gly Ala Pro Tyr Pro Pro Phe Cys Pro Pro Gly Gly Val
    75                  80                  85

tat gct cat cct ggt gtt caa atg ggc tca caa cca caa ggt cct gtt      400
Tyr Ala His Pro Gly Val Gln Met Gly Ser Gln Pro Gln Gly Pro Val
 90                 95                 100                 105

tct caa tca gca tct gga gtt aca acc cct ttg acc att gat gca cca      448
Ser Gln Ser Ala Ser Gly Val Thr Thr Pro Leu Thr Ile Asp Ala Pro
                110                 115                 120

gct aat tca gct gga aac tca gat cat ggg ttc atg aaa aag ctg aaa      496
Ala Asn Ser Ala Gly Asn Ser Asp His Gly Phe Met Lys Lys Leu Lys
            125                 130                 135

gag ttc gat gga ctt gca atg tca ata agc aat aac aaa gtt ggg agt      544
Glu Phe Asp Gly Leu Ala Met Ser Ile Ser Asn Asn Lys Val Gly Ser
        140                 145                 150

gct gaa cat agc agc agt gaa cat agg agt tct cag agc tcc gag aat      592
Ala Glu His Ser Ser Ser Glu His Arg Ser Ser Gln Ser Ser Glu Asn
    155                 160                 165

gat ggc tct agc aat ggt agt gat ggt aat aca act ggg gga gaa caa      640
Asp Gly Ser Ser Asn Gly Ser Asp Gly Asn Thr Thr Gly Gly Glu Gln
170                 175                 180                 185

tct agg agg aaa aga agg caa caa aga tca cca agc act ggt gaa aga      688
Ser Arg Arg Lys Arg Arg Gln Gln Arg Ser Pro Ser Thr Gly Glu Arg
                190                 195                 200

ccc tca tct caa aac agt ctg cct ctt aga ggt gaa aat gag aaa ccc      736
Pro Ser Ser Gln Asn Ser Leu Pro Leu Arg Gly Glu Asn Glu Lys Pro
            205                 210                 215

gat gtg act atg ggg act cct gtt atg ccc aca gca atg agt ttc caa      784
Asp Val Thr Met Gly Thr Pro Val Met Pro Thr Ala Met Ser Phe Gln
        220                 225                 230

aac tct gct ggc atg aac ggt gtg cca cag cca tgg aat gaa aaa gag      832
Asn Ser Ala Gly Met Asn Gly Val Pro Gln Pro Trp Asn Glu Lys Glu
    235                 240                 245

gtt aaa cga gag aag aga aaa cag tca aac cga gaa tct gct agg agg      880
Val Lys Arg Glu Lys Arg Lys Gln Ser Asn Arg Glu Ser Ala Arg Arg
250                 255                 260                 265

tca aga ctg agg aag cag gct gaa aca gaa caa cta tct gtc aaa gtt      928
Ser Arg Leu Arg Lys Gln Ala Glu Thr Glu Gln Leu Ser Val Lys Val
                270                 275                 280

gac gca tta gta gct gag aac atg tct ctg agg tct aaa cta ggc cag      976
Asp Ala Leu Val Ala Glu Asn Met Ser Leu Arg Ser Lys Leu Gly Gln
            285                 290                 295

cta aac aat gag tct gag aaa cta cgg ctg gag aac gaa gct ata ttg      1024
Leu Asn Asn Glu Ser Glu Lys Leu Arg Leu Glu Asn Glu Ala Ile Leu
```

300 305 310

gat caa ctg aaa gcg caa gca aca ggg aaa aca gag aac ctg atc tct 1072
Asp Gln Leu Lys Ala Gln Ala Thr Gly Lys Thr Glu Asn Leu Ile Ser
315 320 325

cga gtt gat aag aac aac tct gta tca ggt agc aaa act gtg cag cat 1120
Arg Val Asp Lys Asn Asn Ser Val Ser Gly Ser Lys Thr Val Gln His
330 335 340 345

caa ctg tta aat gca agt ccg ata acc gat cct gtc gcg gct agc tga 1168
Gln Leu Leu Asn Ala Ser Pro Ile Thr Asp Pro Val Ala Ala Ser *
350 355 360

ccgtggccgc aacaatgaga acccgatatt tcttcctttg ggttgtgatt gtaacttaaa 1228
aggagacttt ttgtttttat tcttagattt gtagctctct gcatagtgag cataaattga 1288
tgtaatatgg tttaagagat tcggtgttct ctggtgtgtg ctgcaaccac ataattggtg 1348
atagataggt ttagttatat aagcaaatgt attagagata aggggagaca tatttgatgg 1408
tcttt 1413

<210> 60
<211> 360
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (248)...(308)
<223> Conserved domain

<400> 60
Met Gly Ser Asn Glu Glu Gly Asn Pro Thr Asn Asn Ser Asp Lys Pro
1 5 10 15
Ser Gln Ala Ala Ala Pro Glu Gln Ser Asn Val His Val Tyr His His
20 25 30
Asp Trp Ala Ala Met Gln Ala Tyr Tyr Gly Pro Arg Val Gly Ile Pro
35 40 45
Gln Tyr Tyr Asn Ser Asn Leu Ala Pro Gly His Ala Pro Pro Pro Tyr
50 55 60
Met Trp Ala Ser Pro Ser Pro Met Met Ala Pro Tyr Gly Ala Pro Tyr
65 70 75 80
Pro Pro Phe Cys Pro Pro Gly Gly Val Tyr Ala His Pro Gly Val Gln
85 90 95
Met Gly Ser Gln Pro Gln Gly Pro Val Ser Gln Ser Ala Ser Gly Val
100 105 110
Thr Thr Pro Leu Thr Ile Asp Ala Pro Ala Asn Ser Ala Gly Asn Ser
115 120 125
Asp His Gly Phe Met Lys Lys Leu Lys Glu Phe Asp Gly Leu Ala Met
130 135 140
Ser Ile Ser Asn Asn Lys Val Gly Ser Ala Glu His Ser Ser Ser Glu
145 150 155 160
His Arg Ser Ser Gln Ser Ser Glu Asn Asp Gly Ser Ser Asn Gly Ser
165 170 175
Asp Gly Asn Thr Thr Gly Gly Glu Gln Ser Arg Arg Lys Arg Arg Gln
180 185 190
Gln Arg Ser Pro Ser Thr Gly Glu Arg Pro Ser Ser Gln Asn Ser Leu
195 200 205

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Pro Leu Arg Gly Glu Asn Glu Lys Pro Asp Val Thr Met Gly Thr Pro
    210                 215                 220
Val Met Pro Thr Ala Met Ser Phe Gln Asn Ser Ala Gly Met Asn Gly
225                 230                 235                 240
Val Pro Gln Pro Trp Asn Glu Lys Glu Val Lys Arg Glu Lys Arg Lys
                245                 250                 255
Gln Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Leu Arg Lys Gln Ala
            260                 265                 270
Glu Thr Glu Gln Leu Ser Val Lys Val Asp Ala Leu Val Ala Glu Asn
        275                 280                 285
Met Ser Leu Arg Ser Lys Leu Gly Gln Leu Asn Asn Glu Ser Glu Lys
    290                 295                 300
Leu Arg Leu Glu Asn Glu Ala Ile Leu Asp Gln Leu Lys Ala Gln Ala
305                 310                 315                 320
Thr Gly Lys Thr Glu Asn Leu Ile Ser Arg Val Asp Lys Asn Asn Ser
                325                 330                 335
Val Ser Gly Ser Lys Thr Val Gln His Gln Leu Leu Asn Ala Ser Pro
            340                 345                 350
Ile Thr Asp Pro Val Ala Ala Ser
        355                 360


<210> 61
<211> 480
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(480)

<400> 61
atg ggt ctt cct gaa gat ttc atc acc gag ctt cag att cca ggt tac      48
Met Gly Leu Pro Glu Asp Phe Ile Thr Glu Leu Gln Ile Pro Gly Tyr
 1               5                  10                  15

ata tta aag ata ctt tac gtc atc ggt ttc ttt aga gac atg gtc gat      96
Ile Leu Lys Ile Leu Tyr Val Ile Gly Phe Phe Arg Asp Met Val Asp
            20                  25                  30

gct ctt tgt cct tac att ggt cta cct agt ttt cta gac cac aac gag     144
Ala Leu Cys Pro Tyr Ile Gly Leu Pro Ser Phe Leu Asp His Asn Glu
        35                  40                  45

acc tct gga ccc gat ccg acc cga cac gct ctc tct acg tca gcg agt     192
Thr Ser Gly Pro Asp Pro Thr Arg His Ala Leu Ser Thr Ser Ala Ser
    50                  55                  60

ctt gct aac gag ttg atc ccg gtg gtt cgg ttc tcg gat ctt ccg acc     240
Leu Ala Asn Glu Leu Ile Pro Val Val Arg Phe Ser Asp Leu Pro Thr
65                  70                  75                  80

gat ccg gaa gat tgt tgt acg gtt tgt ttg tca gat ttt gag tcc gac     288
Asp Pro Glu Asp Cys Cys Thr Val Cys Leu Ser Asp Phe Glu Ser Asp
                85                  90                  95

gat aag gtt agg cag cta ccc aag tgt gga cac gtg ttt cat cat cat     336
```

```
Asp Lys Val Arg Gln Leu Pro Lys Cys Gly His Val Phe His His His
            100                 105                 110

tgt tta gac cgt tgg atc gtt gac tac aac aag atg aaa tgt ccg gtt     384
Cys Leu Asp Arg Trp Ile Val Asp Tyr Asn Lys Met Lys Cys Pro Val
        115                 120                 125

tgt cgg cac cgg ttc tta ccg aaa gaa aag tac acg caa tgt gat tgg     432
Cys Arg His Arg Phe Leu Pro Lys Glu Lys Tyr Thr Gln Cys Asp Trp
    130                 135                 140

ggt tct ggt tca gat tgg ttt agt gat gaa gtg gaa agt acc aac taa     480
Gly Ser Gly Ser Asp Trp Phe Ser Asp Glu Val Glu Ser Thr Asn  *
145                 150                 155


<210> 62
<211> 159
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (86)...(129)
<223> Conserved domain

<400> 62
Met Gly Leu Pro Glu Asp Phe Ile Thr Glu Leu Gln Ile Pro Gly Tyr
 1               5                  10                  15
Ile Leu Lys Ile Leu Tyr Val Ile Gly Phe Phe Arg Asp Met Val Asp
            20                  25                  30
Ala Leu Cys Pro Tyr Ile Gly Leu Pro Ser Phe Leu Asp His Asn Glu
        35                  40                  45
Thr Ser Gly Pro Asp Pro Thr Arg His Ala Leu Ser Thr Ser Ala Ser
    50                  55                  60
Leu Ala Asn Glu Leu Ile Pro Val Val Arg Phe Ser Asp Leu Pro Thr
65                  70                  75                  80
Asp Pro Glu Asp Cys Cys Thr Val Cys Leu Ser Asp Phe Glu Ser Asp
                85                  90                  95
Asp Lys Val Arg Gln Leu Pro Lys Cys Gly His Val Phe His His His
            100                 105                 110
Cys Leu Asp Arg Trp Ile Val Asp Tyr Asn Lys Met Lys Cys Pro Val
        115                 120                 125
Cys Arg His Arg Phe Leu Pro Lys Glu Lys Tyr Thr Gln Cys Asp Trp
    130                 135                 140
Gly Ser Gly Ser Asp Trp Phe Ser Asp Glu Val Glu Ser Thr Asn
145                 150                 155


<210> 63
<211> 1116
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
```

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<222> (89)...(934)

<400> 63
ttggaaccct agaggccttt caagcaaatc atcagggtaa caatttcttg atctttcttt 60
ttagcgaatt tccagttttt ggtcaatc atg gca aac cct tgg tgg acg aac     112
                               Met Ala Asn Pro Trp Trp Thr Asn
                                1               5

cag agt ggt tta gcg ggc atg gtg gac cat tcg gtc tcc tca ggc cat    160
Gln Ser Gly Leu Ala Gly Met Val Asp His Ser Val Ser Ser Gly His
     10                  15                  20

cac caa aac cat cac cac caa agt ctt ctt acc aaa gga gat ctt gga    208
His Gln Asn His His His Gln Ser Leu Leu Thr Lys Gly Asp Leu Gly
 25                  30                  35                  40

ata gcc atg aat cag agc caa gac aac gac caa gac gaa gaa gat gat    256
Ile Ala Met Asn Gln Ser Gln Asp Asn Asp Gln Asp Glu Glu Asp Asp
                 45                  50                  55

cct aga gaa gga gcc gtt gag gtg gtc aac cgt aga cca aga ggt aga    304
Pro Arg Glu Gly Ala Val Glu Val Val Asn Arg Arg Pro Arg Gly Arg
             60                  65                  70

cca cca gga tcc aaa aac aaa ccc aaa gct cca atc ttt gtg aca aga    352
Pro Pro Gly Ser Lys Asn Lys Pro Lys Ala Pro Ile Phe Val Thr Arg
         75                  80                  85

gac agc ccc aac gca ctc cgt agc cat gtc ttg gag atc tcc gac ggc    400
Asp Ser Pro Asn Ala Leu Arg Ser His Val Leu Glu Ile Ser Asp Gly
     90                  95                 100

agt gac gtc gcc gac aca atc gct cac ttc tca aga cgc agg caa cgc    448
Ser Asp Val Ala Asp Thr Ile Ala His Phe Ser Arg Arg Arg Gln Arg
105                 110                 115                 120

ggc gtt tgc gtt ctc agc ggg aca ggc tca gtc gct aac gtc acc ctc    496
Gly Val Cys Val Leu Ser Gly Thr Gly Ser Val Ala Asn Val Thr Leu
                125                 130                 135

cgc caa gcc gcc gca cca gga ggt gtg gtc tct ctc caa ggc agg ttt    544
Arg Gln Ala Ala Ala Pro Gly Gly Val Val Ser Leu Gln Gly Arg Phe
            140                 145                 150

gaa atc tta tct tta acc ggt gct ttc ctc cct gga cct tcc cca ccc    592
Glu Ile Leu Ser Leu Thr Gly Ala Phe Leu Pro Gly Pro Ser Pro Pro
        155                 160                 165

ggg tca acc ggt tta acg gtt tac tta gcc ggg gtc cag ggt cag gtc    640
Gly Ser Thr Gly Leu Thr Val Tyr Leu Ala Gly Val Gln Gly Gln Val
    170                 175                 180

gtt gga ggt agc gtt gta ggc cca ctc tta gcc ata ggg tcg gtc atg    688
Val Gly Gly Ser Val Val Gly Pro Leu Leu Ala Ile Gly Ser Val Met
185                 190                 195                 200

gtg att gct gct act ttc tct aac gct act tat gag aga ttg ccc atg    736
```

Val Ile Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Met
205 210 215

gaa gaa gag gaa gac ggt ggc ggc tca aga cag att cac gga ggc ggt 784
Glu Glu Glu Glu Asp Gly Gly Gly Ser Arg Gln Ile His Gly Gly Gly
220 225 230

gac tca ccg ccc aga atc ggt agt aac ctg cct gat cta tca ggg atg 832
Asp Ser Pro Pro Arg Ile Gly Ser Asn Leu Pro Asp Leu Ser Gly Met
235 240 245

gcc ggg cca ggc tac aat atg ccg ccg cat ctg att cca aat ggg gct 880
Ala Gly Pro Gly Tyr Asn Met Pro Pro His Leu Ile Pro Asn Gly Ala
250 255 260

ggt cag cta ggg cac gaa cca tat aca tgg gtc cac gca aga cca cct 928
Gly Gln Leu Gly His Glu Pro Tyr Thr Trp Val His Ala Arg Pro Pro
265 270 275 280

tac tga ctcagtgagc catttctata tataatggtc tatataaata aatatataga 984
Tyr *

tgaatataag caagcaattt gaggtagtct attacaaagc ttttgctctg gttggaaaaa 1044
taaataagta tcaaagcttt gtttgttctt aatggaaata tagagcttgg gaaggtagaa 1104
agagacgaca tt 1116

<210> 64
<211> 281
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (67)...(74)
<223> Conserved domain

<400> 64
Met Ala Asn Pro Trp Trp Thr Asn Gln Ser Gly Leu Ala Gly Met Val
1 5 10 15
Asp His Ser Val Ser Ser Gly His His Gln Asn His His His Gln Ser
20 25 30
Leu Leu Thr Lys Gly Asp Leu Gly Ile Ala Met Asn Gln Ser Gln Asp
35 40 45
Asn Asp Gln Asp Glu Glu Asp Asp Pro Arg Glu Gly Ala Val Glu Val
50 55 60
Val Asn Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro
65 70 75 80
Lys Ala Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser
85 90 95
His Val Leu Glu Ile Ser Asp Gly Ser Asp Val Ala Asp Thr Ile Ala
100 105 110
His Phe Ser Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Thr
115 120 125
Gly Ser Val Ala Asn Val Thr Leu Arg Gln Ala Ala Ala Pro Gly Gly
130 135 140
Val Val Ser Leu Gln Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ala

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145                 150                 155                 160
Phe Leu Pro Gly Pro Ser Pro Pro Gly Ser Thr Gly Leu Thr Val Tyr
                165                 170                 175
Leu Ala Gly Val Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Pro
            180                 185                 190
Leu Leu Ala Ile Gly Ser Val Met Val Ile Ala Ala Thr Phe Ser Asn
        195                 200                 205
Ala Thr Tyr Glu Arg Leu Pro Met Glu Glu Glu Glu Asp Gly Gly Gly
    210                 215                 220
Ser Arg Gln Ile His Gly Gly Gly Asp Ser Pro Pro Arg Ile Gly Ser
225                 230                 235                 240
Asn Leu Pro Asp Leu Ser Gly Met Ala Gly Pro Gly Tyr Asn Met Pro
                245                 250                 255
Pro His Leu Ile Pro Asn Gly Ala Gly Gln Leu Gly His Glu Pro Tyr
            260                 265                 270
Thr Trp Val His Ala Arg Pro Pro Tyr
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                                  1               5

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Glu Asn Glu Glu Ala Val Thr Arg Cys Lys Glu Arg Lys Gln Leu Met
     10                  15                  20

aaa gac gcc gtc act gct cgt aac gct ttc gcc gcc gct cac tca gct   150
Lys Asp Ala Val Thr Ala Arg Asn Ala Phe Ala Ala Ala His Ser Ala
 25                  30                  35                  40

tac gct atg gct ctt aaa aac acc gga gct gct ctt tcc gat tac tct   198
Tyr Ala Met Ala Leu Lys Asn Thr Gly Ala Ala Leu Ser Asp Tyr Ser
                 45                  50                  55

cac ggc gag ttt tta gtc tct aat cac tcg tct tcc tcc gca gct gca   246
His Gly Glu Phe Leu Val Ser Asn His Ser Ser Ser Ser Ala Ala Ala
             60                  65                  70

gca atc gct tct act tct tct ctt ccc act gct ata tct cct cct ctt   294
Ala Ile Ala Ser Thr Ser Ser Leu Pro Thr Ala Ile Ser Pro Pro Leu
         75                  80                  85

cct tct tcc acc gct ccg gtt tct aat tca acc gct tct tct tcc tcc   342
Pro Ser Ser Thr Ala Pro Val Ser Asn Ser Thr Ala Ser Ser Ser Ser
     90                  95                 100
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gct gcg gtt cct cag ccg att cct gat act ctt cct cct cct cct cct    390
Ala Ala Val Pro Gln Pro Ile Pro Asp Thr Leu Pro Pro Pro Pro Pro
105                 110                 115                 120

cca cca ccg ctt cct ctt caa cgt gct gct act atg ccg gag atg aac    438
Pro Pro Pro Leu Pro Leu Gln Arg Ala Ala Thr Met Pro Glu Met Asn
                125                 130                 135

ggt aga tcc ggt ggt ggt cat gct ggt agt gga ctc aac gga att gaa    486
Gly Arg Ser Gly Gly Gly His Ala Gly Ser Gly Leu Asn Gly Ile Glu
            140                 145                 150

gaa gat gga gcc cta gat aac gat gat gat gac gat gat gat gat gat    534
Glu Asp Gly Ala Leu Asp Asn Asp Asp Asp Asp Asp Asp Asp Asp Asp
        155                 160                 165

gac tct gaa atg gag aat cgt gat cgt ttg att agg aaa tcg aga agc    582
Asp Ser Glu Met Glu Asn Arg Asp Arg Leu Ile Arg Lys Ser Arg Ser
    170                 175                 180

cgt gga ggt agt act aga gga aat agg acg acg att gaa gat cat cat    630
Arg Gly Gly Ser Thr Arg Gly Asn Arg Thr Thr Ile Glu Asp His His
185                 190                 195                 200

ctt cag gag gag aaa gct ccg cca cct ccc cct ttg gcg aat tcg cgg    678
Leu Gln Glu Glu Lys Ala Pro Pro Pro Pro Pro Leu Ala Asn Ser Arg
                205                 210                 215

cca att ccg ccg cca cgt cag cat cag cat caa cat cag caa cag caa    726
Pro Ile Pro Pro Pro Arg Gln His Gln His Gln His Gln Gln Gln Gln
            220                 225                 230

caa caa cct ttc tac gat tac ttc ttc cct aat gtt gag aat atg cct    774
Gln Gln Pro Phe Tyr Asp Tyr Phe Phe Pro Asn Val Glu Asn Met Pro
        235                 240                 245

gga act act tta gaa gat act cct cca caa cca caa cca caa cca aca    822
Gly Thr Thr Leu Glu Asp Thr Pro Pro Gln Pro Gln Pro Gln Pro Thr
    250                 255                 260

agg cct gtg cct cct caa cca cat tca cca gtc gtt act gag gat gac    870
Arg Pro Val Pro Pro Gln Pro His Ser Pro Val Val Thr Glu Asp Asp
265                 270                 275                 280

gaa gat gag gag gag gaa gag gag gaa gag gag gag gaa gag gag acg    918
Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Thr
                285                 290                 295

gtg att gaa cgg aaa cca ctg gtg gag gaa aga ccg aag aga gta gag    966
Val Ile Glu Arg Lys Pro Leu Val Glu Glu Arg Pro Lys Arg Val Glu
            300                 305                 310

gaa gtg acg att gaa ttg gaa aaa gtt act aat ttg aga ggg atg aag    1014
Glu Val Thr Ile Glu Leu Glu Lys Val Thr Asn Leu Arg Gly Met Lys
        315                 320                 325

aag agt aaa ggg ata ggg att ccc gga gag agg aga gga atg cga atg    1062
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Lys Ser Lys Gly Ile Gly Ile Pro Gly Glu Arg Arg Gly Met Arg Met
330 335 340

ccg gtg act gcg acg cat ttg gcg aat gta ttc att gag ctt gat gat 1110
Pro Val Thr Ala Thr His Leu Ala Asn Val Phe Ile Glu Leu Asp Asp
345 350 355 360

aat ttc ttg aaa gct tct gaa agt gct cat gat gtt tct aag atg ctt 1158
Asn Phe Leu Lys Ala Ser Glu Ser Ala His Asp Val Ser Lys Met Leu
365 370 375

gaa gct act agg ctc cat tac cat tct aat ttt gca gat aac cga gga 1206
Glu Ala Thr Arg Leu His Tyr His Ser Asn Phe Ala Asp Asn Arg Gly
380 385 390

cat att gat cac tct gct aga gtg atg cgt gta att aca tgg aat aga 1254
His Ile Asp His Ser Ala Arg Val Met Arg Val Ile Thr Trp Asn Arg
395 400 405

tca ttt aga gga ata cca aat gct gat gat ggg aaa gat gat gtt gat 1302
Ser Phe Arg Gly Ile Pro Asn Ala Asp Asp Gly Lys Asp Asp Val Asp
410 415 420

ttg gaa gag aat gaa act cat gct act gtt ctt gac aaa ttg cta gca 1350
Leu Glu Glu Asn Glu Thr His Ala Thr Val Leu Asp Lys Leu Leu Ala
425 430 435 440

tgg gaa aag aag ctc tat gac gaa gtc aag gct ggc gaa ctc atg aaa 1398
Trp Glu Lys Lys Leu Tyr Asp Glu Val Lys Ala Gly Glu Leu Met Lys
445 450 455

atc gag tac cag aaa aag gtt gct cat tta aat cgg gtg aag aaa cga 1446
Ile Glu Tyr Gln Lys Lys Val Ala His Leu Asn Arg Val Lys Lys Arg
460 465 470

ggt ggc cac tcg gat tca tta gag aga gct aaa gca gca gta agt cat 1494
Gly Gly His Ser Asp Ser Leu Glu Arg Ala Lys Ala Ala Val Ser His
475 480 485

ttg cat aca aga tat ata gtt gat atg caa tcc atg gac tcc aca gtt 1542
Leu His Thr Arg Tyr Ile Val Asp Met Gln Ser Met Asp Ser Thr Val
490 495 500

tca gaa atc aat cgt ctt agg gat gaa caa cta tac cta aag ctc gtt 1590
Ser Glu Ile Asn Arg Leu Arg Asp Glu Gln Leu Tyr Leu Lys Leu Val
505 510 515 520

cac ctt gtt gag gcg atg ggg aag atg tgg gaa atg atg caa ata cat 1638
His Leu Val Glu Ala Met Gly Lys Met Trp Glu Met Met Gln Ile His
525 530 535

cat caa aga caa gct gag atc tca aag gtg ttg aga tct cta gat gtt 1686
His Gln Arg Gln Ala Glu Ile Ser Lys Val Leu Arg Ser Leu Asp Val
540 545 550

tca caa gcg gtg aaa gaa aca aat gat cat cat cac gaa cgc acc atc 1734
Ser Gln Ala Val Lys Glu Thr Asn Asp His His His Glu Arg Thr Ile

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        555                 560                 565

cag ctc ttg gca gtg gtt caa gaa tgg cac acg cag ttt tgc agg atg     1782
Gln Leu Leu Ala Val Val Gln Glu Trp His Thr Gln Phe Cys Arg Met
    570                 575                 580

ata gat cat cag aaa gaa tac ata aaa gca ctt ggc gga tgg cta aag     1830
Ile Asp His Gln Lys Glu Tyr Ile Lys Ala Leu Gly Gly Trp Leu Lys
585                 590                 595                 600

cta aat ctc atc cct atc gaa agc aca ctc aag gag aaa gta tct tcg     1878
Leu Asn Leu Ile Pro Ile Glu Ser Thr Leu Lys Glu Lys Val Ser Ser
                605                 610                 615

cct cct cga gtt ccc aat ccc gca atc caa aaa ctc ctc cac gct tgg     1926
Pro Pro Arg Val Pro Asn Pro Ala Ile Gln Lys Leu Leu His Ala Trp
            620                 625                 630

tat gac cgt tta gac aaa atc ccc gac gaa atg gct aaa agt gcc ata     1974
Tyr Asp Arg Leu Asp Lys Ile Pro Asp Glu Met Ala Lys Ser Ala Ile
        635                 640                 645

atc aat ttc gca gcg gtt gta agc acg ata atg cag cag caa gaa gac     2022
Ile Asn Phe Ala Ala Val Val Ser Thr Ile Met Gln Gln Gln Glu Asp
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gag ata agt ctc aga aac aaa tgc gaa gag aca aga aaa gaa ttg gga     2070
Glu Ile Ser Leu Arg Asn Lys Cys Glu Glu Thr Arg Lys Glu Leu Gly
665                 670                 675                 680

aga aaa att aga cag ttt gag gat tgg tac cac aaa tac atc cag aag     2118
Arg Lys Ile Arg Gln Phe Glu Asp Trp Tyr His Lys Tyr Ile Gln Lys
                685                 690                 695

aga gga ccg gag ggg atg aat ccg gat gaa gcg gat aac gat cat aat     2166
Arg Gly Pro Glu Gly Met Asn Pro Asp Glu Ala Asp Asn Asp His Asn
            700                 705                 710

gat gag gtc gct gtg agg caa ttc aat gta gaa caa att aag aag agg     2214
Asp Glu Val Ala Val Arg Gln Phe Asn Val Glu Gln Ile Lys Lys Arg
        715                 720                 725

ttg gaa gaa gaa gaa gaa gct tac cat aga caa agc cat caa gtt aga     2262
Leu Glu Glu Glu Glu Glu Ala Tyr His Arg Gln Ser His Gln Val Arg
    730                 735                 740

gag aag tca ctg gct agt ctt cga act cgc ctc ccc gag ctt ttt cag     2310
Glu Lys Ser Leu Ala Ser Leu Arg Thr Arg Leu Pro Glu Leu Phe Gln
745                 750                 755                 760

gca atg tcc gag gtt gcg tat tca tgt tcg gat atg tat aga gct ata     2358
Ala Met Ser Glu Val Ala Tyr Ser Cys Ser Asp Met Tyr Arg Ala Ile
                765                 770                 775

acg tat gcg agt aag cgg caa agc caa agc gaa cgg cat cag aaa cct     2406
Thr Tyr Ala Ser Lys Arg Gln Ser Gln Ser Glu Arg His Gln Lys Pro
            780                 785                 790
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Ser Gln Gly Gln Ser Ser  *
        795

ttcttctttg atcttgaata tttaagcaca cacatacata caacgtatag ctaaatcttt 2517
atcattgctt tcttatatta aggttttggc ttttgtaaga aggtttctta catatgagat 2577
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Ala Phe Ala Ala Ala His Ser Ala Tyr Ala Met Ala Leu Lys Asn Thr
        35                  40                  45
Gly Ala Ala Leu Ser Asp Tyr Ser His Gly Glu Phe Leu Val Ser Asn
    50                  55                  60
His Ser Ser Ser Ser Ala Ala Ala Ala Ile Ala Ser Thr Ser Ser Leu
65                  70                  75                  80
Pro Thr Ala Ile Ser Pro Pro Leu Pro Ser Ser Thr Ala Pro Val Ser
                85                  90                  95
Asn Ser Thr Ala Ser Ser Ser Ser Ala Ala Val Pro Gln Pro Ile Pro
            100                 105                 110
Asp Thr Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Leu Gln Arg
        115                 120                 125
Ala Ala Thr Met Pro Glu Met Asn Gly Arg Ser Gly Gly Gly His Ala
    130                 135                 140
Gly Ser Gly Leu Asn Gly Ile Glu Glu Asp Gly Ala Leu Asp Asn Asp
145                 150                 155                 160
Asp Asp Asp Asp Asp Asp Asp Asp Asp Ser Glu Met Glu Asn Arg Asp
                165                 170                 175
Arg Leu Ile Arg Lys Ser Arg Ser Arg Gly Gly Ser Thr Arg Gly Asn
            180                 185                 190
Arg Thr Thr Ile Glu Asp His His Leu Gln Glu Glu Lys Ala Pro Pro
        195                 200                 205
Pro Pro Pro Leu Ala Asn Ser Arg Pro Ile Pro Pro Pro Arg Gln His
    210                 215                 220
Gln His Gln His Gln Gln Gln Gln Gln Gln Pro Phe Tyr Asp Tyr Phe
225                 230                 235                 240
Phe Pro Asn Val Glu Asn Met Pro Gly Thr Thr Leu Glu Asp Thr Pro
                245                 250                 255
Pro Gln Pro Gln Pro Gln Pro Thr Arg Pro Val Pro Pro Gln Pro His
            260                 265                 270
Ser Pro Val Val Thr Glu Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu
        275                 280                 285
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Glu Glu Glu Glu Glu Glu Glu Thr Val Ile Glu Arg Lys Pro Leu Val
290 295 300
Glu Glu Arg Pro Lys Arg Val Glu Glu Val Thr Ile Glu Leu Glu Lys
305 310 315 320
Val Thr Asn Leu Arg Gly Met Lys Lys Ser Lys Gly Ile Gly Ile Pro
325 330 335
Gly Glu Arg Arg Gly Met Arg Met Pro Val Thr Ala Thr His Leu Ala
340 345 350
Asn Val Phe Ile Glu Leu Asp Asp Asn Phe Leu Lys Ala Ser Glu Ser
355 360 365
Ala His Asp Val Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His
370 375 380
Ser Asn Phe Ala Asp Asn Arg Gly His Ile Asp His Ser Ala Arg Val
385 390 395 400
Met Arg Val Ile Thr Trp Asn Arg Ser Phe Arg Gly Ile Pro Asn Ala
405 410 415
Asp Asp Gly Lys Asp Asp Val Asp Leu Glu Glu Asn Glu Thr His Ala
420 425 430
Thr Val Leu Asp Lys Leu Leu Ala Trp Glu Lys Lys Leu Tyr Asp Glu
435 440 445
Val Lys Ala Gly Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ala
450 455 460
His Leu Asn Arg Val Lys Lys Arg Gly Gly His Ser Asp Ser Leu Glu
465 470 475 480
Arg Ala Lys Ala Ala Val Ser His Leu His Thr Arg Tyr Ile Val Asp
485 490 495
Met Gln Ser Met Asp Ser Thr Val Ser Glu Ile Asn Arg Leu Arg Asp
500 505 510
Glu Gln Leu Tyr Leu Lys Leu Val His Leu Val Glu Ala Met Gly Lys
515 520 525
Met Trp Glu Met Met Gln Ile His His Gln Arg Gln Ala Glu Ile Ser
530 535 540
Lys Val Leu Arg Ser Leu Asp Val Ser Gln Ala Val Lys Glu Thr Asn
545 550 555 560
Asp His His His Glu Arg Thr Ile Gln Leu Leu Ala Val Val Gln Glu
565 570 575
Trp His Thr Gln Phe Cys Arg Met Ile Asp His Gln Lys Glu Tyr Ile
580 585 590
Lys Ala Leu Gly Gly Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser
595 600 605
Thr Leu Lys Glu Lys Val Ser Ser Pro Pro Arg Val Pro Asn Pro Ala
610 615 620
Ile Gln Lys Leu Leu His Ala Trp Tyr Asp Arg Leu Asp Lys Ile Pro
625 630 635 640
Asp Glu Met Ala Lys Ser Ala Ile Ile Asn Phe Ala Ala Val Val Ser
645 650 655
Thr Ile Met Gln Gln Gln Glu Asp Glu Ile Ser Leu Arg Asn Lys Cys
660 665 670
Glu Glu Thr Arg Lys Glu Leu Gly Arg Lys Ile Arg Gln Phe Glu Asp
675 680 685
Trp Tyr His Lys Tyr Ile Gln Lys Arg Gly Pro Glu Gly Met Asn Pro
690 695 700
Asp Glu Ala Asp Asn Asp His Asn Asp Glu Val Ala Val Arg Gln Phe
705 710 715 720
Asn Val Glu Gln Ile Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala Tyr
725 730 735
His Arg Gln Ser His Gln Val Arg Glu Lys Ser Leu Ala Ser Leu Arg

740 745 750
Thr Arg Leu Pro Glu Leu Phe Gln Ala Met Ser Glu Val Ala Tyr Ser
755 760 765
Cys Ser Asp Met Tyr Arg Ala Ile Thr Tyr Ala Ser Lys Arg Gln Ser
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Gln Ser Glu Arg His Gln Lys Pro Ser Gln Gly Gln Ser Ser
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ttcttacagt cattactctc tatagggctc gagcggccgc ccgggcaggt ttct atg 177
Met
1

cag atg gtt cac act tcc cgc tcc att gcc cag att ggg ttc ggt gtt 225
Gln Met Val His Thr Ser Arg Ser Ile Ala Gln Ile Gly Phe Gly Val
5 10 15

aag tcg caa tta gta ctc act ata ggg ctc gag cgg ccg ccc ggg cag 273
Lys Ser Gln Leu Val Leu Thr Ile Gly Leu Glu Arg Pro Pro Gly Gln
20 25 30

gta aaa gat caa aca atg tct aaa gaa gct gag atg tcg atc gcg gtg 321
Val Lys Asp Gln Thr Met Ser Lys Glu Ala Glu Met Ser Ile Ala Val
35 40 45

tcg gct ttg ttc cct ggt ttt aga ttc tct cct act gat gtt gaa ctt 369
Ser Ala Leu Phe Pro Gly Phe Arg Phe Ser Pro Thr Asp Val Glu Leu
50 55 60 65

atc tcg tac tat ctt cgt cgt aaa atc gat ggt gat gag aac tct gtt 417
Ile Ser Tyr Tyr Leu Arg Arg Lys Ile Asp Gly Asp Glu Asn Ser Val
70 75 80

gct gtg att gct gag gtc gag att tac aag ttc gag ccg tgg gac ttg 465
Ala Val Ile Ala Glu Val Glu Ile Tyr Lys Phe Glu Pro Trp Asp Leu
85 90 95

cca gag gaa tcg aaa ctg aaa tcg gag aac gag tgg ttt tac ttc tgc 513
Pro Glu Glu Ser Lys Leu Lys Ser Glu Asn Glu Trp Phe Tyr Phe Cys
100 105 110

gcg agg ggg agg aag tac ccg cac ggg tca caa agc cgg cga gcc aca 561
Ala Arg Gly Arg Lys Tyr Pro His Gly Ser Gln Ser Arg Arg Ala Thr
115 120 125

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cag cta gga tat tgg aaa gcg acc ggt aaa gag cgg agt gtt aaa tcc    609
Gln Leu Gly Tyr Trp Lys Ala Thr Gly Lys Glu Arg Ser Val Lys Ser
130                 135                 140                 145

ggg aac caa gtt gtt gga acc aag aga acg ctt gta ttt cat atc ggt    657
Gly Asn Gln Val Val Gly Thr Lys Arg Thr Leu Val Phe His Ile Gly
                150                 155                 160

cgg gct cct cgt ggc gag aga acg gag tgg att atg cat gaa tac tgc    705
Arg Ala Pro Arg Gly Glu Arg Thr Glu Trp Ile Met His Glu Tyr Cys
            165                 170                 175

atc cat gga gcc cca cag gat gca tta gtg gtg tgc cgg tta aga aaa    753
Ile His Gly Ala Pro Gln Asp Ala Leu Val Val Cys Arg Leu Arg Lys
        180                 185                 190

aat gct gat ttt cgg gct agt tcg acc caa aaa att gag gat ggt gtt    801
Asn Ala Asp Phe Arg Ala Ser Ser Thr Gln Lys Ile Glu Asp Gly Val
    195                 200                 205

gtg caa gac gat ggc tac gtt ggc caa aga ggt ggt ttg gac aag gag    849
Val Gln Asp Asp Gly Tyr Val Gly Gln Arg Gly Gly Leu Asp Lys Glu
210                 215                 220                 225

gac aaa tcc tac tat gaa tct gag cat cag ata cca aat ggt gac atc    897
Asp Lys Ser Tyr Tyr Glu Ser Glu His Gln Ile Pro Asn Gly Asp Ile
                230                 235                 240

gca gaa tca tca aat gtt gtt gag gat cag gcc gat acc gat gat gat    945
Ala Glu Ser Ser Asn Val Val Glu Asp Gln Ala Asp Thr Asp Asp Asp
            245                 250                 255

tgt tac gcc gag att ctg aac gat gat ata ata aag ctc gac gaa gaa    993
Cys Tyr Ala Glu Ile Leu Asn Asp Asp Ile Ile Lys Leu Asp Glu Glu
        260                 265                 270

gcg ttg aaa gct agc caa gcg ttt cga cca act aat cca act cat caa    1041
Ala Leu Lys Ala Ser Gln Ala Phe Arg Pro Thr Asn Pro Thr His Gln
    275                 280                 285

gaa aca ata tca agc gag tca tcg agt aag agg tca aaa tgt ggt ata    1089
Glu Thr Ile Ser Ser Glu Ser Ser Ser Lys Arg Ser Lys Cys Gly Ile
290                 295                 300                 305

aaa aaa gaa tca acg gaa aca atg aat tgt tac gct ttg ttc agg atc    1137
Lys Lys Glu Ser Thr Glu Thr Met Asn Cys Tyr Ala Leu Phe Arg Ile
                310                 315                 320

aag aac gtt gcc gga acc gac tcc agc tgg aga ttc ccg aac ccg ttc    1185
Lys Asn Val Ala Gly Thr Asp Ser Ser Trp Arg Phe Pro Asn Pro Phe
            325                 330                 335

aaa atc aag aaa gat gat agc cag aga ttg atg aag aat gtt ctg gcc    1233
Lys Ile Lys Lys Asp Asp Ser Gln Arg Leu Met Lys Asn Val Leu Ala
        340                 345                 350

act act gtt ttc ttg gct atc tta ttt tct ttc ttt tgg act gta tta    1281
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Thr Thr Val Phe Leu Ala Ile Leu Phe Ser Phe Phe Trp Thr Val Leu
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ata gct agg aac taa agctagttac gacatacata ttatttatac ataaataaat   1336
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370

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Gln Val Lys Asp Gln Thr Met Ser Lys Glu Ala Glu Met Ser Ile Ala
        35                  40                  45
Val Ser Ala Leu Phe Pro Gly Phe Arg Phe Ser Pro Thr Asp Val Glu
    50                  55                  60
Leu Ile Ser Tyr Tyr Leu Arg Arg Lys Ile Asp Gly Asp Glu Asn Ser
65                  70                  75                  80
Val Ala Val Ile Ala Glu Val Glu Ile Tyr Lys Phe Glu Pro Trp Asp
                85                  90                  95
Leu Pro Glu Glu Ser Lys Leu Lys Ser Glu Asn Glu Trp Phe Tyr Phe
            100                 105                 110
Cys Ala Arg Gly Arg Lys Tyr Pro His Gly Ser Gln Ser Arg Arg Ala
        115                 120                 125
Thr Gln Leu Gly Tyr Trp Lys Ala Thr Gly Lys Glu Arg Ser Val Lys
    130                 135                 140
Ser Gly Asn Gln Val Val Gly Thr Lys Arg Thr Leu Val Phe His Ile
145                 150                 155                 160
Gly Arg Ala Pro Arg Gly Glu Arg Thr Glu Trp Ile Met His Glu Tyr
                165                 170                 175
Cys Ile His Gly Ala Pro Gln Asp Ala Leu Val Val Cys Arg Leu Arg
            180                 185                 190
Lys Asn Ala Asp Phe Arg Ala Ser Ser Thr Gln Lys Ile Glu Asp Gly
        195                 200                 205
Val Val Gln Asp Asp Gly Tyr Val Gly Gln Arg Gly Gly Leu Asp Lys
    210                 215                 220
Glu Asp Lys Ser Tyr Tyr Glu Ser Glu His Gln Ile Pro Asn Gly Asp
225                 230                 235                 240
Ile Ala Glu Ser Ser Asn Val Val Glu Asp Gln Ala Asp Thr Asp Asp
                245                 250                 255
Asp Cys Tyr Ala Glu Ile Leu Asn Asp Asp Ile Ile Lys Leu Asp Glu
            260                 265                 270
Glu Ala Leu Lys Ala Ser Gln Ala Phe Arg Pro Thr Asn Pro Thr His
        275                 280                 285
Gln Glu Thr Ile Ser Ser Glu Ser Ser Ser Lys Arg Ser Lys Cys Gly
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Ile Lys Lys Glu Ser Thr Glu Thr Met Asn Cys Tyr Ala Leu Phe Arg
305                 310                 315                 320
Ile Lys Asn Val Ala Gly Thr Asp Ser Ser Trp Arg Phe Pro Asn Pro
                325                 330                 335
Phe Lys Ile Lys Lys Asp Asp Ser Gln Arg Leu Met Lys Asn Val Leu
            340                 345                 350
Ala Thr Thr Val Phe Leu Ala Ile Leu Phe Ser Phe Phe Trp Thr Val
        355                 360                 365
Leu Ile Ala Arg Asn
    370


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aacgataatc aagaacgaga gagagagaga gcaagagcaa gagatttcta ctacagaaga 240
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catgtttcga tgtttcgatc tctcttactg tctaaacggc gaaataaaaa gtctgatggg 360
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         Met Ala Gly Ile Asp Asn Lys Ala Ala Val Met Gly Glu Trp
          1               5                  10

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Phe Asp Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu
 15                  20                  25                  30

ggt aga gag ttt tct tta aat tac atc aag aat gag gat tct ttg caa   566
Gly Arg Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln
                 35                  40                  45

acc acc ttt caa gaa agt tca cga gga gct ctt cgt gaa agg att gct   614
Thr Thr Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala
             50                  55                  60

gcg aga tcc ggg ttt aat gca ccg tgg tta aac act gag gat att ctt   662
Ala Arg Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu
         65                  70                  75

cag tcg aaa tct tta acc atc tct tct cct ggt ctt agt cct gca act   710
Gln Ser Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr
     80                  85                  90
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ctg tta gag tct cct gtt ttc ctc tca aac cct ttg cta tct cca aca    758
Leu Leu Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr
 95                 100                 105                 110

acc ggg aag ctc tca tca gta cct tct gat aag gct aaa gct gag tta    806
Thr Gly Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu
                115                 120                 125

ttt gac gac att acc aca tcc tta gcc ttc caa acc att tca gga agt    854
Phe Asp Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser
            130                 135                 140

ggc ctt gat cct act aac atc gct tta gaa ccc gat gat tcc caa gac    902
Gly Leu Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp
        145                 150                 155

tat gaa gaa aga cag ctc ggc ggt tta gga gac tcg atg gct tgt tgt    950
Tyr Glu Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys
    160                 165                 170

gca cct gca gat gat gga tac aac tgg aga aaa tat gga caa aag cta    998
Ala Pro Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu
175                 180                 185                 190

gtt aaa gga agt gag tat ccg cgg agc tat tac aag tgc acg cac ccg    1046
Val Lys Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro
                195                 200                 205

aat tgt gag gcc aag aag aag gtt gaa cgg tct cgg gaa ggt cat att    1094
Asn Cys Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile
            210                 215                 220

ata gag atc ata tac aca gga gat cat ata cac agc aaa cct cca cct    1142
Ile Glu Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro
        225                 230                 235

aac cgc cgg tca ggg att gga tca tcc ggt act ggc caa gac atg caa    1190
Asn Arg Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln
    240                 245                 250

ata gat gca acc gaa tac gaa ggt ttt gct gga acc aat gag aac ata    1238
Ile Asp Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile
255                 260                 265                 270

gaa tgg aca tca cct gta tct gca gag ctc gaa tac gga agc cat tca    1286
Glu Trp Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser
                275                 280                 285

gga tca atg cag gtt caa aac ggg act cat cag ttc ggg tat ggt gat    1334
Gly Ser Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp
            290                 295                 300

gca gca gct gat gcc tta tat aga gat gaa aac gaa gat gat cgc acg    1382
Ala Ala Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr
        305                 310                 315
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tcc cac atg agt gtt tcc ctg act tac gat gga gag gta gaa gag tcc     1430
Ser His Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser
    320                 325                 330

gaa tca aag aga agg aaa cta gaa gct tat gca aca gaa acg agt gga     1478
Glu Ser Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly
335                 340                 345                 350

tca acc aga gcc agc cgt gag cca aga gtt gtg gtg cag acc aca agt     1526
Ser Thr Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser
                355                 360                 365

gac att gac atc ctc gat gat ggt tat cgc tgg cgc aag tat ggg caa     1574
Asp Ile Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln
            370                 375                 380

aaa gtc gtt aaa gga aac ccg aat cca agg agc tac tat aaa tgc aca     1622
Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr
        385                 390                 395

gct aat gga tgt acc gta acg aag cat gta gag aga gcc tct gat gac     1670
Ala Asn Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp
    400                 405                 410

ttc aag agc gta cta aca act tat ata ggc aag cac acc cac gtt gta     1718
Phe Lys Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val
415                 420                 425                 430

cca gca gca cgc aac agc agc cac gtc ggt gca ggc agt tca ggg act     1766
Pro Ala Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr
                435                 440                 445

ctc caa ggc agt tta gcg act cag acc cac aac cac aat gtg cac tat     1814
Leu Gln Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr
            450                 455                 460

cca atg cca cac agt aga tct gag gga ctg gcc aca gcc aac tca tct     1862
Pro Met Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser
        465                 470                 475

cta ttt gac ttc cag tca cac ctg agg cat cct aca ggt ttc tcc gtt     1910
Leu Phe Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val
    480                 485                 490

tac ata ggc caa tct gag ctt tct gat ctt tca atg cct ggt cta act     1958
Tyr Ile Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr
495                 500                 505                 510

att ggg caa gag aag ctt acc agc ctg cag gcg cct gac att ggg gat     2006
Ile Gly Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp
                515                 520                 525

cca act ggc cta atg ttg cag tta gca gca cag ccg aag gtg gaa cca     2054
Pro Thr Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro
            530                 535                 540

gtg tca cca caa cag gga ctt gat ttg tca gcg agc tca ttg ata tgc     2102
```

```
Val Ser Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys
        545                 550                 555

aga gag atg ttg agt aga tta cga cag ata tga aacaaatctc tttgttcact 2155
Arg Glu Met Leu Ser Arg Leu Arg Gln Ile  *
    560                 565

gattgctcaa atttttgaat aaatgaaaaa ttgaganaaa aaaaaaaaaa aaaaaaaaaa 2215
aa                                                                2217

<210> 70
<211> 568
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (178)...(234)
<223> Conserved domain

<221> DOMAIN
<222> (372)...(428)
<223> Conserved domain

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Met Ala Gly Ile Asp Asn Lys Ala Ala Val Met Gly Glu Trp Phe Asp
 1               5                  10                  15
Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu Gly Arg
            20                  25                  30
Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln Thr Thr
        35                  40                  45
Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala Ala Arg
    50                  55                  60
Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu Gln Ser
65                  70                  75                  80
Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu
                85                  90                  95
Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr Thr Gly
            100                 105                 110
Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu Phe Asp
        115                 120                 125
Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser Gly Leu
    130                 135                 140
Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp Tyr Glu
145                 150                 155                 160
Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys Ala Pro
                165                 170                 175
Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys
            180                 185                 190
Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys
        195                 200                 205
Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Ile Glu
    210                 215                 220
Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro Asn Arg
225                 230                 235                 240
Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln Ile Asp
                245                 250                 255
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Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile Glu Trp
            260                 265                 270
Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser Gly Ser
        275                 280                 285
Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp Ala Ala
    290                 295                 300
Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr Ser His
305                 310                 315                 320
Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser Glu Ser
                325                 330                 335
Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly Ser Thr
            340                 345                 350
Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser Asp Ile
        355                 360                 365
Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val
    370                 375                 380
Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ala Asn
385                 390                 395                 400
Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp Phe Lys
                405                 410                 415
Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val Pro Ala
            420                 425                 430
Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr Leu Gln
        435                 440                 445
Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr Pro Met
    450                 455                 460
Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser Leu Phe
465                 470                 475                 480
Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val Tyr Ile
                485                 490                 495
Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr Ile Gly
            500                 505                 510
Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp Pro Thr
        515                 520                 525
Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro Val Ser
    530                 535                 540
Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys Arg Glu
545                 550                 555                 560
Met Leu Ser Arg Leu Arg Gln Ile
                565
```

<210> 71
<211> 1927
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (55)...(1857)

<400> 71

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catctgatct gctctcgaag acgaaagctt cgagtactgg ttgaagctaa agct atg    57
                                                            Met
                                                             1

gga cac gtg aat cta cct gca tca aag cgt ggt aac cct cgt caa tgg    105
```

Gly His Val Asn Leu Pro Ala Ser Lys Arg Gly Asn Pro Arg Gln Trp
5 10 15

cgt ctc ctc gac atc gta acc gct gct ttc ttc ggt atc gta ctt ctc 153
Arg Leu Leu Asp Ile Val Thr Ala Ala Phe Phe Gly Ile Val Leu Leu
20 25 30

ttc ttc atc ctt tta ttc act cct ctt ggt gat tcc atg gcg gct tct 201
Phe Phe Ile Leu Leu Phe Thr Pro Leu Gly Asp Ser Met Ala Ala Ser
35 40 45

ggt cgg caa acg ctg ctt ctc tct acg gcg tca gat ccg agg caa cgg 249
Gly Arg Gln Thr Leu Leu Leu Ser Thr Ala Ser Asp Pro Arg Gln Arg
50 55 60 65

cag cga tta gtg act ttg gtt gaa gct ggt cag cat ttg caa ccg atc 297
Gln Arg Leu Val Thr Leu Val Glu Ala Gly Gln His Leu Gln Pro Ile
70 75 80

gag tat tgt cct gcg gaa gct gtt gct cat atg cct tgt gag gat ccg 345
Glu Tyr Cys Pro Ala Glu Ala Val Ala His Met Pro Cys Glu Asp Pro
85 90 95

aga agg aat agt cag ctt agt aga gag atg aat ttc tat agg gag aga 393
Arg Arg Asn Ser Gln Leu Ser Arg Glu Met Asn Phe Tyr Arg Glu Arg
100 105 110

cat tgt cct ttg cct gag gag act ccg ctc tgt ttg att cct ccg cct 441
His Cys Pro Leu Pro Glu Glu Thr Pro Leu Cys Leu Ile Pro Pro Pro
115 120 125

tct ggt tat aaa att cct gtt ccg tgg cct gag agt ctt cac aag att 489
Ser Gly Tyr Lys Ile Pro Val Pro Trp Pro Glu Ser Leu His Lys Ile
130 135 140 145

tgg cat gca aac atg cca tat aac aaa att gct gac cgg aaa ggt cat 537
Trp His Ala Asn Met Pro Tyr Asn Lys Ile Ala Asp Arg Lys Gly His
150 155 160

caa gga tgg atg aaa agg gaa ggg gaa tac ttt act ttc cca ggc ggt 585
Gln Gly Trp Met Lys Arg Glu Gly Glu Tyr Phe Thr Phe Pro Gly Gly
165 170 175

ggc acg atg ttt cct ggc gga gct ggc caa tac att gaa aag ctt gca 633
Gly Thr Met Phe Pro Gly Gly Ala Gly Gln Tyr Ile Glu Lys Leu Ala
180 185 190

cag tat att ccg ctt aat ggt gga act ttg aga act gct ctt gac atg 681
Gln Tyr Ile Pro Leu Asn Gly Gly Thr Leu Arg Thr Ala Leu Asp Met
195 200 205

gga tgc ggg gta gct agt ttt gga ggt act cta cta tct caa ggc att 729
Gly Cys Gly Val Ala Ser Phe Gly Gly Thr Leu Leu Ser Gln Gly Ile
210 215 220 225

cta gcc ctc tca ttt gct cca aga gat tca cat aaa tct caa att cag 777
Leu Ala Leu Ser Phe Ala Pro Arg Asp Ser His Lys Ser Gln Ile Gln

230 235 240

ttc gct ttg gaa aga gga gtg cct gca ttt gtt gcc atg ctt ggc act 825
Phe Ala Leu Glu Arg Gly Val Pro Ala Phe Val Ala Met Leu Gly Thr
245 250 255

cgt aga ctc ccc ttt cct gca tac tcc ttt gac ctg atg cac tgt tcc 873
Arg Arg Leu Pro Phe Pro Ala Tyr Ser Phe Asp Leu Met His Cys Ser
260 265 270

cga tgt ttg att cct ttt acg gct tac aat gca act tac ttc atc gaa 921
Arg Cys Leu Ile Pro Phe Thr Ala Tyr Asn Ala Thr Tyr Phe Ile Glu
275 280 285

gta gat agg tta ctg cgc cct gga gga tat ctt gta atc tct ggc cca 969
Val Asp Arg Leu Leu Arg Pro Gly Gly Tyr Leu Val Ile Ser Gly Pro
290 295 300 305

cct gta caa tgg cct aaa caa gac aaa gaa tgg gct gat ctt cag gcg 1017
Pro Val Gln Trp Pro Lys Gln Asp Lys Glu Trp Ala Asp Leu Gln Ala
310 315 320

gtg gct aga gct ttg tgc tat gag cta att gcg gtt gat gga aac act 1065
Val Ala Arg Ala Leu Cys Tyr Glu Leu Ile Ala Val Asp Gly Asn Thr
325 330 335

gtc atc tgg aag aag cct gtt gga gat tca tgt cta cct agc cag aat 1113
Val Ile Trp Lys Lys Pro Val Gly Asp Ser Cys Leu Pro Ser Gln Asn
340 345 350

gag ttt ggg ctt gag ttg tgt gat gag tct gtt ccg cca agt gat gca 1161
Glu Phe Gly Leu Glu Leu Cys Asp Glu Ser Val Pro Pro Ser Asp Ala
355 360 365

tgg tat ttt aaa ttg aag agg tgt gtt acc agg cca tca tcc gtc aaa 1209
Trp Tyr Phe Lys Leu Lys Arg Cys Val Thr Arg Pro Ser Ser Val Lys
370 375 380 385

gga gaa cac gct ttg gga act ata tcc aag tgg ccg gag agg ctt act 1257
Gly Glu His Ala Leu Gly Thr Ile Ser Lys Trp Pro Glu Arg Leu Thr
390 395 400

aaa gtt cct tct agg gcc att gtc atg aaa aac gga ttg gat gtg ttt 1305
Lys Val Pro Ser Arg Ala Ile Val Met Lys Asn Gly Leu Asp Val Phe
405 410 415

gaa gca gat gca agg cgg tgg gca aga cgc gtt gct tat tac agg gat 1353
Glu Ala Asp Ala Arg Arg Trp Ala Arg Arg Val Ala Tyr Tyr Arg Asp
420 425 430

tct ctt aac ttg aag ctg aaa tct cca act gtc cgc aat gtc atg gac 1401
Ser Leu Asn Leu Lys Leu Lys Ser Pro Thr Val Arg Asn Val Met Asp
435 440 445

atg aac gca ttc ttc gga ggc ttt gca gca acc ctt gca tct gat cct 1449
Met Asn Ala Phe Phe Gly Gly Phe Ala Ala Thr Leu Ala Ser Asp Pro
450 455 460 465

```
gtg tgg gtt atg aat gtc att cca gct cgg aag cca tta act ctt gac     1497
Val Trp Val Met Asn Val Ile Pro Ala Arg Lys Pro Leu Thr Leu Asp
                470                 475                 480

gtg att tat gac aga ggt ctc atc ggt gtt tac cat gat tgg tgt gaa     1545
Val Ile Tyr Asp Arg Gly Leu Ile Gly Val Tyr His Asp Trp Cys Glu
            485                 490                 495

cca ttt tca aca tat ccc cgc acg tat gat ttc atc cat gta tca gga     1593
Pro Phe Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile His Val Ser Gly
        500                 505                 510

att gaa tca ctg ata aaa cga caa gac tca agc aaa tcg agg tgt agc     1641
Ile Glu Ser Leu Ile Lys Arg Gln Asp Ser Ser Lys Ser Arg Cys Ser
    515                 520                 525

cta gta gat cta atg gta gag atg gac aga ata tta cgt cca gaa gga     1689
Leu Val Asp Leu Met Val Glu Met Asp Arg Ile Leu Arg Pro Glu Gly
530                 535                 540                 545

aag gtt gtg atc cga gac tct cct gag gtg cta gat aaa gtc gca cga     1737
Lys Val Val Ile Arg Asp Ser Pro Glu Val Leu Asp Lys Val Ala Arg
                550                 555                 560

atg gct cat gct gta aga tgg tct tct tcc ata cac gag aaa gaa cct     1785
Met Ala His Ala Val Arg Trp Ser Ser Ser Ile His Glu Lys Glu Pro
            565                 570                 575

gaa tcc cat gga aga gag aag att ctt atc gca acc aaa tct ctc tgg     1833
Glu Ser His Gly Arg Glu Lys Ile Leu Ile Ala Thr Lys Ser Leu Trp
        580                 585                 590

aaa ttg cca tca aac tcc cac tga agacacaaaa gaagaagaaa agaagaagct  1887
Lys Leu Pro Ser Asn Ser His  *
    595                 600

cttctcaatc ttgtaggtac tgtcacttgc tctccagccc                         1927

<210> 72
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<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (1)...(601)
<223> Conserved domain

<400> 72
Met Gly His Val Asn Leu Pro Ala Ser Lys Arg Gly Asn Pro Arg Gln
 1               5                  10                  15
Trp Arg Leu Leu Asp Ile Val Thr Ala Ala Phe Phe Gly Ile Val Leu
            20                  25                  30
Leu Phe Phe Ile Leu Leu Phe Thr Pro Leu Gly Asp Ser Met Ala Ala
        35                  40                  45
Ser Gly Arg Gln Thr Leu Leu Leu Ser Thr Ala Ser Asp Pro Arg Gln
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    50                  55                  60
Arg Gln Arg Leu Val Thr Leu Val Glu Ala Gly Gln His Leu Gln Pro
65                  70                  75                  80
Ile Glu Tyr Cys Pro Ala Glu Ala Val Ala His Met Pro Cys Glu Asp
                85                  90                  95
Pro Arg Arg Asn Ser Gln Leu Ser Arg Glu Met Asn Phe Tyr Arg Glu
            100                 105                 110
Arg His Cys Pro Leu Pro Glu Glu Thr Pro Leu Cys Leu Ile Pro Pro
        115                 120                 125
Pro Ser Gly Tyr Lys Ile Pro Val Pro Trp Pro Glu Ser Leu His Lys
    130                 135                 140
Ile Trp His Ala Asn Met Pro Tyr Asn Lys Ile Ala Asp Arg Lys Gly
145                 150                 155                 160
His Gln Gly Trp Met Lys Arg Glu Gly Glu Tyr Phe Thr Phe Pro Gly
                165                 170                 175
Gly Gly Thr Met Phe Pro Gly Gly Ala Gly Gln Tyr Ile Glu Lys Leu
            180                 185                 190
Ala Gln Tyr Ile Pro Leu Asn Gly Gly Thr Leu Arg Thr Ala Leu Asp
        195                 200                 205
Met Gly Cys Gly Val Ala Ser Phe Gly Gly Thr Leu Leu Ser Gln Gly
    210                 215                 220
Ile Leu Ala Leu Ser Phe Ala Pro Arg Asp Ser His Lys Ser Gln Ile
225                 230                 235                 240
Gln Phe Ala Leu Glu Arg Gly Val Pro Ala Phe Val Ala Met Leu Gly
                245                 250                 255
Thr Arg Arg Leu Pro Phe Pro Ala Tyr Ser Phe Asp Leu Met His Cys
            260                 265                 270
Ser Arg Cys Leu Ile Pro Phe Thr Ala Tyr Asn Ala Thr Tyr Phe Ile
        275                 280                 285
Glu Val Asp Arg Leu Leu Arg Pro Gly Gly Tyr Leu Val Ile Ser Gly
    290                 295                 300
Pro Pro Val Gln Trp Pro Lys Gln Asp Lys Glu Trp Ala Asp Leu Gln
305                 310                 315                 320
Ala Val Ala Arg Ala Leu Cys Tyr Glu Leu Ile Ala Val Asp Gly Asn
                325                 330                 335
Thr Val Ile Trp Lys Lys Pro Val Gly Asp Ser Cys Leu Pro Ser Gln
            340                 345                 350
Asn Glu Phe Gly Leu Glu Leu Cys Asp Glu Ser Val Pro Pro Ser Asp
        355                 360                 365
Ala Trp Tyr Phe Lys Leu Lys Arg Cys Val Thr Arg Pro Ser Ser Val
    370                 375                 380
Lys Gly Glu His Ala Leu Gly Thr Ile Ser Lys Trp Pro Glu Arg Leu
385                 390                 395                 400
Thr Lys Val Pro Ser Arg Ala Ile Val Met Lys Asn Gly Leu Asp Val
                405                 410                 415
Phe Glu Ala Asp Ala Arg Arg Trp Ala Arg Arg Val Ala Tyr Tyr Arg
            420                 425                 430
Asp Ser Leu Asn Leu Lys Leu Lys Ser Pro Thr Val Arg Asn Val Met
        435                 440                 445
Asp Met Asn Ala Phe Phe Gly Gly Phe Ala Ala Thr Leu Ala Ser Asp
    450                 455                 460
Pro Val Trp Val Met Asn Val Ile Pro Ala Arg Lys Pro Leu Thr Leu
465                 470                 475                 480
Asp Val Ile Tyr Asp Arg Gly Leu Ile Gly Val Tyr His Asp Trp Cys
                485                 490                 495
Glu Pro Phe Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile His Val Ser
            500                 505                 510
```

```
Gly Ile Glu Ser Leu Ile Lys Arg Gln Asp Ser Ser Lys Ser Arg Cys
        515                 520                 525
Ser Leu Val Asp Leu Met Val Glu Met Asp Arg Ile Leu Arg Pro Glu
    530                 535                 540
Gly Lys Val Val Ile Arg Asp Ser Pro Glu Val Leu Asp Lys Val Ala
545                 550                 555                 560
Arg Met Ala His Ala Val Arg Trp Ser Ser Ser Ile His Glu Lys Glu
                565                 570                 575
Pro Glu Ser His Gly Arg Glu Lys Ile Leu Ile Ala Thr Lys Ser Leu
            580                 585                 590
Trp Lys Leu Pro Ser Asn Ser His
        595                 600
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<210> 73
<211> 1322
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (51)...(1247)

<400> 73

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                                                       Met Asp
                                                        1

ttg caa ctg aaa caa tgg aga agc cag cag cag caa caa cat cag aca   104
Leu Gln Leu Lys Gln Trp Arg Ser Gln Gln Gln Gln Gln His Gln Thr
        5                  10                  15

gag tca gaa gaa caa cct tct gca gct aag ata cca aaa cat gtc ttt   152
Glu Ser Glu Glu Gln Pro Ser Ala Ala Lys Ile Pro Lys His Val Phe
    20                  25                  30

gac cag att cat tct cac act gca act tct act gct ctt cct ctc ttt   200
Asp Gln Ile His Ser His Thr Ala Thr Ser Thr Ala Leu Pro Leu Phe
 35                  40                  45                  50

acc cct gag cct act tct tct aaa ctc tcc tct ttg tct cct gat tct   248
Thr Pro Glu Pro Thr Ser Ser Lys Leu Ser Ser Leu Ser Pro Asp Ser
                 55                  60                  65

tcc tcc agg ttc ccc aag atg ggg agc ttc ttt agc tgg gca cag tgg   296
Ser Ser Arg Phe Pro Lys Met Gly Ser Phe Phe Ser Trp Ala Gln Trp
             70                  75                  80

caa gaa ctt gaa cta caa gct ctg atc tac agg tac atg ttg gct ggt   344
Gln Glu Leu Glu Leu Gln Ala Leu Ile Tyr Arg Tyr Met Leu Ala Gly
         85                  90                  95

gct gct gtt cct cag gag ctc ctt tta cca atc aag aaa agc ctt ctc   392
Ala Ala Val Pro Gln Glu Leu Leu Leu Pro Ile Lys Lys Ser Leu Leu
    100                 105                 110

cat cta tct cct tcc tac ttt ctt cac cat cct ctt caa cac cta cct   440
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His Leu Ser Pro Ser Tyr Phe Leu His His Pro Leu Gln His Leu Pro
115 120 125 130

cat tac caa cct gct tgg tat ttg gga agg gca gcg atg gat cct gag 488
His Tyr Gln Pro Ala Trp Tyr Leu Gly Arg Ala Ala Met Asp Pro Glu
135 140 145

cca ggc aga tgc agg aga acg gat ggt aag aag tgg aga tgt tca aga 536
Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Arg
150 155 160

gac gtc ttc gct ggc cac aag tat tgc gag cgc cac atg cac cgt ggc 584
Asp Val Phe Ala Gly His Lys Tyr Cys Glu Arg His Met His Arg Gly
165 170 175

cgc aac cgt tca aga aag cct gtg gaa act cca acc acc gtc aat gca 632
Arg Asn Arg Ser Arg Lys Pro Val Glu Thr Pro Thr Thr Val Asn Ala
180 185 190

act gcc acg tcc atg gct tca tca gta gca gcc gca gcc acc act aca 680
Thr Ala Thr Ser Met Ala Ser Ser Val Ala Ala Ala Ala Thr Thr Thr
195 200 205 210

aca gca aca aca aca tct acg ttt gct ttt ggt ggt ggt ggt ggt agt 728
Thr Ala Thr Thr Thr Ser Thr Phe Ala Phe Gly Gly Gly Gly Gly Ser
215 220 225

gag gaa gtg gtt ggt caa gga gga tct ttc ttc ttc tct ggc tct tct 776
Glu Glu Val Val Gly Gln Gly Gly Ser Phe Phe Phe Ser Gly Ser Ser
230 235 240

aac tct tca tct gaa ctt ctc cac ctt agt caa agt tgt tcg gag atg 824
Asn Ser Ser Ser Glu Leu Leu His Leu Ser Gln Ser Cys Ser Glu Met
245 250 255

aag caa gaa agc aac aac atg aac aac aag agg cca tac gag tcc cac 872
Lys Gln Glu Ser Asn Asn Met Asn Asn Lys Arg Pro Tyr Glu Ser His
260 265 270

atc gga ttc agt aac aac aga tca gat gga gga cac atc ctg agg ccc 920
Ile Gly Phe Ser Asn Asn Arg Ser Asp Gly Gly His Ile Leu Arg Pro
275 280 285 290

ttc ttt gac gat tgg cct cgt tct tcg ctc caa gaa gct gac aat agt 968
Phe Phe Asp Asp Trp Pro Arg Ser Ser Leu Gln Glu Ala Asp Asn Ser
295 300 305

tca agc ccc atg agc tca gcc act tgt ctc tcc atc tcc atg ccc ggg 1016
Ser Ser Pro Met Ser Ser Ala Thr Cys Leu Ser Ile Ser Met Pro Gly
310 315 320

aac tct tcc tca gac gtc tct ctg aag ctg tcc aca ggc aac gaa gag 1064
Asn Ser Ser Ser Asp Val Ser Leu Lys Leu Ser Thr Gly Asn Glu Glu
325 330 335

gga gcc cgg agc aac aac aat ggg aga gat cag caa aac atg agc tgg 1112
Gly Ala Arg Ser Asn Asn Asn Gly Arg Asp Gln Gln Asn Met Ser Trp

```
 340                 345                 350

tgg agc ggt gga ggt tcc aac cac cat cat cac aac atg ggc gga cca    1160
Trp Ser Gly Gly Gly Ser Asn His His His His Asn Met Gly Gly Pro
355                 360                 365                 370

ttg gcc gaa gcc ctg aga tct tct tcc tca tct tcc cca acc agt gtt    1208
Leu Ala Glu Ala Leu Arg Ser Ser Ser Ser Ser Ser Pro Thr Ser Val
                375                 380                 385

ctc cat cag ctt ggt gtc tcg aca caa gcc ttt cat tga ccagtgtaaa     1257
Leu His Gln Leu Gly Val Ser Thr Gln Ala Phe His  *
            390                 395

accaacacaa caatgcggtt tttactgtgt ttttggtttt tatccaaatt tcctgtataa 1317
agagg                                                              1322
```

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<210> 74
<211> 398
<212> PRT
<213> Arabidopsis thaliana

<400> 74
Met Asp Leu Gln Leu Lys Gln Trp Arg Ser Gln Gln Gln Gln Gln His
 1               5                  10                  15
Gln Thr Glu Ser Glu Glu Gln Pro Ser Ala Ala Lys Ile Pro Lys His
            20                  25                  30
Val Phe Asp Gln Ile His Ser His Thr Ala Thr Ser Thr Ala Leu Pro
        35                  40                  45
Leu Phe Thr Pro Glu Pro Thr Ser Ser Lys Leu Ser Ser Leu Ser Pro
    50                  55                  60
Asp Ser Ser Ser Arg Phe Pro Lys Met Gly Ser Phe Phe Ser Trp Ala
65                  70                  75                  80
Gln Trp Gln Glu Leu Glu Leu Gln Ala Leu Ile Tyr Arg Tyr Met Leu
                85                  90                  95
Ala Gly Ala Ala Val Pro Gln Glu Leu Leu Leu Pro Ile Lys Lys Ser
            100                 105                 110
Leu Leu His Leu Ser Pro Ser Tyr Phe Leu His His Pro Leu Gln His
        115                 120                 125
Leu Pro His Tyr Gln Pro Ala Trp Tyr Leu Gly Arg Ala Ala Met Asp
    130                 135                 140
Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys
145                 150                 155                 160
Ser Arg Asp Val Phe Ala Gly His Lys Tyr Cys Glu Arg His Met His
                165                 170                 175
Arg Gly Arg Asn Arg Ser Arg Lys Pro Val Glu Thr Pro Thr Thr Val
            180                 185                 190
Asn Ala Thr Ala Thr Ser Met Ala Ser Ser Val Ala Ala Ala Ala Thr
        195                 200                 205
Thr Thr Thr Ala Thr Thr Thr Ser Thr Phe Ala Phe Gly Gly Gly Gly
    210                 215                 220
Gly Ser Glu Glu Val Val Gly Gln Gly Gly Ser Phe Phe Phe Ser Gly
225                 230                 235                 240
Ser Ser Asn Ser Ser Ser Glu Leu Leu His Leu Ser Gln Ser Cys Ser
                245                 250                 255
Glu Met Lys Gln Glu Ser Asn Asn Met Asn Asn Lys Arg Pro Tyr Glu
            260                 265                 270
```

```
Ser His Ile Gly Phe Ser Asn Asn Arg Ser Asp Gly Gly His Ile Leu
        275                 280                 285
Arg Pro Phe Phe Asp Asp Trp Pro Arg Ser Ser Leu Gln Glu Ala Asp
    290                 295                 300
Asn Ser Ser Ser Pro Met Ser Ser Ala Thr Cys Leu Ser Ile Ser Met
305                 310                 315                 320
Pro Gly Asn Ser Ser Ser Asp Val Ser Leu Lys Leu Ser Thr Gly Asn
                325                 330                 335
Glu Glu Gly Ala Arg Ser Asn Asn Asn Gly Arg Asp Gln Gln Asn Met
            340                 345                 350
Ser Trp Trp Ser Gly Gly Gly Ser Asn His His His His Asn Met Gly
        355                 360                 365
Gly Pro Leu Ala Glu Ala Leu Arg Ser Ser Ser Ser Ser Ser Pro Thr
    370                 375                 380
Ser Val Leu His Gln Leu Gly Val Ser Thr Gln Ala Phe His
385                 390                 395
```

<210> 75
<211> 1191
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (50)...(1096)

<400> 75

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ctctcaccaa cataatcaaa gaagctttcc tcacgaattc aagatcgcc atg tcc tcc 58
                                                      Met Ser Ser
                                                       1

gag gat tgg gat ctc ttc gcc gtc gtc aga agc tgc agc tct tct gtt    106
Glu Asp Trp Asp Leu Phe Ala Val Val Arg Ser Cys Ser Ser Ser Val
    5                   10                  15

tcc acc acc aat tct tgt gct ggt cat gaa gac gac ata gga aac tgt    154
Ser Thr Thr Asn Ser Cys Ala Gly His Glu Asp Asp Ile Gly Asn Cys
20                  25                  30                  35

aaa caa caa caa gat cct cct cct cct cct ctg ttt caa gct tct tct    202
Lys Gln Gln Gln Asp Pro Pro Pro Pro Pro Leu Phe Gln Ala Ser Ser
                40                  45                  50

tct tgc aac gag tta caa gat tct tgc aaa cca ttt tta ccc gtt act    250
Ser Cys Asn Glu Leu Gln Asp Ser Cys Lys Pro Phe Leu Pro Val Thr
            55                  60                  65

act act act act act act tgg tct cct cct cct cta ctt cct cct cct    298
Thr Thr Thr Thr Thr Thr Trp Ser Pro Pro Pro Leu Leu Pro Pro Pro
        70                  75                  80

aaa gcc tca tca cca tct ccc aat atc tta cta aaa caa gaa caa gta    346
Lys Ala Ser Ser Pro Ser Pro Asn Ile Leu Leu Lys Gln Glu Gln Val
    85                  90                  95

ctt ctc gaa tca caa gat caa aaa cct cct ctt agt gtt agg gtt ttc    394
```

```
Leu Leu Glu Ser Gln Asp Gln Lys Pro Pro Leu Ser Val Arg Val Phe
100                 105                 110                 115

cca cca tcc act tct tct tct gtc ttt gtt ttt aga ggt caa cgc gac      442
Pro Pro Ser Thr Ser Ser Ser Val Phe Val Phe Arg Gly Gln Arg Asp
                120                 125                 130

cag ctt ctt caa caa caa tcc caa cct ccc ctt cga tct aga aaa aga      490
Gln Leu Leu Gln Gln Gln Ser Gln Pro Pro Leu Arg Ser Arg Lys Arg
            135                 140                 145

aag aat cag caa aaa aga acc ata tgt cat gta acg caa gag aat ctt      538
Lys Asn Gln Gln Lys Arg Thr Ile Cys His Val Thr Gln Glu Asn Leu
        150                 155                 160

tct tct gat ttg tgg gct tgg cgt aaa tac ggt caa aaa ccc atc aaa      586
Ser Ser Asp Leu Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys
    165                 170                 175

ggc tct cct tat cca agg aat tat tac aga tgt agt agc tca aaa gga      634
Gly Ser Pro Tyr Pro Arg Asn Tyr Tyr Arg Cys Ser Ser Ser Lys Gly
180                 185                 190                 195

tgt tta gca cga aaa caa gtt gaa aga agt aat tta gat cct aat atc      682
Cys Leu Ala Arg Lys Gln Val Glu Arg Ser Asn Leu Asp Pro Asn Ile
                200                 205                 210

ttc atc gtt act tac acc gga gaa cac act cat cca cgt cct act cac      730
Phe Ile Val Thr Tyr Thr Gly Glu His Thr His Pro Arg Pro Thr His
            215                 220                 225

cgg aac tct ctc gcc gga agt act cgt aac aaa tct cag ccc gtt aac      778
Arg Asn Ser Leu Ala Gly Ser Thr Arg Asn Lys Ser Gln Pro Val Asn
        230                 235                 240

ccg gtt cct aaa ccg gac aca tct cct tta tcg gat aca gta aaa gaa      826
Pro Val Pro Lys Pro Asp Thr Ser Pro Leu Ser Asp Thr Val Lys Glu
    245                 250                 255

gag att cat ctt tct ccg acg aca ccg ttg aaa gga aac gat gac gtt      874
Glu Ile His Leu Ser Pro Thr Thr Pro Leu Lys Gly Asn Asp Asp Val
260                 265                 270                 275

caa gaa acg aat gga gat gaa gat atg gtt ggt caa gaa gtc aac atg      922
Gln Glu Thr Asn Gly Asp Glu Asp Met Val Gly Gln Glu Val Asn Met
                280                 285                 290

gaa gag gaa gag gag gaa gaa gaa gtg gaa gaa gat gat gaa gaa gaa      970
Glu Glu Glu Glu Glu Glu Glu Glu Val Glu Glu Asp Asp Glu Glu Glu
            295                 300                 305

gaa gat gat gat gac gtg gat gat ctt ttg ata cca aat tta gcg gtg     1018
Glu Asp Asp Asp Asp Val Asp Asp Leu Leu Ile Pro Asn Leu Ala Val
        310                 315                 320

aga gat cga gat gat ttg ttc ttc gct gga agt ttt cca tct tgg tcc     1066
Arg Asp Arg Asp Asp Leu Phe Phe Ala Gly Ser Phe Pro Ser Trp Ser
```

325 330 335

gcc gga tcc gcc ggt gac ggt ggt gga tga tgaaaacgaa taaaatctca 1116
Ala Gly Ser Ala Gly Asp Gly Gly Gly *
340 345

atttacaatt tacaaaaaga aaaaagtcag tttttaatta ttatttttgt ttgttaaaac 1176
ttgacattta ttgtg 1191

<210> 76
<211> 348
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (175)...(222)
<223> Conserved domain

<400> 76
Met Ser Ser Glu Asp Trp Asp Leu Phe Ala Val Val Arg Ser Cys Ser
1 5 10 15
Ser Ser Val Ser Thr Thr Asn Ser Cys Ala Gly His Glu Asp Asp Ile
20 25 30
Gly Asn Cys Lys Gln Gln Gln Asp Pro Pro Pro Pro Pro Leu Phe Gln
35 40 45
Ala Ser Ser Ser Cys Asn Glu Leu Gln Asp Ser Cys Lys Pro Phe Leu
50 55 60
Pro Val Thr Thr Thr Thr Thr Thr Thr Trp Ser Pro Pro Pro Leu Leu
65 70 75 80
Pro Pro Pro Lys Ala Ser Ser Pro Ser Pro Asn Ile Leu Leu Lys Gln
85 90 95
Glu Gln Val Leu Leu Glu Ser Gln Asp Gln Lys Pro Pro Leu Ser Val
100 105 110
Arg Val Phe Pro Pro Ser Thr Ser Ser Ser Val Phe Val Phe Arg Gly
115 120 125
Gln Arg Asp Gln Leu Leu Gln Gln Gln Ser Gln Pro Pro Leu Arg Ser
130 135 140
Arg Lys Arg Lys Asn Gln Gln Lys Arg Thr Ile Cys His Val Thr Gln
145 150 155 160
Glu Asn Leu Ser Ser Asp Leu Trp Ala Trp Arg Lys Tyr Gly Gln Lys
165 170 175
Pro Ile Lys Gly Ser Pro Tyr Pro Arg Asn Tyr Tyr Arg Cys Ser Ser
180 185 190
Ser Lys Gly Cys Leu Ala Arg Lys Gln Val Glu Arg Ser Asn Leu Asp
195 200 205
Pro Asn Ile Phe Ile Val Thr Tyr Thr Gly Glu His Thr His Pro Arg
210 215 220
Pro Thr His Arg Asn Ser Leu Ala Gly Ser Thr Arg Asn Lys Ser Gln
225 230 235 240
Pro Val Asn Pro Val Pro Lys Pro Asp Thr Ser Pro Leu Ser Asp Thr
245 250 255
Val Lys Glu Glu Ile His Leu Ser Pro Thr Thr Pro Leu Lys Gly Asn
260 265 270
Asp Asp Val Gln Glu Thr Asn Gly Asp Glu Asp Met Val Gly Gln Glu
275 280 285
Val Asn Met Glu Glu Glu Glu Glu Glu Glu Glu Val Glu Glu Asp Asp

```
    290                     295                     300
Glu Glu Glu Glu Asp Asp Asp Asp Val Asp Asp Leu Leu Ile Pro Asn
305                 310                     315                 320
Leu Ala Val Arg Asp Arg Asp Asp Leu Phe Phe Ala Gly Ser Phe Pro
                325                     330                 335
Ser Trp Ser Ala Gly Ser Ala Gly Asp Gly Gly Gly
            340                     345
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<210> 77
<211> 1155
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (76)...(1077)

<400> 77

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attcacatta ctaatctctc aagatttcac aattttcttg tgattttctc tcagtttctt 60
atttcgtttc ataac atg gat gcc atg agt agc gta gac gag agc tct aca  111
                 Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr
                  1               5                  10

act aca gat tcc att ccg gcg aga aag tca tcg tct ccg gcg agt tta   159
Thr Thr Asp Ser Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu
        15                  20                  25

cta tat aga atg gga agc gga aca agc gtg gta ctt gat tca gag aac   207
Leu Tyr Arg Met Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn
    30                  35                  40

ggt gtc gaa gtc gaa gtc gaa gcc gaa tca aga aag ctt cct tct tca   255
Gly Val Glu Val Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser
45                  50                  55                  60

aga ttc aaa ggt gtt gtt cct caa cca aat gga aga tgg gga gct cag   303
Arg Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
                65                  70                  75

att tac gag aaa cat caa cgc gtg tgg ctt ggt act ttc aac gag gaa   351
Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu
            80                  85                  90

gac gaa gca gct cgt gct tac gac gtc gcg gct cac cgt ttc cgt ggc   399
Asp Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly
        95                  100                 105

cgc gat gcc gtt act aat ttc aaa gac acg acg ttc gaa gaa gag gtt   447
Arg Asp Ala Val Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val
    110                 115                 120

gag ttc tta aac gcg cat tcg aaa tca gag atc gta gat atg ttg aga   495
Glu Phe Leu Asn Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg
125                 130                 135                 140

aaa cac act tac aaa gaa gag tta gac caa agg aaa cgt aac cgt gac   543
```

Lys His Thr Tyr Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp
145 150 155

ggt aac gga aaa gag acg acg gcg ttt gct ttg gct tcg atg gtg gtt 591
Gly Asn Gly Lys Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val
160 165 170

atg acg ggg ttt aaa acg gcg gag tta ctg ttt gag aaa acg gta acg 639
Met Thr Gly Phe Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr
175 180 185

cca agt gac gtc ggg aaa cta aac cgt tta gtt ata cca aaa cac caa 687
Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln
190 195 200

gcg gag aaa cat ttt ccg tta ccg tta ggt aat aat aac gtc tcc gtt 735
Ala Glu Lys His Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val
205 210 215 220

aaa ggt atg ctg ttg aat ttc gaa gac gtt aac ggg aaa gtg tgg agg 783
Lys Gly Met Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg
225 230 235

ttc cgt tac tct tat tgg aat agt agt caa agt tat gtg ttg acc aaa 831
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
240 245 250

ggt tgg agt aga ttc gtt aaa gag aag aga ctt tgt gct ggt gat ttg 879
Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu
255 260 265

atc agt ttt aaa aga tcc aac gat caa gat caa aaa ttc ttt atc ggg 927
Ile Ser Phe Lys Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly
270 275 280

tgg aaa tcg aaa tcc ggg ttg gat cta gag acg ggt cgg gtt atg aga 975
Trp Lys Ser Lys Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg
285 290 295 300

ttg ttt ggg gtt gat att tct tta aac gcc gtc gtt gta gtg aag gaa 1023
Leu Phe Gly Val Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu
305 310 315

aca acg gag gtg tta atg tcg tcg tta agg tgt aag aag caa cga gtt 1071
Thr Thr Glu Val Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val
320 325 330

ttg taa taacaattta acaacttggg aaagaaaaaa aagctttttg attttaattt 1127
Leu *

ctcttcaacg ttaatcttgc tgagatta 1155

<210> 78
<211> 333
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (59)...(124)
<223> Conserved domain

<400> 78
Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser
1 5 10 15
Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met
20 25 30
Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val
35 40 45
Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly
50 55 60
Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65 70 75 80
His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
85 90 95
Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val
100 105 110
Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn
115 120 125
Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
130 135 140
Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys
145 150 155 160
Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe
165 170 175
Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val
180 185 190
Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His
195 200 205
Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu
210 215 220
Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser
225 230 235 240
Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
245 250 255
Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys
260 265 270
Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys
275 280 285
Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val
290 295 300
Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu Thr Thr Glu Val
305 310 315 320
Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val Leu
325 330

<210> 79
<211> 1029
<212> DNA
<213> Arabidopsis thaliana

<220>

<221> CDS
<222> (1)...(1029)

<400> 79
atg gag aat ccg gtg ggt tta aga ttc cgt ccg acc gac aag gag atc 48
Met Glu Asn Pro Val Gly Leu Arg Phe Arg Pro Thr Asp Lys Glu Ile
1 5 10 15

gtc gtc gat tac ctc cga cca aaa aac tcc gat agg gac acg agt cat 96
Val Val Asp Tyr Leu Arg Pro Lys Asn Ser Asp Arg Asp Thr Ser His
20 25 30

gtt gat cga gtc att agc aca gtc act atc cgt agc ttc gac cct tgg 144
Val Asp Arg Val Ile Ser Thr Val Thr Ile Arg Ser Phe Asp Pro Trp
35 40 45

gag tta cct tgc cag tct agg atc aaa ctg aaa gat gag tct tgg tgt 192
Glu Leu Pro Cys Gln Ser Arg Ile Lys Leu Lys Asp Glu Ser Trp Cys
50 55 60

ttc ttc agc cct aag gag aac aaa tat ggc aga ggt gat caa caa att 240
Phe Phe Ser Pro Lys Glu Asn Lys Tyr Gly Arg Gly Asp Gln Gln Ile
65 70 75 80

aga aaa acg aaa tct ggt tac tgg aag att act ggc aaa cca aag cct 288
Arg Lys Thr Lys Ser Gly Tyr Trp Lys Ile Thr Gly Lys Pro Lys Pro
85 90 95

atc ttg cgt aac cgc caa gag atc ggt gag aaa aag gtt ttg atg ttt 336
Ile Leu Arg Asn Arg Gln Glu Ile Gly Glu Lys Lys Val Leu Met Phe
100 105 110

tac atg agt aag gaa ctt ggt gga tcc aaa tcc gac tgg gtt atg cac 384
Tyr Met Ser Lys Glu Leu Gly Gly Ser Lys Ser Asp Trp Val Met His
115 120 125

gag tac cat gct ttc tct cct act cag atg atg atg aca tat aca ata 432
Glu Tyr His Ala Phe Ser Pro Thr Gln Met Met Met Thr Tyr Thr Ile
130 135 140

tgt aaa gtt atg ttt aag ggt gac gtg aga gag att tct tct tct tct 480
Cys Lys Val Met Phe Lys Gly Asp Val Arg Glu Ile Ser Ser Ser Ser
145 150 155 160

gct tct tat ggt agt gaa att gag cag agt cgt gac tct tta atc cct 528
Ala Ser Tyr Gly Ser Glu Ile Glu Gln Ser Arg Asp Ser Leu Ile Pro
165 170 175

ctt ctt gtg aac gat tct gag gaa gaa gct caa atc gag gat gct ata 576
Leu Leu Val Asn Asp Ser Glu Glu Glu Ala Gln Ile Glu Asp Ala Ile
180 185 190

cca ata gag gaa tgg gaa aca tgg ttg act gat gat ggt gtt gat gag 624
Pro Ile Glu Glu Trp Glu Thr Trp Leu Thr Asp Asp Gly Val Asp Glu
195 200 205

cag gtg aat cat att atg aat atg aaa gat gat cgc aac aac cac agg 672

Gln Val Asn His Ile Met Asn Met Lys Asp Asp Arg Asn Asn His Arg
210 215 220

cct caa aag cca ttg act ggt gtc ttg att gac gat agt agt gat gat 720
Pro Gln Lys Pro Leu Thr Gly Val Leu Ile Asp Asp Ser Ser Asp Asp
225 230 235 240

gat gat gat tct gat ttg cta tct cca aca aca aat tct att gaa aat 768
Asp Asp Asp Ser Asp Leu Leu Ser Pro Thr Thr Asn Ser Ile Glu Asn
245 250 255

tcg agc act tgt gat agt ttt ggt agc tca gac caa atc aac tta gtg 816
Ser Ser Thr Cys Asp Ser Phe Gly Ser Ser Asp Gln Ile Asn Leu Val
260 265 270

tca cta act caa gag gtg agc caa gct ctg ata acc agt att gat aca 864
Ser Leu Thr Gln Glu Val Ser Gln Ala Leu Ile Thr Ser Ile Asp Thr
275 280 285

ccc gag aag att aag agt cct tat gat gat gca caa ggg act ggg gct 912
Pro Glu Lys Ile Lys Ser Pro Tyr Asp Asp Ala Gln Gly Thr Gly Ala
290 295 300

gga ggg caa aaa ttg ggt caa gag act cga gag aag aaa cga gct ggt 960
Gly Gly Gln Lys Leu Gly Gln Glu Thr Arg Glu Lys Lys Arg Ala Gly
305 310 315 320

ttc ttt cac agg atg ata caa ata ttc gtc aag aaa att cac caa tgt 1008
Phe Phe His Arg Met Ile Gln Ile Phe Val Lys Lys Ile His Gln Cys
325 330 335

tct tct atc tca aga aca taa 1029
Ser Ser Ile Ser Arg Thr *
340

<210> 80
<211> 342
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (10)...(149)
<223> Conserved domain

<400> 80
Met Glu Asn Pro Val Gly Leu Arg Phe Arg Pro Thr Asp Lys Glu Ile
1 5 10 15
Val Val Asp Tyr Leu Arg Pro Lys Asn Ser Asp Arg Asp Thr Ser His
20 25 30
Val Asp Arg Val Ile Ser Thr Val Thr Ile Arg Ser Phe Asp Pro Trp
35 40 45
Glu Leu Pro Cys Gln Ser Arg Ile Lys Leu Lys Asp Glu Ser Trp Cys
50 55 60
Phe Phe Ser Pro Lys Glu Asn Lys Tyr Gly Arg Gly Asp Gln Gln Ile
65 70 75 80

```
Arg Lys Thr Lys Ser Gly Tyr Trp Lys Ile Thr Gly Lys Pro Lys Pro
                85                  90                  95
Ile Leu Arg Asn Arg Gln Glu Ile Gly Glu Lys Lys Val Leu Met Phe
            100                 105                 110
Tyr Met Ser Lys Glu Leu Gly Gly Ser Lys Ser Asp Trp Val Met His
        115                 120                 125
Glu Tyr His Ala Phe Ser Pro Thr Gln Met Met Met Thr Tyr Thr Ile
    130                 135                 140
Cys Lys Val Met Phe Lys Gly Asp Val Arg Glu Ile Ser Ser Ser Ser
145                 150                 155                 160
Ala Ser Tyr Gly Ser Glu Ile Glu Gln Ser Arg Asp Ser Leu Ile Pro
                165                 170                 175
Leu Leu Val Asn Asp Ser Glu Glu Glu Ala Gln Ile Glu Asp Ala Ile
            180                 185                 190
Pro Ile Glu Glu Trp Glu Thr Trp Leu Thr Asp Asp Gly Val Asp Glu
        195                 200                 205
Gln Val Asn His Ile Met Asn Met Lys Asp Asp Arg Asn Asn His Arg
    210                 215                 220
Pro Gln Lys Pro Leu Thr Gly Val Leu Ile Asp Asp Ser Ser Asp Asp
225                 230                 235                 240
Asp Asp Asp Ser Asp Leu Leu Ser Pro Thr Thr Asn Ser Ile Glu Asn
                245                 250                 255
Ser Ser Thr Cys Asp Ser Phe Gly Ser Ser Asp Gln Ile Asn Leu Val
            260                 265                 270
Ser Leu Thr Gln Glu Val Ser Gln Ala Leu Ile Thr Ser Ile Asp Thr
        275                 280                 285
Pro Glu Lys Ile Lys Ser Pro Tyr Asp Asp Ala Gln Gly Thr Gly Ala
    290                 295                 300
Gly Gly Gln Lys Leu Gly Gln Glu Thr Arg Glu Lys Lys Arg Ala Gly
305                 310                 315                 320
Phe Phe His Arg Met Ile Gln Ile Phe Val Lys Lys Ile His Gln Cys
                325                 330                 335
Ser Ser Ile Ser Arg Thr
            340


<210> 81
<211> 1514
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (148)...(1254)

<400> 81
actctcttaa ctttcgtttc ttctcctacc ttcttttacc aacctttcct ttctcttaca 60
cacatatata tatacatata tagagagaga gaagaggaca aagagttgaa agatgaagac 120
tctcatgtct tcatagaaac aagtgat atg tgc gct aag aaa gaa gaa gaa gaa 174
                              Met Cys Ala Lys Lys Glu Glu Glu Glu
                               1               5

gaa gaa gaa gaa gac agt tct gaa gcc atg aac aac ata caa aat tac   222
Glu Glu Glu Glu Asp Ser Ser Glu Ala Met Asn Asn Ile Gln Asn Tyr
 10                  15                  20                  25

caa aat gac ctc ttc ttt cac caa ctc atc tct cat cat cac cat cat   270
```

Gln Asn Asp Leu Phe Phe His Gln Leu Ile Ser His His His His His
30 35 40

cat cat gat cct tct caa tct gaa act ttg gga gca tcc ggt aac gtt 318
His His Asp Pro Ser Gln Ser Glu Thr Leu Gly Ala Ser Gly Asn Val
45 50 55

gga tct ggt ttc act atc ttc tct caa gat tcc gtc tct cca ata tgg 366
Gly Ser Gly Phe Thr Ile Phe Ser Gln Asp Ser Val Ser Pro Ile Trp
60 65 70

tct cta cct cca cct acc tcg atc caa cca cca ttt gat cag ttt cct 414
Ser Leu Pro Pro Pro Thr Ser Ile Gln Pro Pro Phe Asp Gln Phe Pro
75 80 85

cct cct tct tct tct cca gca tct ttc tac gga agt ttc ttc aac aga 462
Pro Pro Ser Ser Ser Pro Ala Ser Phe Tyr Gly Ser Phe Phe Asn Arg
90 95 100 105

agt cga gct cat cat cag gga tta cag ttt ggg tac gag ggt ttt ggt 510
Ser Arg Ala His His Gln Gly Leu Gln Phe Gly Tyr Glu Gly Phe Gly
110 115 120

gga gcc acg tca gca gca cat cat cat cat gaa caa ctt cgg atc ttg 558
Gly Ala Thr Ser Ala Ala His His His His Glu Gln Leu Arg Ile Leu
125 130 135

tcg gaa gct tta ggt ccg gta gta caa gcc ggg tcc ggt cct ttt ggg 606
Ser Glu Ala Leu Gly Pro Val Val Gln Ala Gly Ser Gly Pro Phe Gly
140 145 150

tta caa gct gag tta ggg aag atg aca gca caa gag atc atg gac gct 654
Leu Gln Ala Glu Leu Gly Lys Met Thr Ala Gln Glu Ile Met Asp Ala
155 160 165

aaa gct ttg gct gct tca aag agt cat agt gaa gct gag aga aga aga 702
Lys Ala Leu Ala Ala Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg
170 175 180 185

aga gag aga atc aat aat cat ctc gct aag ctc cgt agc ata tta ccc 750
Arg Glu Arg Ile Asn Asn His Leu Ala Lys Leu Arg Ser Ile Leu Pro
190 195 200

aac acc acc aaa acg gat aaa gcg tcg tta cta gct gaa gtg atc caa 798
Asn Thr Thr Lys Thr Asp Lys Ala Ser Leu Leu Ala Glu Val Ile Gln
205 210 215

cat gtg aaa gag ttg aag aga gag act tca gtg atc tca gag aca aat 846
His Val Lys Glu Leu Lys Arg Glu Thr Ser Val Ile Ser Glu Thr Asn
220 225 230

ctt gtc cca acg gaa agc gat gag tta acg gta gct ttc acg gag gag 894
Leu Val Pro Thr Glu Ser Asp Glu Leu Thr Val Ala Phe Thr Glu Glu
235 240 245

gaa gaa acc gga gat ggc aga ttt gta att aaa gcg tcg ctt tgc tgt 942
Glu Glu Thr Gly Asp Gly Arg Phe Val Ile Lys Ala Ser Leu Cys Cys

```
250                 255                 260                 265

gaa gac agg tcg gat ctc ttg cct gac atg att aaa aca ttg aaa gct    990
Glu Asp Arg Ser Asp Leu Leu Pro Asp Met Ile Lys Thr Leu Lys Ala
                270                 275                 280

atg cgt ctc aaa acg ctc aag gcg gag ata acc acc gtt ggg gga cga    1038
Met Arg Leu Lys Thr Leu Lys Ala Glu Ile Thr Thr Val Gly Gly Arg
            285                 290                 295

gtc aag aac gtt ttg ttt gtt acc gga gaa gag agc tcc ggt gag gaa    1086
Val Lys Asn Val Leu Phe Val Thr Gly Glu Glu Ser Ser Gly Glu Glu
        300                 305                 310

gtg gag gaa gag tac tgt ata ggg acg att gag gaa gct ttg aaa gcg    1134
Val Glu Glu Glu Tyr Cys Ile Gly Thr Ile Glu Glu Ala Leu Lys Ala
    315                 320                 325

gtg atg gag aag agc aat gta gag gaa tca tct tct tct gga aat gct    1182
Val Met Glu Lys Ser Asn Val Glu Glu Ser Ser Ser Ser Gly Asn Ala
330                 335                 340                 345

aag aga cag aga atg agt agt cac aac act atc act atc gtc gaa caa    1230
Lys Arg Gln Arg Met Ser Ser His Asn Thr Ile Thr Ile Val Glu Gln
                350                 355                 360

caa caa caa tat aat cag agg taa tcaatttttt acttaaatcg cttttttttc   1284
Gln Gln Gln Tyr Asn Gln Arg  *
            365

ttactttcgg tgtatctact acgtgtgttg tttgctggtt atggaaatga atgttgtacg 1344
tcacgttata ctatagatat atgtgtgttt gtgtgtatgt ataacggaag tatttgtatc 1404
cgttgtggtc ttggactttt ggtttggttc taagatactt atttttaaaa acttgtatcg 1464
ttgagttggt tttctagata tgcttaatgg gagtatgtga cgaaaaaaaa            1514

<210> 82
<211> 368
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (167)...(242)
<223> Conserved domain

<400> 82
Met Cys Ala Lys Lys Glu Glu Glu Glu Glu Glu Glu Glu Asp Ser Ser
 1               5                  10                  15
Glu Ala Met Asn Asn Ile Gln Asn Tyr Gln Asn Asp Leu Phe Phe His
            20                  25                  30
Gln Leu Ile Ser His His His His His His His Asp Pro Ser Gln Ser
        35                  40                  45
Glu Thr Leu Gly Ala Ser Gly Asn Val Gly Ser Gly Phe Thr Ile Phe
    50                  55                  60
Ser Gln Asp Ser Val Ser Pro Ile Trp Ser Leu Pro Pro Pro Thr Ser
65                  70                  75                  80
Ile Gln Pro Pro Phe Asp Gln Phe Pro Pro Pro Ser Ser Ser Pro Ala
```

```
                85                  90                  95
Ser Phe Tyr Gly Ser Phe Phe Asn Arg Ser Arg Ala His His Gln Gly
            100                 105                 110
Leu Gln Phe Gly Tyr Glu Gly Phe Gly Gly Ala Thr Ser Ala Ala His
        115                 120                 125
His His His Glu Gln Leu Arg Ile Leu Ser Glu Ala Leu Gly Pro Val
    130                 135                 140
Val Gln Ala Gly Ser Gly Pro Phe Gly Leu Gln Ala Glu Leu Gly Lys
145                 150                 155                 160
Met Thr Ala Gln Glu Ile Met Asp Ala Lys Ala Leu Ala Ala Ser Lys
                165                 170                 175
Ser His Ser Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile Asn Asn His
            180                 185                 190
Leu Ala Lys Leu Arg Ser Ile Leu Pro Asn Thr Thr Lys Thr Asp Lys
        195                 200                 205
Ala Ser Leu Leu Ala Glu Val Ile Gln His Val Lys Glu Leu Lys Arg
    210                 215                 220
Glu Thr Ser Val Ile Ser Glu Thr Asn Leu Val Pro Thr Glu Ser Asp
225                 230                 235                 240
Glu Leu Thr Val Ala Phe Thr Glu Glu Glu Glu Thr Gly Asp Gly Arg
                245                 250                 255
Phe Val Ile Lys Ala Ser Leu Cys Cys Glu Asp Arg Ser Asp Leu Leu
            260                 265                 270
Pro Asp Met Ile Lys Thr Leu Lys Ala Met Arg Leu Lys Thr Leu Lys
        275                 280                 285
Ala Glu Ile Thr Thr Val Gly Gly Arg Val Lys Asn Val Leu Phe Val
    290                 295                 300
Thr Gly Glu Glu Ser Ser Gly Glu Glu Val Glu Glu Glu Tyr Cys Ile
305                 310                 315                 320
Gly Thr Ile Glu Glu Ala Leu Lys Ala Val Met Glu Lys Ser Asn Val
                325                 330                 335
Glu Glu Ser Ser Ser Ser Gly Asn Ala Lys Arg Gln Arg Met Ser Ser
            340                 345                 350
His Asn Thr Ile Thr Ile Val Glu Gln Gln Gln Gln Tyr Asn Gln Arg
        355                 360                 365
```

<210> 83
<211> 1383
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (243)...(1190)

<400> 83

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ttcttgctta gtatcattct ttgtcgtgtt cttttaatta accttttgca atttgtcttg 60
tgtttctcac aacacaaaaa cttgtaaaag tgttaaaaaa tcaagatctg aaaaatctta 120
tcaccgcttc taggtttttc agtttttttt cttccttttc ctgatctaaa ttaacttata 180
tttcttaggg tttcacttct tgaaacattt aatcagaatt aattaacctc tctagggctt 240
tc atg gcg aat cca tgg tgg aca gga caa gtg aac cta tcc ggc ctc    287
   Met Ala Asn Pro Trp Trp Thr Gly Gln Val Asn Leu Ser Gly Leu
    1               5                  10                  15

gaa acg acg ccg cct ggt tcc tct cag tta aag aaa cca gat ctc cac   335
Glu Thr Thr Pro Pro Gly Ser Ser Gln Leu Lys Lys Pro Asp Leu His
```

```
                20                      25                      30

atc tcc atg aac atg gcc atg gac tca ggt cac aat aat cat cac cat     383
Ile Ser Met Asn Met Ala Met Asp Ser Gly His Asn Asn His His His
            35                      40                      45

cac caa gaa gtc gat aac aac aac aac gac gac gat aga gac aac ttg     431
His Gln Glu Val Asp Asn Asn Asn Asn Asp Asp Asp Arg Asp Asn Leu
        50                      55                      60

agt gga gac gac cac gag cca cgt gaa gga gcc gta gaa gcc ccc acg     479
Ser Gly Asp Asp His Glu Pro Arg Glu Gly Ala Val Glu Ala Pro Thr
    65                      70                      75

cgc cgt cca cgt gga cgt cct gct ggt tcc aag aac aaa cca aag cca     527
Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro
80                      85                      90                  95

ccg atc ttc gtc act cgc gat tct cca aat gct ctc aag agc cat gtc     575
Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Lys Ser His Val
                100                     105                     110

atg gag atc gct agt ggg act gac gtc atc gaa acc cta gct act ttt     623
Met Glu Ile Ala Ser Gly Thr Asp Val Ile Glu Thr Leu Ala Thr Phe
            115                     120                     125

gct agg cgg cgt caa cgt ggc atc tgc atc ttg agc gga aat ggc aca     671
Ala Arg Arg Arg Gln Arg Gly Ile Cys Ile Leu Ser Gly Asn Gly Thr
        130                     135                     140

gtg gct aac gtc acc ctc cgt caa ccc tcg acc gct gcc gtt gcg gcg     719
Val Ala Asn Val Thr Leu Arg Gln Pro Ser Thr Ala Ala Val Ala Ala
    145                     150                     155

gct cct ggt ggt gcg gct gtt ttg gct tta caa ggg agg ttt gag att     767
Ala Pro Gly Gly Ala Ala Val Leu Ala Leu Gln Gly Arg Phe Glu Ile
160                     165                     170                     175

ctt tct tta acc ggt tct ttc ttg cca gga ccg gct cca cct ggt tcc     815
Leu Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser
                180                     185                     190

acc ggt tta acg att tac tta gcc ggt ggt caa ggt cag gtt gtt gga     863
Thr Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly
            195                     200                     205

gga agc gtg gtg ggc cca ttg atg gca gca ggt ccg gtg atg ctg atc     911
Gly Ser Val Val Gly Pro Leu Met Ala Ala Gly Pro Val Met Leu Ile
        210                     215                     220

gcc gcc acg ttc tct aac gcg act tac gag aga ttg cca ttg gag gag     959
Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Glu Glu
    225                     230                     235

gaa gag gca gca gag aga ggc ggt ggt gga ggc agc gga gga gtg gtt     1007
Glu Glu Ala Ala Glu Arg Gly Gly Gly Gly Gly Ser Gly Gly Val Val
240                     245                     250                     255
```

```
ccg ggg cag ctc gga ggc gga ggt tcg cca cta agc agc ggt gct ggt   1055
Pro Gly Gln Leu Gly Gly Gly Gly Ser Pro Leu Ser Ser Gly Ala Gly
                260                 265                 270

gga ggc gac ggt aac caa gga ctt ccg gtg tat aat atg ccg gga aat   1103
Gly Gly Asp Gly Asn Gln Gly Leu Pro Val Tyr Asn Met Pro Gly Asn
            275                 280                 285

ctt gtt tct aat ggt ggc agt ggt gga gga gga cag atg agc ggc caa   1151
Leu Val Ser Asn Gly Gly Ser Gly Gly Gly Gly Gln Met Ser Gly Gln
        290                 295                 300

gaa gct tat ggt tgg gct caa gct agg tca gga ttt taa cgtgcgttaa    1200
Glu Ala Tyr Gly Trp Ala Gln Ala Arg Ser Gly Phe  *
    305                 310                 315

aatggttttt aatttacaga agttaacaat aagattataa tgatgtttat tatgatgatg 1260
aaaaccagtc agttgctact tgttactagt gagctatata gtttgtggac attatattat 1320
gttctctctt gactatgatt attatttgct aaatttcact tagctaaaaa aaaaaaaaaa 1380
aaa                                                               1383
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<210> 84
<211> 315
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (75)...(94)
<223> Conserved domain

<221> DOMAIN
<222> (162)...(206)
<223> Conserved domain

<400> 84

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Met Ala Asn Pro Trp Trp Thr Gly Gln Val Asn Leu Ser Gly Leu Glu
 1               5                  10                  15
Thr Thr Pro Pro Gly Ser Ser Gln Leu Lys Lys Pro Asp Leu His Ile
            20                  25                  30
Ser Met Asn Met Ala Met Asp Ser Gly His Asn Asn His His His His
        35                  40                  45
Gln Glu Val Asp Asn Asn Asn Asn Asp Asp Asp Arg Asp Asn Leu Ser
    50                  55                  60
Gly Asp Asp His Glu Pro Arg Glu Gly Ala Val Glu Ala Pro Thr Arg
65                  70                  75                  80
Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro
                85                  90                  95
Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Lys Ser His Val Met
            100                 105                 110
Glu Ile Ala Ser Gly Thr Asp Val Ile Glu Thr Leu Ala Thr Phe Ala
        115                 120                 125
Arg Arg Arg Gln Arg Gly Ile Cys Ile Leu Ser Gly Asn Gly Thr Val
    130                 135                 140
Ala Asn Val Thr Leu Arg Gln Pro Ser Thr Ala Ala Val Ala Ala Ala
145                 150                 155                 160
```

Pro Gly Gly Ala Ala Val Leu Ala Leu Gln Gly Arg Phe Glu Ile Leu
165 170 175
Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser Thr
180 185 190
Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly
195 200 205
Ser Val Val Gly Pro Leu Met Ala Ala Gly Pro Val Met Leu Ile Ala
210 215 220
Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Glu Glu Glu
225 230 235 240
Glu Ala Ala Glu Arg Gly Gly Gly Gly Gly Ser Gly Gly Val Val Pro
245 250 255
Gly Gln Leu Gly Gly Gly Gly Ser Pro Leu Ser Ser Gly Ala Gly Gly
260 265 270
Gly Asp Gly Asn Gln Gly Leu Pro Val Tyr Asn Met Pro Gly Asn Leu
275 280 285
Val Ser Asn Gly Gly Ser Gly Gly Gly Gly Gln Met Ser Gly Gln Glu
290 295 300
Ala Tyr Gly Trp Ala Gln Ala Arg Ser Gly Phe
305 310 315

<210> 85
<211> 799
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (52)...(798)

<400> 85
cgccgtcact ctcctcccgg tgccgcacat tagcaacact actcccgacg a atg gag 57
Met Glu
1

acg acg acg ccg cag tca aaa tca agt gtg tcc cac cga ccg ccg ttg 105
Thr Thr Thr Pro Gln Ser Lys Ser Ser Val Ser His Arg Pro Pro Leu
5 10 15

gga aga gaa gac tgg tgg agt gag gaa gcg acg gcg acg ctg gta gaa 153
Gly Arg Glu Asp Trp Trp Ser Glu Glu Ala Thr Ala Thr Leu Val Glu
20 25 30

gcc tgg ggc aat cgt tac gtc aag ctg aac cac gga aat ctc cgg cag 201
Ala Trp Gly Asn Arg Tyr Val Lys Leu Asn His Gly Asn Leu Arg Gln
35 40 45 50

aat gac tgg aaa gac gtc gcc gac gcc gtt aac tct aga cac ggt gat 249
Asn Asp Trp Lys Asp Val Ala Asp Ala Val Asn Ser Arg His Gly Asp
55 60 65

aac agc cgt aag aag acc gac tta cag tgt aag aac cgg gtc gat act 297
Asn Ser Arg Lys Lys Thr Asp Leu Gln Cys Lys Asn Arg Val Asp Thr
70 75 80

ttg aag aag aag tac aaa aca gag aaa gct aaa ctc tcg ccg tcg act 345

```
Leu Lys Lys Lys Tyr Lys Thr Glu Lys Ala Lys Leu Ser Pro Ser Thr
        85                  90                  95

tgg cgt ttc tat aac cgc ctc gat gtt cta atc ggt ccc gtt gtg aag     393
Trp Arg Phe Tyr Asn Arg Leu Asp Val Leu Ile Gly Pro Val Val Lys
    100                 105                 110

aaa tcg gct ggc gga gtt gtc aaa tca gcg cct ttt aag aat cat ctg     441
Lys Ser Ala Gly Gly Val Val Lys Ser Ala Pro Phe Lys Asn His Leu
115                 120                 125                 130

aat cca act gga tcg aac tct act gga agc tct ctt gaa gat gat gat     489
Asn Pro Thr Gly Ser Asn Ser Thr Gly Ser Ser Leu Glu Asp Asp Asp
                135                 140                 145

gag gat gat gat gag gtt ggt gat tgg gaa ttc gtt gct agg aag cat     537
Glu Asp Asp Asp Glu Val Gly Asp Trp Glu Phe Val Ala Arg Lys His
            150                 155                 160

cct cgt gtg gaa gag gta gat ctg agt gaa gga tca acg tgt agg gaa     585
Pro Arg Val Glu Glu Val Asp Leu Ser Glu Gly Ser Thr Cys Arg Glu
        165                 170                 175

cta gct acg gcg att ctc aag ttt gga gaa gtt tac gag aga att gaa     633
Leu Ala Thr Ala Ile Leu Lys Phe Gly Glu Val Tyr Glu Arg Ile Glu
    180                 185                 190

ggg aag aag caa cag atg atg att gag ttg gag aag cag aga atg gaa     681
Gly Lys Lys Gln Gln Met Met Ile Glu Leu Glu Lys Gln Arg Met Glu
195                 200                 205                 210

gtg aca aag gag gta gag tta aaa cga atg aac atg ttg atg gag atg     729
Val Thr Lys Glu Val Glu Leu Lys Arg Met Asn Met Leu Met Glu Met
                215                 220                 225

cag tta gag att gag aaa tca aag cac cgg aaa cgc gca agt gct tca     777
Gln Leu Glu Ile Glu Lys Ser Lys His Arg Lys Arg Ala Ser Ala Ser
            230                 235                 240

ggt aag aag aac tca cat tag g                                       799
Gly Lys Lys Asn Ser His  *
        245
```

<210> 86
<211> 248
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (19)...(110)
<223> Conserved domain

<221> DOMAIN
<222> (173)...(232)
<223> Conserved domain

```
<400> 86
Met Glu Thr Thr Thr Pro Gln Ser Lys Ser Ser Val Ser His Arg Pro
 1               5                  10                  15
Pro Leu Gly Arg Glu Asp Trp Trp Ser Glu Glu Ala Thr Ala Thr Leu
            20                  25                  30
Val Glu Ala Trp Gly Asn Arg Tyr Val Lys Leu Asn His Gly Asn Leu
        35                  40                  45
Arg Gln Asn Asp Trp Lys Asp Val Ala Asp Ala Val Asn Ser Arg His
    50                  55                  60
Gly Asp Asn Ser Arg Lys Lys Thr Asp Leu Gln Cys Lys Asn Arg Val
65                  70                  75                  80
Asp Thr Leu Lys Lys Lys Tyr Lys Thr Glu Lys Ala Lys Leu Ser Pro
                85                  90                  95
Ser Thr Trp Arg Phe Tyr Asn Arg Leu Asp Val Leu Ile Gly Pro Val
            100                 105                 110
Val Lys Lys Ser Ala Gly Gly Val Val Lys Ser Ala Pro Phe Lys Asn
        115                 120                 125
His Leu Asn Pro Thr Gly Ser Asn Ser Thr Gly Ser Ser Leu Glu Asp
    130                 135                 140
Asp Asp Glu Asp Asp Asp Glu Val Gly Asp Trp Glu Phe Val Ala Arg
145                 150                 155                 160
Lys His Pro Arg Val Glu Glu Val Asp Leu Ser Glu Gly Ser Thr Cys
                165                 170                 175
Arg Glu Leu Ala Thr Ala Ile Leu Lys Phe Gly Glu Val Tyr Glu Arg
            180                 185                 190
Ile Glu Gly Lys Lys Gln Gln Met Met Ile Glu Leu Glu Lys Gln Arg
        195                 200                 205
Met Glu Val Thr Lys Glu Val Glu Leu Lys Arg Met Asn Met Leu Met
    210                 215                 220
Glu Met Gln Leu Glu Ile Glu Lys Ser Lys His Arg Lys Arg Ala Ser
225                 230                 235                 240
Ala Ser Gly Lys Lys Asn Ser His
                245


<210> 87
<211> 866
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (46)...(837)

<400> 87
gtgtttgtag ttgaaactta ttcttccctt tttttgtttt taggt atg gag act ctg 57
                                                  Met Glu Thr Leu
                                                   1

cat cca ttc tct cac cta cct atc tct gac cac cgg ttc gtt gtt caa    105
His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg Phe Val Val Gln
 5                  10                  15                  20

gag atg gtg agc tta cac agc tcg agt agc ggt agc tgg act aaa gaa    153
Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser Trp Thr Lys Glu
                25                  30                  35
```

```
gag aac aag atg ttc gaa cga gct ctt gcg ata tac gct gaa gac tcg    201
Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr Ala Glu Asp Ser
            40                  45                  50

cct gat cgc tgg ttt aaa gtt gct tcc atg atc cct gga aag act gtt    249
Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro Gly Lys Thr Val
        55                  60                  65

ttt gat gtt atg aag caa tat agt aag ctt gaa gaa gac gtt ttc gat    297
Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu Asp Val Phe Asp
    70                  75                  80

att gaa gca gga cgt gtt ccc att cct ggt tat cct gca gct tct tct    345
Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro Ala Ala Ser Ser
85                  90                  95                  100

ccc ttg ggg ttt gac acg gac atg tgt cgt aaa cgg cct agt gga gct    393
Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg Pro Ser Gly Ala
                105                 110                 115

aga gga tct gat caa gat cga aag aaa gga gtc cct tgg aca gag gaa    441
Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro Trp Thr Glu Glu
            120                 125                 130

gaa cac agg aga ttc ttg tta ggc ctt ctc aag tac ggt aaa gga gat    489
Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly Lys Gly Asp
        135                 140                 145

tgg aga aac ata tcg aga aac ttc gtg gtg tca aag acg cca acg caa    537
Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys Thr Pro Thr Gln
    150                 155                 160

gtg gcg agc cac gcc caa aag tat tac cag aga cag ctc tcc gga gcc    585
Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu Ser Gly Ala
165                 170                 175                 180

aag gac aaa cgc agg cca agt atc cat gac atc aca acc ggc aat ctt    633
Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr Gly Asn Leu
                185                 190                 195

ctc aat gcc aat ctc aac cgt tcc ttt tcc gat cat aga gat att ctc    681
Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His Arg Asp Ile Leu
            200                 205                 210

cct gat tta ggg ttt atc gat aag gat gat acg gag gag gga gta ata    729
Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu Glu Gly Val Ile
        215                 220                 225

ttt atg ggt cag aat ctc tct tca gaa aat ctg ttt tct cca tca cca    777
Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe Ser Pro Ser Pro
    230                 235                 240

act tca ttc gaa gct gcc att aac ttc gcc gga gaa aat gtc ttc agt    825
Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu Asn Val Phe Ser
245                 250                 255                 260
```

```
gcc gga gct taa ggcaacatag aatccccaaa ctcagcggc                   866
Ala Gly Ala  *


<210> 88
<211> 263
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (33)...(81)
<223> Conserved domain

<221> DOMAIN
<222> (129)...(183)
<223> Conserved domain

<400> 88
Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg
 1               5                  10                  15
Phe Val Val Gln Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser
            20                  25                  30
Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr
        35                  40                  45
Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro
    50                  55                  60
Gly Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu
65                  70                  75                  80
Asp Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro
                85                  90                  95
Ala Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg
            100                 105                 110
Pro Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro
        115                 120                 125
Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr
    130                 135                 140
Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys
145                 150                 155                 160
Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln
                165                 170                 175
Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr
            180                 185                 190
Thr Gly Asn Leu Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His
        195                 200                 205
Arg Asp Ile Leu Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu
    210                 215                 220
Glu Gly Val Ile Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe
225                 230                 235                 240
Ser Pro Ser Pro Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu
                245                 250                 255
Asn Val Phe Ser Ala Gly Ala
            260


<210> 89
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<211> 1200
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1200)

<400> 89
atg gaa gga gaa act cat caa tcg gag ccg tta cct tta gca tct gga 48
Met Glu Gly Glu Thr His Gln Ser Glu Pro Leu Pro Leu Ala Ser Gly
1 5 10 15

gat tcc gat gaa ggg atc agt gct gcg att gag gcg gag ctt gct gag 96
Asp Ser Asp Glu Gly Ile Ser Ala Ala Ile Glu Ala Glu Leu Ala Glu
20 25 30

tta gct gct gga gat tca agc ggc ggt ggt ggt tgc ggc ggc gga gga 144
Leu Ala Ala Gly Asp Ser Ser Gly Gly Gly Gly Cys Gly Gly Gly Gly
35 40 45

gga ggg att agg agt aaa gtc aaa gga cct tgg tct acg gag gaa gac 192
Gly Gly Ile Arg Ser Lys Val Lys Gly Pro Trp Ser Thr Glu Glu Asp
50 55 60

gcg gtt ctt acg aag ctt gtg agg aaa cta gga ccg agg aat tgg agt 240
Ala Val Leu Thr Lys Leu Val Arg Lys Leu Gly Pro Arg Asn Trp Ser
65 70 75 80

ttg atc gct cgt gga atc cct ggt cgt tct ggt aaa tct tgt cga ttg 288
Leu Ile Ala Arg Gly Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu
85 90 95

cgt tgg tgt aat cag ctt gac cct tgt ctc aag cgt aaa cct ttc tct 336
Arg Trp Cys Asn Gln Leu Asp Pro Cys Leu Lys Arg Lys Pro Phe Ser
100 105 110

gat gag gaa gat cgt atg ata att tct gct cac gcg gtt cac gga aac 384
Asp Glu Glu Asp Arg Met Ile Ile Ser Ala His Ala Val His Gly Asn
115 120 125

aaa tgg gca gtg att gcg aaa ctg tta act gga aga aca gat aac gct 432
Lys Trp Ala Val Ile Ala Lys Leu Leu Thr Gly Arg Thr Asp Asn Ala
130 135 140

atc aag aac cat tgg aac tca act ctt aga cgt aaa tac gca gat cta 480
Ile Lys Asn His Trp Asn Ser Thr Leu Arg Arg Lys Tyr Ala Asp Leu
145 150 155 160

tgg aat aat ggt caa tgg atg gct aat tca gtt act acc gct tcc gtc 528
Trp Asn Asn Gly Gln Trp Met Ala Asn Ser Val Thr Thr Ala Ser Val
165 170 175

aaa aac gaa aat gtc gat gaa aca act aat cct cca tcc tca aaa caa 576
Lys Asn Glu Asn Val Asp Glu Thr Thr Asn Pro Pro Ser Ser Lys Gln
180 185 190

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cag ttg cct caa gga gat atc aat tcc tcc ccg cca aag cct cca caa     624
Gln Leu Pro Gln Gly Asp Ile Asn Ser Ser Pro Pro Lys Pro Pro Gln
    195                 200                 205

gtg agt gat gtt gta atg gaa gag gca gct aat gaa cct caa gaa cct     672
Val Ser Asp Val Val Met Glu Glu Ala Ala Asn Glu Pro Gln Glu Pro
    210                 215                 220

caa gaa caa caa gaa caa gct cca ccg gta gtg agt aac gtt cca aca     720
Gln Glu Gln Gln Glu Gln Ala Pro Pro Val Val Ser Asn Val Pro Thr
225                 230                 235                 240

gaa aat aac gtg ttt cgc ccc gtg gct cgc gtt ggt gca ttc agt atc     768
Glu Asn Asn Val Phe Arg Pro Val Ala Arg Val Gly Ala Phe Ser Ile
                245                 250                 255

tat aac cca acc agc cag aaa aat ggt tac aga gac tac aat ata gtt     816
Tyr Asn Pro Thr Ser Gln Lys Asn Gly Tyr Arg Asp Tyr Asn Ile Val
            260                 265                 270

cca tgt gag gga ccg ttg att caa gca gct aaa ccc gat tca ttg gct     864
Pro Cys Glu Gly Pro Leu Ile Gln Ala Ala Lys Pro Asp Ser Leu Ala
        275                 280                 285

ggt aaa ttt cta caa tct ctt tgt gat gaa cct caa atc ccg tca aaa     912
Gly Lys Phe Leu Gln Ser Leu Cys Asp Glu Pro Gln Ile Pro Ser Lys
    290                 295                 300

tgt ggt cac ggc tgc tct act ctt cca gct gaa act aag ttc tca cgt     960
Cys Gly His Gly Cys Ser Thr Leu Pro Ala Glu Thr Lys Phe Ser Arg
305                 310                 315                 320

aac tcg gtg ttg gga cct gag ttt gtg gat tat gaa gag cct tct gcg    1008
Asn Ser Val Leu Gly Pro Glu Phe Val Asp Tyr Glu Glu Pro Ser Ala
                325                 330                 335

gtt ttc aac caa gaa cta ata tct ata gca acc gat ttg aac aac att    1056
Val Phe Asn Gln Glu Leu Ile Ser Ile Ala Thr Asp Leu Asn Asn Ile
            340                 345                 350

gca tgg ata aag agt ggc ctt gac aat gct gtt gtc aga gaa gca gaa    1104
Ala Trp Ile Lys Ser Gly Leu Asp Asn Ala Val Val Arg Glu Ala Glu
        355                 360                 365

cag agt ttg aag atg gat aat tac aat tat aat gat cct cga atc aag    1152
Gln Ser Leu Lys Met Asp Asn Tyr Asn Tyr Asn Asp Pro Arg Ile Lys
    370                 375                 380

ttt act gga atg atg cct aga caa gat ttc ttc tgt gca aga agc tga    1200
Phe Thr Gly Met Met Pro Arg Gln Asp Phe Phe Cys Ala Arg Ser  *
385                 390                 395
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<210> 90
<211> 399
<212> PRT

<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (56)...(154)
<223> Conserved domain

<400> 90
Met Glu Gly Glu Thr His Gln Ser Glu Pro Leu Pro Leu Ala Ser Gly
1 5 10 15
Asp Ser Asp Glu Gly Ile Ser Ala Ala Ile Glu Ala Glu Leu Ala Glu
20 25 30
Leu Ala Ala Gly Asp Ser Ser Gly Gly Gly Gly Cys Gly Gly Gly Gly
35 40 45
Gly Gly Ile Arg Ser Lys Val Lys Gly Pro Trp Ser Thr Glu Glu Asp
50 55 60
Ala Val Leu Thr Lys Leu Val Arg Lys Leu Gly Pro Arg Asn Trp Ser
65 70 75 80
Leu Ile Ala Arg Gly Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu
85 90 95
Arg Trp Cys Asn Gln Leu Asp Pro Cys Leu Lys Arg Lys Pro Phe Ser
100 105 110
Asp Glu Glu Asp Arg Met Ile Ile Ser Ala His Ala Val His Gly Asn
115 120 125
Lys Trp Ala Val Ile Ala Lys Leu Leu Thr Gly Arg Thr Asp Asn Ala
130 135 140
Ile Lys Asn His Trp Asn Ser Thr Leu Arg Arg Lys Tyr Ala Asp Leu
145 150 155 160
Trp Asn Asn Gly Gln Trp Met Ala Asn Ser Val Thr Thr Ala Ser Val
165 170 175
Lys Asn Glu Asn Val Asp Glu Thr Thr Asn Pro Pro Ser Ser Lys Gln
180 185 190
Gln Leu Pro Gln Gly Asp Ile Asn Ser Ser Pro Pro Lys Pro Pro Gln
195 200 205
Val Ser Asp Val Val Met Glu Glu Ala Ala Asn Glu Pro Gln Glu Pro
210 215 220
Gln Glu Gln Gln Glu Gln Ala Pro Pro Val Val Ser Asn Val Pro Thr
225 230 235 240
Glu Asn Asn Val Phe Arg Pro Val Ala Arg Val Gly Ala Phe Ser Ile
245 250 255
Tyr Asn Pro Thr Ser Gln Lys Asn Gly Tyr Arg Asp Tyr Asn Ile Val
260 265 270
Pro Cys Glu Gly Pro Leu Ile Gln Ala Ala Lys Pro Asp Ser Leu Ala
275 280 285
Gly Lys Phe Leu Gln Ser Leu Cys Asp Glu Pro Gln Ile Pro Ser Lys
290 295 300
Cys Gly His Gly Cys Ser Thr Leu Pro Ala Glu Thr Lys Phe Ser Arg
305 310 315 320
Asn Ser Val Leu Gly Pro Glu Phe Val Asp Tyr Glu Glu Pro Ser Ala
325 330 335
Val Phe Asn Gln Glu Leu Ile Ser Ile Ala Thr Asp Leu Asn Asn Ile
340 345 350
Ala Trp Ile Lys Ser Gly Leu Asp Asn Ala Val Val Arg Glu Ala Glu
355 360 365
Gln Ser Leu Lys Met Asp Asn Tyr Asn Tyr Asn Asp Pro Arg Ile Lys
370 375 380
Phe Thr Gly Met Met Pro Arg Gln Asp Phe Phe Cys Ala Arg Ser

385 390 395

<210> 91
<211> 1040
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (82)...(879)

<400> 91
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ctttagggac accaaatcta ttcaacctaa aagccttctt ttcccctata ttgaccaact 60
ttttagcgaa tcagaagagg a atg gat gag gta tct cgt tct cat aca ccg   111
                        Met Asp Glu Val Ser Arg Ser His Thr Pro
                         1               5                  10

caa ttt cta tca agt gat cat cag cac tat cac cat caa aac gct gga   159
Gln Phe Leu Ser Ser Asp His Gln His Tyr His His Gln Asn Ala Gly
                15                  20                  25

cga caa aaa cgc ggc aga gaa gaa gaa gga gtt gaa ccc aac aat ata   207
Arg Gln Lys Arg Gly Arg Glu Glu Glu Gly Val Glu Pro Asn Asn Ile
            30                  35                  40

ggg gaa gac cta gcc acc ttt cct tcc gga gaa gag aat atc aag aag   255
Gly Glu Asp Leu Ala Thr Phe Pro Ser Gly Glu Glu Asn Ile Lys Lys
        45                  50                  55

aga agg cca cgt ggc aga cct gct ggt tcc aag aac aaa ccc aaa gca   303
Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Ala
    60                  65                  70

cca atc ata gtc act cgc gac tcc gcg aac gcc ttc aga tgt cac gtc   351
Pro Ile Ile Val Thr Arg Asp Ser Ala Asn Ala Phe Arg Cys His Val
75                  80                  85                  90

atg gag ata acc aac gcc tgc gat gta atg gaa agc cta gcc gtc ttc   399
Met Glu Ile Thr Asn Ala Cys Asp Val Met Glu Ser Leu Ala Val Phe
                95                  100                 105

gct aga cgc cgt cag cgt ggc gtt tgc gtc ttg acc gga aac ggg gcc   447
Ala Arg Arg Arg Gln Arg Gly Val Cys Val Leu Thr Gly Asn Gly Ala
            110                 115                 120

gtt aca aac gtc acc gtt aga caa cct ggc gga ggc gtc gtc agt tta   495
Val Thr Asn Val Thr Val Arg Gln Pro Gly Gly Gly Val Val Ser Leu
        125                 130                 135

cac gga cgg ttt gag att ctt tct ctc tcg ggt tcg ttt ctt cct cca   543
His Gly Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro
    140                 145                 150

ccg gca cca cca gct gcg tct ggt tta aag gtt tac tta gcc ggt ggt   591
Pro Ala Pro Pro Ala Ala Ser Gly Leu Lys Val Tyr Leu Ala Gly Gly
155                 160                 165                 170
```

```
caa ggt caa gtg atc gga ggc agt gtg gtg gga ccg ctt acg gca tca     639
Gln Gly Gln Val Ile Gly Gly Ser Val Val Gly Pro Leu Thr Ala Ser
                175                 180                 185

agt ccg gtg gtc gtt atg gca gct tca ttt gga aac gca tct tac gag     687
Ser Pro Val Val Val Met Ala Ala Ser Phe Gly Asn Ala Ser Tyr Glu
            190                 195                 200

agg ctg cca cta gag gag gag gag gaa act gaa aga gaa ata gat gga     735
Arg Leu Pro Leu Glu Glu Glu Glu Glu Thr Glu Arg Glu Ile Asp Gly
        205                 210                 215

aac gcg gct agg gcg att gga acg caa acg cag aaa cag tta atg caa     783
Asn Ala Ala Arg Ala Ile Gly Thr Gln Thr Gln Lys Gln Leu Met Gln
    220                 225                 230

gat gcg aca tcg ttt att ggg tcg ccg tcg aat tta att aac tct gtt     831
Asp Ala Thr Ser Phe Ile Gly Ser Pro Ser Asn Leu Ile Asn Ser Val
235                 240                 245                 250

tcg ttg cca ggt gaa gct tat tgg gga acg caa cga ccg tct ttc taa     879
Ser Leu Pro Gly Glu Ala Tyr Trp Gly Thr Gln Arg Pro Ser Phe  *
                255                 260                 265

gataatatca ttgataatat aagtttcgtc ttcttattct ttttcacttt ttaccttttt 939
cactttctta ggttttgttt taacgtttga ttaatacctg aaggttttg gaaaattttc 999
gatcggataa aaggatttat gttgcgagcc gaaacgcggc c                   1040
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<210> 92
<211> 265
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (53)...(73)
<223> Conserved domain

<221> DOMAIN
<222> (121)...(165)
<223> Conserved domain

<400> 92

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Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp
 1               5                  10                  15
His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg
            20                  25                  30
Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr
        35                  40                  45
Phe Pro Ser Gly Glu Glu Asn Ile Lys Lys Arg Arg Pro Arg Gly Arg
    50                  55                  60
Pro Ala Gly Ser Lys Asn Lys Pro Lys Ala Pro Ile Ile Val Thr Arg
65                  70                  75                  80
Asp Ser Ala Asn Ala Phe Arg Cys His Val Met Glu Ile Thr Asn Ala
                85                  90                  95
Cys Asp Val Met Glu Ser Leu Ala Val Phe Ala Arg Arg Arg Gln Arg
```

```
                100                 105                 110
Gly Val Cys Val Leu Thr Gly Asn Gly Ala Val Thr Asn Val Thr Val
            115                 120                 125
Arg Gln Pro Gly Gly Gly Val Val Ser Leu His Gly Arg Phe Glu Ile
    130                 135                 140
Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala
145                 150                 155                 160
Ser Gly Leu Lys Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Ile Gly
                165                 170                 175
Gly Ser Val Val Gly Pro Leu Thr Ala Ser Ser Pro Val Val Val Met
            180                 185                 190
Ala Ala Ser Phe Gly Asn Ala Ser Tyr Glu Arg Leu Pro Leu Glu Glu
        195                 200                 205
Glu Glu Glu Thr Glu Arg Glu Ile Asp Gly Asn Ala Ala Arg Ala Ile
    210                 215                 220
Gly Thr Gln Thr Gln Lys Gln Leu Met Gln Asp Ala Thr Ser Phe Ile
225                 230                 235                 240
Gly Ser Pro Ser Asn Leu Ile Asn Ser Val Ser Leu Pro Gly Glu Ala
                245                 250                 255
Tyr Trp Gly Thr Gln Arg Pro Ser Phe
            260                 265


<210> 93
<211> 1072
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (87)...(977)

<400> 93
aaaagataac gtagccatta acttttatgc attaactcct tcatttcttt ttgtgctcgt 60
ttggttgaga gagagagagg ctatat atg atg ttc caa caa gat tac cct cat  113
                             Met Met Phe Gln Gln Asp Tyr Pro His
                              1               5

ggc ttt tca ctc gtg gaa aca tcc tta agt tac gaa atg ttg gat tac   161
Gly Phe Ser Leu Val Glu Thr Ser Leu Ser Tyr Glu Met Leu Asp Tyr
 10                  15                  20                  25

ttt caa aac atc gtc gtt tcg aac tct gaa gac gtg gcg tca cag caa   209
Phe Gln Asn Ile Val Val Ser Asn Ser Glu Asp Val Ala Ser Gln Gln
                 30                  35                  40

aat tcc att tcg tcc tct tct tat tca tca gcg aca ctc tcc tgc tcc   257
Asn Ser Ile Ser Ser Ser Ser Tyr Ser Ser Ala Thr Leu Ser Cys Ser
             45                  50                  55

ata aca gag caa aaa tct cac tta act gaa aag tta tct cct cta cga   305
Ile Thr Glu Gln Lys Ser His Leu Thr Glu Lys Leu Ser Pro Leu Arg
         60                  65                  70

gaa aga tat ggt tgc ggt gac ttt ctg tcg cgg aag agg aga agg aga   353
Glu Arg Tyr Gly Cys Gly Asp Phe Leu Ser Arg Lys Arg Arg Arg Arg
     75                  80                  85
```

agt gaa aaa acg att gta gat aaa gag aat caa agg atg aat cac att 401
Ser Glu Lys Thr Ile Val Asp Lys Glu Asn Gln Arg Met Asn His Ile
90 95 100 105

gcc gtc gag cgt aac cgg aga aaa cag atg aat cat ttt ctg tct atc 449
Ala Val Glu Arg Asn Arg Arg Lys Gln Met Asn His Phe Leu Ser Ile
110 115 120

ctc aag tct atg atg cct ctc tct tat tct caa cct aat gac caa gca 497
Leu Lys Ser Met Met Pro Leu Ser Tyr Ser Gln Pro Asn Asp Gln Ala
125 130 135

tca atc ata gaa ggg acc att agc tat ctg aag aag cta gaa caa cgt 545
Ser Ile Ile Glu Gly Thr Ile Ser Tyr Leu Lys Lys Leu Glu Gln Arg
140 145 150

ctc caa tct ctc gaa gcc caa tta aaa gct act aaa ctc aat caa tca 593
Leu Gln Ser Leu Glu Ala Gln Leu Lys Ala Thr Lys Leu Asn Gln Ser
155 160 165

cca aat ata ttt tcc gac ttc ttc atg ttc cct caa tac tcc acc gcc 641
Pro Asn Ile Phe Ser Asp Phe Phe Met Phe Pro Gln Tyr Ser Thr Ala
170 175 180 185

act gcc act gcc acc gcc act gcc tcc tca tcc tcc tcg agc cac cac 689
Thr Ala Thr Ala Thr Ala Thr Ala Ser Ser Ser Ser Ser Ser His His
190 195 200

cat cac aag cga cta gag gtg gtt gct gac gtg gag gtt aca atg gta 737
His His Lys Arg Leu Glu Val Val Ala Asp Val Glu Val Thr Met Val
205 210 215

gaa aga cat gcc aac att aaa gtg tta acg aag aca cag cca aga ttg 785
Glu Arg His Ala Asn Ile Lys Val Leu Thr Lys Thr Gln Pro Arg Leu
220 225 230

ctc ttc aag att atc aat gag ttt aac tct tta ggt tta agt act ctt 833
Leu Phe Lys Ile Ile Asn Glu Phe Asn Ser Leu Gly Leu Ser Thr Leu
235 240 245

cat ctc aac ctc aca act tcc aaa gac atg tct ctc ttc act ttt agc 881
His Leu Asn Leu Thr Thr Ser Lys Asp Met Ser Leu Phe Thr Phe Ser
250 255 260 265

gtc aag gta gag gca gat tgt caa ttg acg cct tct ggt aat gag gtc 929
Val Lys Val Glu Ala Asp Cys Gln Leu Thr Pro Ser Gly Asn Glu Val
270 275 280

gca aat acg gtg cat gaa gtc gtt aga aga gtt cac aag gaa cgt tga 977
Ala Asn Thr Val His Glu Val Val Arg Arg Val His Lys Glu Arg *
285 290 295

attttgttta catactagct aactttgaaa ttctatttta ttgtataaac aatctcttat 1037
gtgtgtaatt tacatatata caattaatta acatt 1072

<210> 94

<211> 296
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (92)...(161)
<223> Conserved domain

<400> 94
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Met Met Phe Gln Gln Asp Tyr Pro His Gly Phe Ser Leu Val Glu Thr
 1               5                  10                  15
Ser Leu Ser Tyr Glu Met Leu Asp Tyr Phe Gln Asn Ile Val Val Ser
            20                  25                  30
Asn Ser Glu Asp Val Ala Ser Gln Gln Asn Ser Ile Ser Ser Ser Ser
        35                  40                  45
Tyr Ser Ser Ala Thr Leu Ser Cys Ser Ile Thr Glu Gln Lys Ser His
    50                  55                  60
Leu Thr Glu Lys Leu Ser Pro Leu Arg Glu Arg Tyr Gly Cys Gly Asp
65                  70                  75                  80
Phe Leu Ser Arg Lys Arg Arg Arg Arg Ser Glu Lys Thr Ile Val Asp
                85                  90                  95
Lys Glu Asn Gln Arg Met Asn His Ile Ala Val Glu Arg Asn Arg Arg
            100                 105                 110
Lys Gln Met Asn His Phe Leu Ser Ile Leu Lys Ser Met Met Pro Leu
        115                 120                 125
Ser Tyr Ser Gln Pro Asn Asp Gln Ala Ser Ile Ile Glu Gly Thr Ile
    130                 135                 140
Ser Tyr Leu Lys Lys Leu Glu Gln Arg Leu Gln Ser Leu Glu Ala Gln
145                 150                 155                 160
Leu Lys Ala Thr Lys Leu Asn Gln Ser Pro Asn Ile Phe Ser Asp Phe
                165                 170                 175
Phe Met Phe Pro Gln Tyr Ser Thr Ala Thr Ala Thr Ala Thr Ala Thr
            180                 185                 190
Ala Ser Ser Ser Ser Ser Ser His His His His Lys Arg Leu Glu Val
        195                 200                 205
Val Ala Asp Val Glu Val Thr Met Val Glu Arg His Ala Asn Ile Lys
    210                 215                 220
Val Leu Thr Lys Thr Gln Pro Arg Leu Leu Phe Lys Ile Ile Asn Glu
225                 230                 235                 240
Phe Asn Ser Leu Gly Leu Ser Thr Leu His Leu Asn Leu Thr Thr Ser
                245                 250                 255
Lys Asp Met Ser Leu Phe Thr Phe Ser Val Lys Val Glu Ala Asp Cys
            260                 265                 270
Gln Leu Thr Pro Ser Gly Asn Glu Val Ala Asn Thr Val His Glu Val
        275                 280                 285
Val Arg Arg Val His Lys Glu Arg
    290                 295
```

<210> 95
<211> 876
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS

<222> (1)...(876)

<400> 95

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atg gag gct cga tgt gac ttt tgt gga acc gaa aaa gca tta atc tac     48
Met Glu Ala Arg Cys Asp Phe Cys Gly Thr Glu Lys Ala Leu Ile Tyr
 1               5                  10                  15

tgc aaa tct gat tcg gct aaa ctt tgt tta aac tgt gac gtt aat gta     96
Cys Lys Ser Asp Ser Ala Lys Leu Cys Leu Asn Cys Asp Val Asn Val
            20                  25                  30

cac tca gcg aat cct ctg tct caa aga cac acg cga tct cta ctc tgc    144
His Ser Ala Asn Pro Leu Ser Gln Arg His Thr Arg Ser Leu Leu Cys
        35                  40                  45

gag aaa tgt tcc tta caa ccc acg gca gta cac tgt atg aac gaa aat    192
Glu Lys Cys Ser Leu Gln Pro Thr Ala Val His Cys Met Asn Glu Asn
    50                  55                  60

gtt tct ctt tgc caa gga tgt cag tgg acc gct agt aac tgc act ggt    240
Val Ser Leu Cys Gln Gly Cys Gln Trp Thr Ala Ser Asn Cys Thr Gly
65                  70                  75                  80

tta gga cac aga ctt cag agt ctg aac cct tac tct gat tgt cct tct    288
Leu Gly His Arg Leu Gln Ser Leu Asn Pro Tyr Ser Asp Cys Pro Ser
                85                  90                  95

cca tca gat ttc ggc aag atc tgg tct tca act tta gaa cct tct gtc    336
Pro Ser Asp Phe Gly Lys Ile Trp Ser Ser Thr Leu Glu Pro Ser Val
            100                 105                 110

aca agt ttg gtc tct cca ttt tct gat acc ctg ctc cag gaa tta gac    384
Thr Ser Leu Val Ser Pro Phe Ser Asp Thr Leu Leu Gln Glu Leu Asp
        115                 120                 125

gat tgg aat ggt tca tca act tcc gtg gtt aca caa act cag aac ctt    432
Asp Trp Asn Gly Ser Ser Thr Ser Val Val Thr Gln Thr Gln Asn Leu
    130                 135                 140

aaa gac tat tct tct ttc ttt cct atg gaa tct aat ctt cca aaa gtg    480
Lys Asp Tyr Ser Ser Phe Phe Pro Met Glu Ser Asn Leu Pro Lys Val
145                 150                 155                 160

ata gaa gag gaa tgt tct ggt ttg gat cta tgc gaa ggg ata aac tta    528
Ile Glu Glu Glu Cys Ser Gly Leu Asp Leu Cys Glu Gly Ile Asn Leu
                165                 170                 175

gat gat gcg ccg ttg aat ttc aac gca agc aat gat ata atc gga tgt    576
Asp Asp Ala Pro Leu Asn Phe Asn Ala Ser Asn Asp Ile Ile Gly Cys
            180                 185                 190

tca tca ctt gac aat acc aaa tgt tac gag tac gag gat tct ttt aag    624
Ser Ser Leu Asp Asn Thr Lys Cys Tyr Glu Tyr Glu Asp Ser Phe Lys
        195                 200                 205

gaa gag aat aac att ggc ctt cct tca tta ctg ctt cct act tta tcc    672
Glu Glu Asn Asn Ile Gly Leu Pro Ser Leu Leu Leu Pro Thr Leu Ser
```

```
    210                 215                 220

ggg aac gtt gta ccg aac atg tca ctt tcg atg tct aac ctc aca gga      720
Gly Asn Val Val Pro Asn Met Ser Leu Ser Met Ser Asn Leu Thr Gly
225                 230                 235                 240

gaa agc aat gcg act gat tac caa gat tgc gga att tca cca ggg ttt      768
Glu Ser Asn Ala Thr Asp Tyr Gln Asp Cys Gly Ile Ser Pro Gly Phe
                245                 250                 255

ctc ata gga gat tcg cca tgg gaa tcg aat gtt gaa gtt agt ttt aat      816
Leu Ile Gly Asp Ser Pro Trp Glu Ser Asn Val Glu Val Ser Phe Asn
            260                 265                 270

cca aaa tta agg gat gag gct aaa aag aga tac aaa caa aag aaa tca      864
Pro Lys Leu Arg Asp Glu Ala Lys Lys Arg Tyr Lys Gln Lys Lys Ser
        275                 280                 285

aag cgc atg taa                                                      876
Lys Arg Met  *
    290


<210> 96
<211> 291
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (5)...(28)
<223> Conserved domain

<221> DOMAIN
<222> (48)...(71)
<223> Conserved domain

<400> 96
Met Glu Ala Arg Cys Asp Phe Cys Gly Thr Glu Lys Ala Leu Ile Tyr
 1               5                  10                  15
Cys Lys Ser Asp Ser Ala Lys Leu Cys Leu Asn Cys Asp Val Asn Val
            20                  25                  30
His Ser Ala Asn Pro Leu Ser Gln Arg His Thr Arg Ser Leu Leu Cys
        35                  40                  45
Glu Lys Cys Ser Leu Gln Pro Thr Ala Val His Cys Met Asn Glu Asn
    50                  55                  60
Val Ser Leu Cys Gln Gly Cys Gln Trp Thr Ala Ser Asn Cys Thr Gly
65                  70                  75                  80
Leu Gly His Arg Leu Gln Ser Leu Asn Pro Tyr Ser Asp Cys Pro Ser
                85                  90                  95
Pro Ser Asp Phe Gly Lys Ile Trp Ser Ser Thr Leu Glu Pro Ser Val
            100                 105                 110
Thr Ser Leu Val Ser Pro Phe Ser Asp Thr Leu Leu Gln Glu Leu Asp
        115                 120                 125
Asp Trp Asn Gly Ser Ser Thr Ser Val Val Thr Gln Thr Gln Asn Leu
    130                 135                 140
Lys Asp Tyr Ser Ser Phe Phe Pro Met Glu Ser Asn Leu Pro Lys Val
```

```
145                 150                 155                 160
Ile Glu Glu Glu Cys Ser Gly Leu Asp Leu Cys Glu Gly Ile Asn Leu
                165                 170                 175
Asp Asp Ala Pro Leu Asn Phe Asn Ala Ser Asn Asp Ile Ile Gly Cys
            180                 185                 190
Ser Ser Leu Asp Asn Thr Lys Cys Tyr Glu Tyr Glu Asp Ser Phe Lys
        195                 200                 205
Glu Glu Asn Asn Ile Gly Leu Pro Ser Leu Leu Leu Pro Thr Leu Ser
    210                 215                 220
Gly Asn Val Val Pro Asn Met Ser Leu Ser Met Ser Asn Leu Thr Gly
225                 230                 235                 240
Glu Ser Asn Ala Thr Asp Tyr Gln Asp Cys Gly Ile Ser Pro Gly Phe
                245                 250                 255
Leu Ile Gly Asp Ser Pro Trp Glu Ser Asn Val Glu Val Ser Phe Asn
            260                 265                 270
Pro Lys Leu Arg Asp Glu Ala Lys Lys Arg Tyr Lys Gln Lys Lys Ser
        275                 280                 285
Lys Arg Met
    290
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<210> 97
<211> 727
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (82)...(570)

<400> 97

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accaaactca aaaaacacaa accacaagag gatcatttca ttttttattg tttcgtttta 60
atcatcatca tcagaagaaa a atg gtt gcg ata tcg gag atc aag tcg acg   111
                        Met Val Ala Ile Ser Glu Ile Lys Ser Thr
                         1               5                  10

gtg gat gtc acg gcg gcg aat tgt ttg atg ctt tta tct aga gtt gga   159
Val Asp Val Thr Ala Ala Asn Cys Leu Met Leu Leu Ser Arg Val Gly
                15                  20                  25

caa gaa aac gtt gac ggt ggc gat caa aaa cgc gtt ttc aca tgt aaa   207
Gln Glu Asn Val Asp Gly Gly Asp Gln Lys Arg Val Phe Thr Cys Lys
            30                  35                  40

acg tgt ttg aag cag ttt cat tcg ttc caa gcc tta gga ggt cac cgt   255
Thr Cys Leu Lys Gln Phe His Ser Phe Gln Ala Leu Gly Gly His Arg
        45                  50                  55

gcg agt cac aag aag cct aac aac gac gct ttg tcg tct gga ttg atg   303
Ala Ser His Lys Lys Pro Asn Asn Asp Ala Leu Ser Ser Gly Leu Met
    60                  65                  70

aag aag gtg aaa acg tcg tcg cat cct tgt ccc ata tgt gga gtg gag   351
Lys Lys Val Lys Thr Ser Ser His Pro Cys Pro Ile Cys Gly Val Glu
75                  80                  85                  90

ttt ccg atg gga caa gct ttg gga gga cac atg agg aga cac agg aac   399
```

```
Phe Pro Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn
                95                  100                 105

gag agt ggg gct gct ggt ggc gcg ttg gtt aca cgc gct ttg ttg ccg     447
Glu Ser Gly Ala Ala Gly Gly Ala Leu Val Thr Arg Ala Leu Leu Pro
            110                 115                 120

gag ccc acg gtg act acg ttg aag aaa tct agc agt ggg aag aga gtg     495
Glu Pro Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val
        125                 130                 135

gct tgt ttg gat ctg agt cta ggg atg gtg gac aat ttg aat ctc aag     543
Ala Cys Leu Asp Leu Ser Leu Gly Met Val Asp Asn Leu Asn Leu Lys
    140                 145                 150

ttg gag ctt gga aga aca gtt tat tga ttttatttat tttccttaaa           590
Leu Glu Leu Gly Arg Thr Val Tyr  *
155                 160

ttttctgaat atatttgttt ctctcattct ttgaattttt cttaatattc tagattatac 650
atacatccgc agatttagga aactttcata gagtgtaatc ttttctttct gtaaaaatat 710
attttacttg tagcaaa                                                727

<210> 98
<211> 162
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (41)...(61)
<223> Conserved domain

<221> DOMAIN
<222> (84)...(104)
<223> Conserved domain

<400> 98
Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala
 1               5                  10                  15
Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp Gly
            20                  25                  30
Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln Phe
        35                  40                  45
His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Pro
    50                  55                  60
Asn Asn Asp Ala Leu Ser Ser Gly Leu Met Lys Lys Val Lys Thr Ser
65                  70                  75                  80
Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala
                85                  90                  95
Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Gly Ala Ala Gly
            100                 105                 110
Gly Ala Leu Val Thr Arg Ala Leu Leu Pro Glu Pro Thr Val Thr Thr
        115                 120                 125
Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu Asp Leu Ser
    130                 135                 140
Leu Gly Met Val Asp Asn Leu Asn Leu Lys Leu Glu Leu Gly Arg Thr
```

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145                 150                 155                 160
Val Tyr
```

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<210> 99
<211> 785
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (38)...(472)

<400> 99
cttcttcttc acatcgatca tcatacaaca acaaaaa atg gat tac aga gaa tcc   55
                                         Met Asp Tyr Arg Glu Ser
                                          1               5

acc ggt gaa agt cag tca aag tac aaa gga atc cgt cgt cgg aaa tgg   103
Thr Gly Glu Ser Gln Ser Lys Tyr Lys Gly Ile Arg Arg Arg Lys Trp
             10                  15                  20

ggc aaa tgg gta tca gag att aga gtt ccg gga act cgt gac cgt ctc   151
Gly Lys Trp Val Ser Glu Ile Arg Val Pro Gly Thr Arg Asp Arg Leu
         25                  30                  35

tgg tta ggt tca ttc tca aca gca gaa ggt gcc gcc gta gca cac gac   199
Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly Ala Ala Val Ala His Asp
     40                  45                  50

gtt gct ttc ttc tgt tta cac caa cct gat tct tta gaa tct ctc aat   247
Val Ala Phe Phe Cys Leu His Gln Pro Asp Ser Leu Glu Ser Leu Asn
 55                  60                  65                  70

ttc cct cat ttg ctt aat cct tca ctc gtt tcc aga act tct ccg aga   295
Phe Pro His Leu Leu Asn Pro Ser Leu Val Ser Arg Thr Ser Pro Arg
                 75                  80                  85

tct atc cag caa gct gct tct aac gcc ggc atg gcc att gac gcc gga   343
Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly Met Ala Ile Asp Ala Gly
             90                  95                  100

atc gtc cac agt acc agc gtg aac tct gga tgc gga gat acg acg acg   391
Ile Val His Ser Thr Ser Val Asn Ser Gly Cys Gly Asp Thr Thr Thr
         105                 110                 115

tat tac gag aat gga gct gat caa gtg gag ccg ttg aat att tca gtg   439
Tyr Tyr Glu Asn Gly Ala Asp Gln Val Glu Pro Leu Asn Ile Ser Val
     120                 125                 130

tat gat tat ctg ggc ggc cac gat cac gtt tga tttatctcga cggtcatgat 492
Tyr Asp Tyr Leu Gly Gly His Asp His Val  *
135                 140

cacgtttgat cttcttttga gtaagatttt gtaccataat caaaacaggt gtggtgctaa 552
aatcttactc aaaacaagat taggtaccac agagaaacaa tcaaatggtt gtgaatatac 612
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attataaggt tttgattaat gtttgtttca ctgatttagt gaagtttggt ccattgtata 672
caaatctatt caagaaacct agcgcgagat catgtttcgt gattgaagat tgagattttt 732
aagtattcgt aatatttttg taaaatacaa ataaaaaaaa aaaaaaaaaa aaa        785

<210> 100
<211> 144
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (11)...(80)
<223> Conserved domain

<400> 100
Met Asp Tyr Arg Glu Ser Thr Gly Glu Ser Gln Ser Lys Tyr Lys Gly
 1               5                  10                  15
Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
            20                  25                  30
Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
        35                  40                  45
Ala Ala Val Ala His Asp Val Ala Phe Phe Cys Leu His Gln Pro Asp
    50                  55                  60
Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Asn Pro Ser Leu Val
65                  70                  75                  80
Ser Arg Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
                85                  90                  95
Met Ala Ile Asp Ala Gly Ile Val His Ser Thr Ser Val Asn Ser Gly
            100                 105                 110
Cys Gly Asp Thr Thr Thr Tyr Tyr Glu Asn Gly Ala Asp Gln Val Glu
        115                 120                 125
Pro Leu Asn Ile Ser Val Tyr Asp Tyr Leu Gly Gly His Asp His Val
    130                 135                 140


<210> 101
<211> 1008
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (33)...(695)

<400> 101
tggatcaaca agaccatgga cagtctggag ct atg aac tat ggc aca aac cca   53
                                    Met Asn Tyr Gly Thr Asn Pro
                                     1               5

tac caa acc aac ccg atg agc acc act gct gct act gta gca gga ggt   101
Tyr Gln Thr Asn Pro Met Ser Thr Thr Ala Ala Thr Val Ala Gly Gly
        10                  15                  20

gcg gca caa cca ggc cag ctg gcg ttc cac cag atc cat cag cag cag   149
Ala Ala Gln Pro Gly Gln Leu Ala Phe His Gln Ile His Gln Gln Gln
    25                  30                  35
```

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cag cag caa cag ctg gca cag cag ctt caa gca ttt tgg gag aac caa    197
Gln Gln Gln Gln Leu Ala Gln Gln Leu Gln Ala Phe Trp Glu Asn Gln
 40                 45                  50                  55

ttc aaa gag att gag aag act acc gat ttc aag aac cac agc ctt ccc    245
Phe Lys Glu Ile Glu Lys Thr Thr Asp Phe Lys Asn His Ser Leu Pro
                60                  65                  70

ctt gcg aga atc aag aaa atc atg aaa gcg gat gaa gat gtc cgt atg    293
Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met
            75                  80                  85

atc tcg gct gag gcg ccg gtc gtg ttt gca agg gcc tgt gag atg ttc    341
Ile Ser Ala Glu Ala Pro Val Val Phe Ala Arg Ala Cys Glu Met Phe
        90                  95                 100

atc ctg gag ctg aca ctc agg tcg tgg aac cac act gag gag aat aag    389
Ile Leu Glu Leu Thr Leu Arg Ser Trp Asn His Thr Glu Glu Asn Lys
    105                 110                 115

agg cgg acg ttg cag aag aac gat att gct gct gct gtg act aga acc    437
Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Val Thr Arg Thr
120                 125                 130                 135

gat att ttt gat ttc ctt gtg gat att gtt ccc cgg gag gat ctc cga    485
Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Glu Asp Leu Arg
                140                 145                 150

gat gaa gtc ttg gga agt att ccg agg ggc act gtc ccg gaa gct gct    533
Asp Glu Val Leu Gly Ser Ile Pro Arg Gly Thr Val Pro Glu Ala Ala
            155                 160                 165

gct gct ggt tac ccg tat gga tac ttg cct gca gga act gct cca ata    581
Ala Ala Gly Tyr Pro Tyr Gly Tyr Leu Pro Ala Gly Thr Ala Pro Ile
        170                 175                 180

gga aat ccg gga atg gtt atg ggt aat ccc ggt ggt gcg tat cca cct    629
Gly Asn Pro Gly Met Val Met Gly Asn Pro Gly Gly Ala Tyr Pro Pro
    185                 190                 195

aat cct tat atg ggt caa cca atg tgg caa caa cag gca cct gac caa    677
Asn Pro Tyr Met Gly Gln Pro Met Trp Gln Gln Gln Ala Pro Asp Gln
200                 205                 210                 215

cct gac cag gaa aat tag caagaaactg tgagtcttcc agcttcgcgg           725
Pro Asp Gln Glu Asn  *
                220

ccgctctaga caggcctcgt accggatcct ctagctagag ctttcgttcg tatcatcggt 785
ttcgacaacg ttcgtcaagt tcaatgcatc agtttcattg cgcacacacc agaatcctac 845
tgagtttgag tattatggca ttgggaaaac tgtttttctt gtccatttgt tgtgcttgta 905
atttactgtg ttttttattc ggttttcgct atcgaactgt gaaatggaaa tggatggaga 965
agagttaatg aatgatatgg ccttttgttc attctcaaat taa                   1008
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<210> 102
<211> 220
<212> PRT

<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (57)...(156)
<223> Conserved domain

<400> 102
Met Asn Tyr Gly Thr Asn Pro Tyr Gln Thr Asn Pro Met Ser Thr Thr
 1   5   10   15
Ala Ala Thr Val Ala Gly Gly Ala Ala Gln Pro Gly Gln Leu Ala Phe
            20   25   30
His Gln Ile His Gln Gln Gln Gln Gln Gln Gln Leu Ala Gln Gln Leu
        35   40   45
Gln Ala Phe Trp Glu Asn Gln Phe Lys Glu Ile Glu Lys Thr Thr Asp
    50   55   60
Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys
65   70   75   80
Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val Phe
                85   90   95
Ala Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg Ser Trp
            100   105   110
Asn His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile
        115   120   125
Ala Ala Ala Val Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile
    130   135   140
Val Pro Arg Glu Asp Leu Arg Asp Glu Val Leu Gly Ser Ile Pro Arg
145   150   155   160
Gly Thr Val Pro Glu Ala Ala Ala Ala Gly Tyr Pro Tyr Gly Tyr Leu
                165   170   175
Pro Ala Gly Thr Ala Pro Ile Gly Asn Pro Gly Met Val Met Gly Asn
            180   185   190
Pro Gly Gly Ala Tyr Pro Pro Asn Pro Tyr Met Gly Gln Pro Met Trp
        195   200   205
Gln Gln Gln Ala Pro Asp Gln Pro Asp Gln Glu Asn
    210   215   220

<210> 103
<211> 1409
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (224)...(1093)

<400> 103
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tttcatttgg agaggacacg ctgacaagct gactctagca gatctgggac cgtcgaccca 120
cgcgtccgaa ttgattagga taggatcagg atcatcctca acaacctcct cctaattcct 180
cctccattca tagtaacaat aatattaaga aagagggtaa act atg tca gaa tta 235
                                                Met Ser Glu Leu
                                                 1

tta cag ttg cct cca ggt ttc cga ttt cac cct acc gat gaa gag ctt 283
Leu Gln Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu

5 10 15 20

gtc atg cac tat ctc tgc cgc aaa tgt gcc tct cag tcc atc gcc gtt 331
Val Met His Tyr Leu Cys Arg Lys Cys Ala Ser Gln Ser Ile Ala Val
25 30 35

ccg atc atc gct gag atc gat ctc tac aaa tac gat cca tgg gag ctt 379
Pro Ile Ile Ala Glu Ile Asp Leu Tyr Lys Tyr Asp Pro Trp Glu Leu
40 45 50

cct ggt tta gcc ttg tat ggt gag aag gaa tgg tac ttc ttc tct ccc 427
Pro Gly Leu Ala Leu Tyr Gly Glu Lys Glu Trp Tyr Phe Phe Ser Pro
55 60 65

agg gac aga aaa tat ccc aac ggt tcg cgt cct aac cgg tcc gct ggt 475
Arg Asp Arg Lys Tyr Pro Asn Gly Ser Arg Pro Asn Arg Ser Ala Gly
70 75 80

tct ggt tac tgg aaa gct acc gga gct gat aaa ccg atc gga cta cct 523
Ser Gly Tyr Trp Lys Ala Thr Gly Ala Asp Lys Pro Ile Gly Leu Pro
85 90 95 100

aaa ccg gtc gga att aag aaa gct ctt gtt ttc tac gcc ggc aaa gct 571
Lys Pro Val Gly Ile Lys Lys Ala Leu Val Phe Tyr Ala Gly Lys Ala
105 110 115

cca aag gga gag aaa acc aat tgg atc atg cac gag tac cgt ctc gcc 619
Pro Lys Gly Glu Lys Thr Asn Trp Ile Met His Glu Tyr Arg Leu Ala
120 125 130

gac gtt gac cgg tcc gtt cgc aag aag aag aat agt ctc agg ctg gat 667
Asp Val Asp Arg Ser Val Arg Lys Lys Lys Asn Ser Leu Arg Leu Asp
135 140 145

gat tgg gtt ctc tgc cgg att tac aac aaa aaa gga gct acc gag agg 715
Asp Trp Val Leu Cys Arg Ile Tyr Asn Lys Lys Gly Ala Thr Glu Arg
150 155 160

cgg gga cca ccg cct ccg gtt gtt tac ggc gac gaa atc atg gag gag 763
Arg Gly Pro Pro Pro Pro Val Val Tyr Gly Asp Glu Ile Met Glu Glu
165 170 175 180

aag ccg aag gtg acg gag atg gtt atg cct ccg ccg ccg caa cag aca 811
Lys Pro Lys Val Thr Glu Met Val Met Pro Pro Pro Pro Gln Gln Thr
185 190 195

agt gag ttc gcg tat ttc gac acg tcg gat tcg gtg ccg aag ctg cat 859
Ser Glu Phe Ala Tyr Phe Asp Thr Ser Asp Ser Val Pro Lys Leu His
200 205 210

act acg gat tcg agt tgc tcg gag cag gtg gtg tcg ccg gag ttc acg 907
Thr Thr Asp Ser Ser Cys Ser Glu Gln Val Val Ser Pro Glu Phe Thr
215 220 225

agc gag gtt cag agc gag ccc aag tgg aaa gat tgg tcg gcc gta agt 955
Ser Glu Val Gln Ser Glu Pro Lys Trp Lys Asp Trp Ser Ala Val Ser
230 235 240

```
aat gac aat aac aat acc ctt gat ttt ggg ttt aat tac att gat gcc    1003
Asn Asp Asn Asn Asn Thr Leu Asp Phe Gly Phe Asn Tyr Ile Asp Ala
245                 250                 255                 260

acc gtg gat aac gcg ttt gga gga gga ggg agt agt aat cag atg ttt    1051
Thr Val Asp Asn Ala Phe Gly Gly Gly Gly Ser Ser Asn Gln Met Phe
                265                 270                 275

ccg cta cag gat atg ttc atg tac atg cag aag cct tac tag            1093
Pro Leu Gln Asp Met Phe Met Tyr Met Gln Lys Pro Tyr  *
            280                 285

aagggaattc ctttcctgcc gccgaaacgc aacgcaaaac gaccctcgtt tttgcgttta 1153
tggcaacacg agaccgtttt atatggtcaa tgagtgtgcc gattcggcca ttagatttct 1213
gttcagtctt cgtttattct atagaccgtc cgatttcaga tcatccctaa tcggacggtg 1273
gtcgttggat gtatcagtag tgtattactg tgttaggtag aagaaaatcc acttgttctt 1333
aaattggcat aaaagtcaga agctaatatt tatatgtgcc gcaatcaatt taatattttc 1393
tgtctaaaaa aaaaaa                                                 1409

<210> 104
<211> 289
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (10)...(155)
<223> Conserved domain

<400> 104
Met Ser Glu Leu Leu Gln Leu Pro Pro Gly Phe Arg Phe His Pro Thr
 1               5                  10                  15
Asp Glu Glu Leu Val Met His Tyr Leu Cys Arg Lys Cys Ala Ser Gln
            20                  25                  30
Ser Ile Ala Val Pro Ile Ile Ala Glu Ile Asp Leu Tyr Lys Tyr Asp
        35                  40                  45
Pro Trp Glu Leu Pro Gly Leu Ala Leu Tyr Gly Glu Lys Glu Trp Tyr
    50                  55                  60
Phe Phe Ser Pro Arg Asp Arg Lys Tyr Pro Asn Gly Ser Arg Pro Asn
65                  70                  75                  80
Arg Ser Ala Gly Ser Gly Tyr Trp Lys Ala Thr Gly Ala Asp Lys Pro
                85                  90                  95
Ile Gly Leu Pro Lys Pro Val Gly Ile Lys Lys Ala Leu Val Phe Tyr
            100                 105                 110
Ala Gly Lys Ala Pro Lys Gly Glu Lys Thr Asn Trp Ile Met His Glu
        115                 120                 125
Tyr Arg Leu Ala Asp Val Asp Arg Ser Val Arg Lys Lys Lys Asn Ser
    130                 135                 140
Leu Arg Leu Asp Asp Trp Val Leu Cys Arg Ile Tyr Asn Lys Lys Gly
145                 150                 155                 160
Ala Thr Glu Arg Arg Gly Pro Pro Pro Pro Val Val Tyr Gly Asp Glu
                165                 170                 175
Ile Met Glu Glu Lys Pro Lys Val Thr Glu Met Val Met Pro Pro Pro
            180                 185                 190
Pro Gln Gln Thr Ser Glu Phe Ala Tyr Phe Asp Thr Ser Asp Ser Val
        195                 200                 205
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Pro Lys Leu His Thr Thr Asp Ser Ser Cys Ser Glu Gln Val Val Ser
    210                 215                 220
Pro Glu Phe Thr Ser Glu Val Gln Ser Glu Pro Lys Trp Lys Asp Trp
225                 230                 235                 240
Ser Ala Val Ser Asn Asp Asn Asn Asn Thr Leu Asp Phe Gly Phe Asn
                245                 250                 255
Tyr Ile Asp Ala Thr Val Asp Asn Ala Phe Gly Gly Gly Gly Ser Ser
            260                 265                 270
Asn Gln Met Phe Pro Leu Gln Asp Met Phe Met Tyr Met Gln Lys Pro
        275                 280                 285
Tyr


<210> 105
<211> 1481
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (181)...(1188)

<400> 105
cgacccacgc gtccgagatt ctctcccagc tagctttctc aattcatttt tctttcttca 60
tcttcttctt gtgtgatctc tctttccaaa taagcttatc attcttacaa aaatatttct 120
gggtttctga tattgttctt gttctcttga atctttatta cttgaaaaac atataaagtg 180
atg gcg gtt gtg gtt gaa gaa ggt gtg gtg ttg aat cat gga ggt gaa   228
Met Ala Val Val Val Glu Glu Gly Val Val Leu Asn His Gly Gly Glu
 1               5                  10                  15

gag ctt gtg gat ttg cca cct ggt ttc agg ttt cat cca aca gac gaa   276
Glu Leu Val Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu
            20                  25                  30

gag atc ata aca tgt tac ctt aag gag aag gtt tta aac agc cga ttc   324
Glu Ile Ile Thr Cys Tyr Leu Lys Glu Lys Val Leu Asn Ser Arg Phe
        35                  40                  45

acg gct gtg gcc atg gga gaa gct gat ctc aac aag tgt gag cct tgg   372
Thr Ala Val Ala Met Gly Glu Ala Asp Leu Asn Lys Cys Glu Pro Trp
    50                  55                  60

gat ttg cca aag agg gca aag atg ggg gag aaa gag ttc tac ttc ttc   420
Asp Leu Pro Lys Arg Ala Lys Met Gly Glu Lys Glu Phe Tyr Phe Phe
65                  70                  75                  80

tgt caa agg gac agg aag tat ccg act ggg atg agg acg aac cgt gcg   468
Cys Gln Arg Asp Arg Lys Tyr Pro Thr Gly Met Arg Thr Asn Arg Ala
                85                  90                  95

acg gag tca gga tac tgg aaa gcc acc ggg aag gat aag gag atc ttc   516
Thr Glu Ser Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe
            100                 105                 110

aaa ggc aaa ggt tgt ctc gtt ggg atg aag aaa aca ctt gtg ttt tat   564
Lys Gly Lys Gly Cys Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr
```

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        115                 120                 125

aga gga aga gct cca aaa ggt gaa aag act aat tgg gtc atg cat gaa    612
Arg Gly Arg Ala Pro Lys Gly Glu Lys Thr Asn Trp Val Met His Glu
    130                 135                 140

tat cgt ctt gaa ggc aaa tat tcg tat tac aat ctc cca aaa tct gca    660
Tyr Arg Leu Glu Gly Lys Tyr Ser Tyr Tyr Asn Leu Pro Lys Ser Ala
145                 150                 155                 160

agg gac gaa tgg gtc gtg tgt agg gtt ttt cac aag aac aat cct tct    708
Arg Asp Glu Trp Val Val Cys Arg Val Phe His Lys Asn Asn Pro Ser
                165                 170                 175

acc aca acc caa cca atg acg aga ata ccc gtt gaa gat ttc aca agg    756
Thr Thr Thr Gln Pro Met Thr Arg Ile Pro Val Glu Asp Phe Thr Arg
            180                 185                 190

atg gat tct cta gag aac att gat cat ctc cta gac ttc tca tct ctt    804
Met Asp Ser Leu Glu Asn Ile Asp His Leu Leu Asp Phe Ser Ser Leu
        195                 200                 205

cct cct ctc ata gac ccg agt ttc atg agt caa acc gaa caa cca aac    852
Pro Pro Leu Ile Asp Pro Ser Phe Met Ser Gln Thr Glu Gln Pro Asn
    210                 215                 220

ttc aaa ccc atc aac cct cca act tac gat atc tca tca cca atc caa    900
Phe Lys Pro Ile Asn Pro Pro Thr Tyr Asp Ile Ser Ser Pro Ile Gln
225                 230                 235                 240

ccc cat cat ttc aat tct tac caa tca atc ttt aac cac cag gtt ttt    948
Pro His His Phe Asn Ser Tyr Gln Ser Ile Phe Asn His Gln Val Phe
                245                 250                 255

ggt tct gct tcg ggc tct acg tac aac aac aac aac gag atg atc aag    996
Gly Ser Ala Ser Gly Ser Thr Tyr Asn Asn Asn Asn Glu Met Ile Lys
            260                 265                 270

atg gag caa tca ctt gtt agt gta tct caa gaa aca tgc cta agc tca    1044
Met Glu Gln Ser Leu Val Ser Val Ser Gln Glu Thr Cys Leu Ser Ser
        275                 280                 285

gat gtg aac gcg aac atg act aca acc acg gag gta tct tcg ggt cct    1092
Asp Val Asn Ala Asn Met Thr Thr Thr Thr Glu Val Ser Ser Gly Pro
    290                 295                 300

gta atg aaa caa gaa atg ggg atg atg gga atg gtg aat ggt agc aag    1140
Val Met Lys Gln Glu Met Gly Met Met Gly Met Val Asn Gly Ser Lys
305                 310                 315                 320

tcg tat gaa gat cta tgt gac ttg agg ggg gac ttg tgg gac ttc taa    1188
Ser Tyr Glu Asp Leu Cys Asp Leu Arg Gly Asp Leu Trp Asp Phe  *
                325                 330                 335

ttaatcattt gactgtggtg aaagagtata tttgttggga tttaaatcat gttagttaat 1248
acatatacat ataggattta ctagaggctt aatcctagtt aactattttc acttcattga 1308
tattatttaa ttagttgatt gtttaattag tttatacttt atagtgtggt taaaaaagaa 1368
```

```
aagaaaggat tgtgataatt tgggatttta gtgcataagt tatatctcaa tgtaaactgt 1428
atttgtatcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa        1481

<210> 106
<211> 335
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (21)...(149)
<223> Conserved domain

<400> 106
Met Ala Val Val Val Glu Glu Gly Val Val Leu Asn His Gly Gly Glu
 1               5                  10                  15
Glu Leu Val Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu
            20                  25                  30
Glu Ile Ile Thr Cys Tyr Leu Lys Glu Lys Val Leu Asn Ser Arg Phe
        35                  40                  45
Thr Ala Val Ala Met Gly Glu Ala Asp Leu Asn Lys Cys Glu Pro Trp
    50                  55                  60
Asp Leu Pro Lys Arg Ala Lys Met Gly Glu Lys Glu Phe Tyr Phe Phe
65                  70                  75                  80
Cys Gln Arg Asp Arg Lys Tyr Pro Thr Gly Met Arg Thr Asn Arg Ala
                85                  90                  95
Thr Glu Ser Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe
            100                 105                 110
Lys Gly Lys Gly Cys Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr
        115                 120                 125
Arg Gly Arg Ala Pro Lys Gly Glu Lys Thr Asn Trp Val Met His Glu
    130                 135                 140
Tyr Arg Leu Glu Gly Lys Tyr Ser Tyr Tyr Asn Leu Pro Lys Ser Ala
145                 150                 155                 160
Arg Asp Glu Trp Val Val Cys Arg Val Phe His Lys Asn Asn Pro Ser
                165                 170                 175
Thr Thr Thr Gln Pro Met Thr Arg Ile Pro Val Glu Asp Phe Thr Arg
            180                 185                 190
Met Asp Ser Leu Glu Asn Ile Asp His Leu Leu Asp Phe Ser Ser Leu
        195                 200                 205
Pro Pro Leu Ile Asp Pro Ser Phe Met Ser Gln Thr Glu Gln Pro Asn
    210                 215                 220
Phe Lys Pro Ile Asn Pro Pro Thr Tyr Asp Ile Ser Ser Pro Ile Gln
225                 230                 235                 240
Pro His His Phe Asn Ser Tyr Gln Ser Ile Phe Asn His Gln Val Phe
                245                 250                 255
Gly Ser Ala Ser Gly Ser Thr Tyr Asn Asn Asn Asn Glu Met Ile Lys
            260                 265                 270
Met Glu Gln Ser Leu Val Ser Val Ser Gln Glu Thr Cys Leu Ser Ser
        275                 280                 285
Asp Val Asn Ala Asn Met Thr Thr Thr Thr Glu Val Ser Ser Gly Pro
    290                 295                 300
Val Met Lys Gln Glu Met Gly Met Met Gly Met Val Asn Gly Ser Lys
305                 310                 315                 320
Ser Tyr Glu Asp Leu Cys Asp Leu Arg Gly Asp Leu Trp Asp Phe
                325                 330                 335
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<210> 107
<211> 1130
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (116)...(1024)

<221> misc_feature
<222> 1100
<223> n = A,T,C or G

<400> 107
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ccaagatcga ctcttacttc gaatctctct caactttctt cctcagctta cgggaacttc 60
cacacatata catccacaag aacccatatc gaagattcat cctacatata tttac atg  118
                                                              Met
                                                               1

gat cag tac tca tcc tct ttg gtc gat act tca tta gat ctc act att   166
Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr Ile
            5                  10                  15

ggc gtt act cgt atg cga gtt gaa gaa gat cca ccg aca agt gct ttg   214
Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu
        20                  25                  30

gtg gaa gaa tta aac cga gtt agt gct gag aac aag aag ctc tcg gag   262
Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser Glu
    35                  40                  45

atg cta act ttg atg tgt gac aac tac aac gtc ttg agg aag caa ctt   310
Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln Leu
 50                  55                  60                  65

atg gaa tat gtt aac aag agc aac ata acc gag agg gat caa atc agc   358
Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile Ser
                70                  75                  80

cct ccc aag aaa cgc aaa tcc ccg gcg aga gag gac gca ttc agc tgc   406
Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser Cys
            85                  90                  95

gcg gtt att ggc gga gtg tcg gag agt agc tca acg gat caa gat gag   454
Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp Glu
        100                 105                 110

tat ttg tgt aag aag cag aga gaa gag act gtc gtg aag gag aaa gtc   502
Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys Val
    115                 120                 125

tca agg gtc tat tac aag acc gaa gct tct gac act acc ctc gtt gtg   550
Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val Val
130                 135                 140                 145

aaa gat ggg tat caa tgg agg aaa tat gga cag aaa gtg act aga gac   598
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Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp
                150                 155                 160

aat cca tct cca aga gct tac ttc aaa tgt gct tgt gct cca agc tgt      646
Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser Cys
            165                 170                 175

tct gtc aaa aag aag gtt cag aga agt gtg gag gat cag tcc gtg tta      694
Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val Leu
        180                 185                 190

gtt gca act tat gag ggt gaa cac aac cat cca atg cca tcg cag atc      742
Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln Ile
    195                 200                 205

gat tca aac aat ggc tta aac cgc cac atc tct cat ggt ggt tca gct      790
Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser Ala
210                 215                 220                 225

tca aca ccc gtt gca gca aac aga aga agt agc ttg act gtg ccg gtg      838
Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro Val
                230                 235                 240

act acc gta gat atg att gaa tcg aag aaa gtg acg agc cca acg tca      886
Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser
            245                 250                 255

aga atc gat ttt ccc caa gtt cag aaa ctt ttg gtg gag caa atg gct      934
Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met Ala
        260                 265                 270

tct tcc tta acc aaa gat cct aac ttt aca gca gct tta gca gca gct      982
Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Ala
    275                 280                 285

gtt acc gga aaa ttg tat caa cag aat cat acc gag aaa tag              1024
Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys  *
290                 295                 300

tttagcttca aattccgtta gagtttttag atttgaattt gtcatgagta agagaaagag 1084
agtagattat aatccnttgt gatactgaaa aaaaaaaaaa aaaaaa                1130

<210> 108
<211> 302
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (146)...(203)
<223> Conserved domain

<400> 108
Met Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr
 1               5                  10                  15
Ile Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala
            20                  25                  30
```

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Leu Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser
        35                  40                  45
Glu Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln
    50                  55                  60
Leu Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile
65                  70                  75                  80
Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser
                85                  90                  95
Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp
            100                 105                 110
Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys
        115                 120                 125
Val Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val
    130                 135                 140
Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg
145                 150                 155                 160
Asp Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser
                165                 170                 175
Cys Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val
            180                 185                 190
Leu Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln
        195                 200                 205
Ile Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser
    210                 215                 220
Ala Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro
225                 230                 235                 240
Val Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr
                245                 250                 255
Ser Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met
            260                 265                 270
Ala Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala
        275                 280                 285
Ala Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
    290                 295                 300


<210> 109
<211> 1449
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1449)

<400> 109
atg gtg gct atg ttt caa gaa gat aat gga aca tct tct gta gct tca      48
Met Val Ala Met Phe Gln Glu Asp Asn Gly Thr Ser Ser Val Ala Ser
 1               5                  10                  15

tca cca ctt caa gtc ttc tca act atg tca ctc aac aga ccg act ctc      96
Ser Pro Leu Gln Val Phe Ser Thr Met Ser Leu Asn Arg Pro Thr Leu
            20                  25                  30

ctc gct tct tca tct ccg ttt cat tgt ctc aaa gat ctc aaa cca gag      144
Leu Ala Ser Ser Ser Pro Phe His Cys Leu Lys Asp Leu Lys Pro Glu
        35                  40                  45
```

gag cgt ggt ctc tac tta atc cac ctc ttg cta act tgt gcc aac cac 192
Glu Arg Gly Leu Tyr Leu Ile His Leu Leu Leu Thr Cys Ala Asn His
50 55 60

gtg gct tca ggt agc ctc caa aac gct aac gca gcg ctc gag cag ctc 240
Val Ala Ser Gly Ser Leu Gln Asn Ala Asn Ala Ala Leu Glu Gln Leu
65 70 75 80

tct cac ctc gct tct cct gac ggc gac acg atg cag cga atc gct gct 288
Ser His Leu Ala Ser Pro Asp Gly Asp Thr Met Gln Arg Ile Ala Ala
85 90 95

tac ttc acc gaa gcg ctt gct aac aga atc ctt aag tcc tgg cct ggt 336
Tyr Phe Thr Glu Ala Leu Ala Asn Arg Ile Leu Lys Ser Trp Pro Gly
100 105 110

ctt tac aag gct ctt aac gca act cag aca aga act aac aat gtc tct 384
Leu Tyr Lys Ala Leu Asn Ala Thr Gln Thr Arg Thr Asn Asn Val Ser
115 120 125

gag gag att cat gtt aga aga ctc ttc ttt gag atg ttc ccg ata ctc 432
Glu Glu Ile His Val Arg Arg Leu Phe Phe Glu Met Phe Pro Ile Leu
130 135 140

aaa gtc tct tac ttg ctc act aat cga gct ata ctc gag gct atg gaa 480
Lys Val Ser Tyr Leu Leu Thr Asn Arg Ala Ile Leu Glu Ala Met Glu
145 150 155 160

gga gag aag atg gtt cat gtg att gat ctc gat gct tct gag cca gct 528
Gly Glu Lys Met Val His Val Ile Asp Leu Asp Ala Ser Glu Pro Ala
165 170 175

caa tgg ctt gct ttg ctt caa gct ttt aac tct agg cct gaa ggt cca 576
Gln Trp Leu Ala Leu Leu Gln Ala Phe Asn Ser Arg Pro Glu Gly Pro
180 185 190

cct cat ttg aga atc act ggt gtt cat cac cag aag gaa gtg ctt gaa 624
Pro His Leu Arg Ile Thr Gly Val His His Gln Lys Glu Val Leu Glu
195 200 205

caa atg gct cat aga ctc att gag gaa gca gag aaa ctc gat atc ccg 672
Gln Met Ala His Arg Leu Ile Glu Glu Ala Glu Lys Leu Asp Ile Pro
210 215 220

ttt cag ttt aat ccc gtt gtg agt agg tta gac tgt tta aat gta gaa 720
Phe Gln Phe Asn Pro Val Val Ser Arg Leu Asp Cys Leu Asn Val Glu
225 230 235 240

cag ttg cgg gtt aaa aca gga gag gcc tta gcc gtt agc tcg gtt ctt 768
Gln Leu Arg Val Lys Thr Gly Glu Ala Leu Ala Val Ser Ser Val Leu
245 250 255

caa ttg cat acc ttc ttg gcc tct gat gat gat ctc atg aga aag aac 816
Gln Leu His Thr Phe Leu Ala Ser Asp Asp Asp Leu Met Arg Lys Asn
260 265 270

```
tgc gct tta cgg ttt cag aac aac cct agt gga gtt gac ttg cag aga     864
Cys Ala Leu Arg Phe Gln Asn Asn Pro Ser Gly Val Asp Leu Gln Arg
        275                 280                 285

gtt cta atg atg agc cat ggc tct gca gct gag gca cgt gag aat gat     912
Val Leu Met Met Ser His Gly Ser Ala Ala Glu Ala Arg Glu Asn Asp
    290                 295                 300

atg agt aac aac aat ggg tat agc cct agc ggt gac tcg gcc tca tct     960
Met Ser Asn Asn Asn Gly Tyr Ser Pro Ser Gly Asp Ser Ala Ser Ser
305                 310                 315                 320

ttg cct tta cca agt tca gga agg act gat agc ttc ctc aat gct att     1008
Leu Pro Leu Pro Ser Ser Gly Arg Thr Asp Ser Phe Leu Asn Ala Ile
                325                 330                 335

tgg ggt ttg tct cca aag gtc atg gtg gtc act gag caa gac tca gac     1056
Trp Gly Leu Ser Pro Lys Val Met Val Val Thr Glu Gln Asp Ser Asp
            340                 345                 350

cac aac ggc tcc aca cta atg gag agg cta tta gaa tca ctt tac acc     1104
His Asn Gly Ser Thr Leu Met Glu Arg Leu Leu Glu Ser Leu Tyr Thr
        355                 360                 365

tac gca gca ttg ttt gat tgc ttg gaa aca aaa gtt cca aga acg tct     1152
Tyr Ala Ala Leu Phe Asp Cys Leu Glu Thr Lys Val Pro Arg Thr Ser
    370                 375                 380

caa gat agg atc aaa gtg gag aag atg ctc ttc ggg gag gag atc aag     1200
Gln Asp Arg Ile Lys Val Glu Lys Met Leu Phe Gly Glu Glu Ile Lys
385                 390                 395                 400

aac atc ata tcc tgc gag gga ttt gag aga aga gaa aga cac gag aag     1248
Asn Ile Ile Ser Cys Glu Gly Phe Glu Arg Arg Glu Arg His Glu Lys
                405                 410                 415

ctt gag aaa tgg agc cag agg atc gat ttg gct ggt ttt ggg aat gtt     1296
Leu Glu Lys Trp Ser Gln Arg Ile Asp Leu Ala Gly Phe Gly Asn Val
            420                 425                 430

cct ctt agc tat tat gcg atg ttg cag gct agg aga ttg ctt caa ggg     1344
Pro Leu Ser Tyr Tyr Ala Met Leu Gln Ala Arg Arg Leu Leu Gln Gly
        435                 440                 445

tgc ggt ttt gat ggg tat aga atc aag gaa gag agc ggg tgc gca gta     1392
Cys Gly Phe Asp Gly Tyr Arg Ile Lys Glu Glu Ser Gly Cys Ala Val
    450                 455                 460

att tgc tgg caa gat cga cct cta tac tcg gta tca gct tgg aga tgc     1440
Ile Cys Trp Gln Asp Arg Pro Leu Tyr Ser Val Ser Ala Trp Arg Cys
465                 470                 475                 480

agg aag tga                                                         1449
Arg Lys  *
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<210> 110
<211> 482
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (225)...(242)
<223> Conserved domain

<400> 110
Met Val Ala Met Phe Gln Glu Asp Asn Gly Thr Ser Ser Val Ala Ser
1 5 10 15
Ser Pro Leu Gln Val Phe Ser Thr Met Ser Leu Asn Arg Pro Thr Leu
20 25 30
Leu Ala Ser Ser Ser Pro Phe His Cys Leu Lys Asp Leu Lys Pro Glu
35 40 45
Glu Arg Gly Leu Tyr Leu Ile His Leu Leu Leu Thr Cys Ala Asn His
50 55 60
Val Ala Ser Gly Ser Leu Gln Asn Ala Asn Ala Ala Leu Glu Gln Leu
65 70 75 80
Ser His Leu Ala Ser Pro Asp Gly Asp Thr Met Gln Arg Ile Ala Ala
85 90 95
Tyr Phe Thr Glu Ala Leu Ala Asn Arg Ile Leu Lys Ser Trp Pro Gly
100 105 110
Leu Tyr Lys Ala Leu Asn Ala Thr Gln Thr Arg Thr Asn Asn Val Ser
115 120 125
Glu Glu Ile His Val Arg Arg Leu Phe Phe Glu Met Phe Pro Ile Leu
130 135 140
Lys Val Ser Tyr Leu Leu Thr Asn Arg Ala Ile Leu Glu Ala Met Glu
145 150 155 160
Gly Glu Lys Met Val His Val Ile Asp Leu Asp Ala Ser Glu Pro Ala
165 170 175
Gln Trp Leu Ala Leu Leu Gln Ala Phe Asn Ser Arg Pro Glu Gly Pro
180 185 190
Pro His Leu Arg Ile Thr Gly Val His His Gln Lys Glu Val Leu Glu
195 200 205
Gln Met Ala His Arg Leu Ile Glu Glu Ala Glu Lys Leu Asp Ile Pro
210 215 220
Phe Gln Phe Asn Pro Val Val Ser Arg Leu Asp Cys Leu Asn Val Glu
225 230 235 240
Gln Leu Arg Val Lys Thr Gly Glu Ala Leu Ala Val Ser Ser Val Leu
245 250 255
Gln Leu His Thr Phe Leu Ala Ser Asp Asp Asp Leu Met Arg Lys Asn
260 265 270
Cys Ala Leu Arg Phe Gln Asn Asn Pro Ser Gly Val Asp Leu Gln Arg
275 280 285
Val Leu Met Met Ser His Gly Ser Ala Ala Glu Ala Arg Glu Asn Asp
290 295 300
Met Ser Asn Asn Asn Gly Tyr Ser Pro Ser Gly Asp Ser Ala Ser Ser
305 310 315 320
Leu Pro Leu Pro Ser Ser Gly Arg Thr Asp Ser Phe Leu Asn Ala Ile
325 330 335
Trp Gly Leu Ser Pro Lys Val Met Val Val Thr Glu Gln Asp Ser Asp
340 345 350
His Asn Gly Ser Thr Leu Met Glu Arg Leu Leu Glu Ser Leu Tyr Thr
355 360 365

```
Tyr Ala Ala Leu Phe Asp Cys Leu Glu Thr Lys Val Pro Arg Thr Ser
    370                 375                 380
Gln Asp Arg Ile Lys Val Glu Lys Met Leu Phe Gly Glu Glu Ile Lys
385                 390                 395                 400
Asn Ile Ile Ser Cys Glu Gly Phe Glu Arg Arg Glu Arg His Glu Lys
                405                 410                 415
Leu Glu Lys Trp Ser Gln Arg Ile Asp Leu Ala Gly Phe Gly Asn Val
            420                 425                 430
Pro Leu Ser Tyr Tyr Ala Met Leu Gln Ala Arg Arg Leu Leu Gln Gly
        435                 440                 445
Cys Gly Phe Asp Gly Tyr Arg Ile Lys Glu Glu Ser Gly Cys Ala Val
    450                 455                 460
Ile Cys Trp Gln Asp Arg Pro Leu Tyr Ser Val Ser Ala Trp Arg Cys
465                 470                 475                 480
Arg Lys
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<210> 111
<211> 1388
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (280)...(1095)

<400> 111
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ctgccggctg tcgggttttc tgaatcgatt ctccttcacc aacttcttct ctggttctgt 120
tcgattctga tttttttca aggtcaattt tttcttctct ttaaactctg caaaatcgtg 180
atcgattaaa ttcacctcag ggttttttga tttctgaaag aagttaatct tcttcgaagg 240
cgattgcaaa agagtgctct gctgtgaatt tccactgag atg caa tca aaa ccg    294
                                          Met Gln Ser Lys Pro
                                           1               5

gga aga gaa aac gaa gag gaa gtc aat aat cac cat gct gtt cag cag   342
Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His His Ala Val Gln Gln
                 10                  15                  20

ccg atg atg tat gca gag ccc tgg tgg aaa aac aac tcc ttt ggt gtt   390
Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn Asn Ser Phe Gly Val
            25                  30                  35

gta cct caa gcg aga cct tct gga att cca tca aat tcc tct tct ttg   438
Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser Asn Ser Ser Ser Leu
        40                  45                  50

gat tgc ccc aat ggt tcc gag tca aac gat gtt cat tca gca tct gaa   486
Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val His Ser Ala Ser Glu
    55                  60                  65

gac ggt gcg ttg aat ggt gaa aac gat ggc act tgg aag gat tca caa   534
Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr Trp Lys Asp Ser Gln
 70                  75                  80                  85

gct gca act tcc tct cgt tca gat aat cac gga atg gaa gga aat gac   582
```

Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly Met Glu Gly Asn Asp
90 95 100

cca gcg ctc tct atc cgt aac atg cat gat cag cca ctt gta caa cca 630
Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln Pro Leu Val Gln Pro
105 110 115

cca gag ctt gtt gga cac tat atc gct tgt gtc cca aac cca tat cag 678
Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val Pro Asn Pro Tyr Gln
120 125 130

gat cca tat tat ggg gga ttg atg gga gca tat ggt cat cag caa ttg 726
Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr Gly His Gln Gln Leu
135 140 145

ggt ttt cgt cca tat ctt gga atg cct cgt gaa aga aca gct ctg cca 774
Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu Arg Thr Ala Leu Pro
150 155 160 165

ctt gac atg gca caa gag ccc gtt tat gtg aat gca aag cag tac gag 822
Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn Ala Lys Gln Tyr Glu
170 175 180

gga att cta agg cga aga aaa gca cgt gcc aag gca gag cta gag agg 870
Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys Ala Glu Leu Glu Arg
185 190 195

aaa gtc atc cgg gac aga aag cca tat ctt cac gag tca aga cac aag 918
Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His Glu Ser Arg His Lys
200 205 210

cat gca atg aga agg gca cga gcg agt gga ggc cgg ttt gcg aag aaa 966
His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly Arg Phe Ala Lys Lys
215 220 225

agt gag gta gaa gcg gga gag gat gca gga ggg aga gac aga gaa agg 1014
Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly Arg Asp Arg Glu Arg
230 235 240 245

ggt tca gca acc aac tca tca ggc tct gaa caa gtt gag aca gac tct 1062
Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln Val Glu Thr Asp Ser
250 255 260

aat gag acc ctg aat tct tct ggt gca cca taa taaaaaaagc caaagctctg 1115
Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro *
265 270

agaggagaga gagacacaca ctttggctaa tataatccat tgcctcaaac cggcaaatca 1175
ttcttggctt tttcgttttt gtgtttgcta gttgttcttg tcagagtctc atattgtgtg 1235
ggtttaacag ttatgatgaa tgtacaaaga gcgagttatg ttaggtgtta gattttggag 1295
acaagagaca aaggaatagc aagtaggtct tgtttttatt ctttgacctt ttttttctct 1355
tttgcaaaat tgaaaaatac gtttgcttaa aaa 1388

<210> 112
<211> 271
<212> PRT
<213> Arabidopsis thaliana

<400> 112
Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His
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His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn
            20   25   30
Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser
        35   40   45
Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val
    50   55   60
His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr
65   70   75   80
Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly
                85   90   95
Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln
            100   105   110
Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val
        115   120   125
Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr
    130   135   140
Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu
145   150   155   160
Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn
                165   170   175
Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys
            180   185   190
Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His
        195   200   205
Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly
    210   215   220
Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly
225   230   235   240
Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln
                245   250   255
Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
            260   265   270

<210> 113
<211> 832
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (103)...(528)

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gagcgtttcg tagaaaaatt cgatttctct aaagccctaa aactaaaacg actatcccca 60
attccaagtt ctagggtttc catcttcccc aatctagtat aa atg gcg gat acg 114
                                               Met Ala Asp Thr
                                               1

cct tcg agc cca gct gga gat ggc gga gaa agc ggc ggt tcc gtt agg 162
Pro Ser Ser Pro Ala Gly Asp Gly Gly Glu Ser Gly Gly Ser Val Arg
5   10   15   20

```
gag cag gat cga tac ctt cct ata gct aat atc agc agg atc atg aag    210
Glu Gln Asp Arg Tyr Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys
                25                  30                  35

aaa gcg ttg cct cct aat ggt aag att gga aaa gat gct aag gat aca    258
Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp Ala Lys Asp Thr
            40                  45                  50

gtt cag gaa tgc gtc tct gag ttc atc agc ttc atc act agc gag gcc    306
Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala
        55                  60                  65

agt gat aag tgt caa aaa gag aaa agg aaa act gtg aat ggt gat gat    354
Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val Asn Gly Asp Asp
    70                  75                  80

ttg ttg tgg gca atg gca aca tta gga ttt gag gat tac ctg gaa cct    402
Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Leu Glu Pro
 85                  90                  95                 100

cta aag ata tac cta gcg agg tac agg gag ttg gag ggt gat aat aag    450
Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu Gly Asp Asn Lys
                105                 110                 115

gga tca gga aag agt gga gat gga tca aat aga gat gct ggt ggc ggt    498
Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp Ala Gly Gly Gly
            120                 125                 130

gtt tct ggt gaa gaa atg ccg agc tgg taa aagaagttgc aagtagtgat     548
Val Ser Gly Glu Glu Met Pro Ser Trp  *
        135                 140

taagaacaat cgccaaatga tcaagggaaa ttagagatca gtgagttgtt tatagttgag 608
ctgatcgaca actatttcgg gtttactctc aatttcggtt atgttagttt gaacgtttgg 668
tttattgttt ccggtttagt tggttgtatt taaagatttc tctgttagat gttgagaaca 728
cttgaatgaa ggaaaaattt gtccacatcc tgttgttatt ttcgattcac tttcggaatt 788
tcatagctaa tttattctca tttaatacca aatccttaaa ttaa                  832

<210> 114
<211> 141
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (20)...(109)
<223> Conserved domain

<400> 114
Met Ala Asp Thr Pro Ser Ser Pro Ala Gly Asp Gly Gly Glu Ser Gly
 1               5                  10                  15
Gly Ser Val Arg Glu Gln Asp Arg Tyr Leu Pro Ile Ala Asn Ile Ser
            20                  25                  30
Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
        35                  40                  45
Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
    50                  55                  60
```

```
Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
65                  70                  75                  80
Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
                85                  90                  95
Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
            100                 105                 110
Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
        115                 120                 125
Ala Gly Gly Gly Val Ser Gly Glu Glu Met Pro Ser Trp
    130                 135                 140
```

<210> 115
<211> 1662
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1662)

<400> 115

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atg ggt gat aca gag aag tgt aac agt gat atg atc cag aga ctt cat      48
Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His
 1               5                  10                  15

tca tct ttc ggc act act tct tct tcc att ccc aaa aat ccc att tct      96
Ser Ser Phe Gly Thr Thr Ser Ser Ser Ile Pro Lys Asn Pro Ile Ser
            20                  25                  30

cag ctc gat tta aac cct aat ttc atc cgc tca tca gct cct caa ttc     144
Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe
        35                  40                  45

tcc aag cct ttc agt gac agt ggc aaa cga atc ggt gtt cct ccg tcg     192
Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser
    50                  55                  60

cac ccc aac tta atc cca ccg act tct ccg ttt tct cag atc ccg acc     240
His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr
65                  70                  75                  80

acc cga caa ccc ggt tcg cat aat ttt aac ccg gga gga gct aat cat     288
Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His
                85                  90                  95

tca cgg tca atg tca cag ccc aac tct ttc ttc tct ttt gac tcc tta     336
Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu
            100                 105                 110

cct ccg tta agc cct tct ccg ttt cga gat cac gat gtt tca atg gag     384
Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu
        115                 120                 125

gat aga gat tcc ggc gtg ttt aac agc aac cat tcg ttg cct cca tcg     432
Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser
    130                 135                 140
```

```
ccg ttc acg agg tgt aat tcg acc tct tct agc tcc ttg aga gtc ggt    480
Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Ser Leu Arg Val Gly
145                 150                 155                 160

gag agt tta cct ccg aga aag tct cat aga cgc tcc aac agt gat atc    528
Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile
                165                 170                 175

ccc agt ggg ttt aat tcg atg cct ttg atc cct ccg aga cca ttg gag    576
Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu
            180                 185                 190

agg tct ttt tct ggt ggg gag tgt gct gat tgg tca aag tct aat cct    624
Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro
        195                 200                 205

ttt gtg aag aag gaa tcg agc tgc gaa agg gaa ggt gtc gga gag aga    672
Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg
    210                 215                 220

gaa gct atg gat gat ctc ttc tca gca tat atg aat ctt gaa aac att    720
Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile
225                 230                 235                 240

gat gtg ttg aac tcc tct gaa gct gat gat agc aag aac ggt aat gag    768
Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu
                245                 250                 255

aat agg gat gat atg gag agc agc aga gca agc ggg acc aag act aac    816
Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn
            260                 265                 270

ggt agt gat acg gaa gga gag agc agc agt gtc aat gag agt gcc aat    864
Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn
        275                 280                 285

aat aat atg aat tct tct ggt gaa aag aga gag agc gtg aag aga aga    912
Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg
    290                 295                 300

gcg gct gga gga gat att gct cct acc acc aga cat tac agg agt gtt    960
Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val
305                 310                 315                 320

tca gtg gac agt tgt ttc atg gag aag ttg tct ttt ggt gat gaa tct    1008
Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser
                325                 330                 335

cta aag ccg cct cct tct cct gga tct atg tca agg aaa gtt tcc cct    1056
Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro
            340                 345                 350

acc aat tcg gtt gat ggg aac tcg ggt gct gct ttt agc atc gag ttc    1104
Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe
        355                 360                 365
```

aat aac ggt gag ttt act gca gcg gaa atg aag aag atc atg gca aat 1152
Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn
370 375 380

gat aaa cta gca gag atg gcc atg tct gac cct aaa cgt gtc aaa agg 1200
Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg
385 390 395 400

aat gat cct ctt ttc aga atc tta gcg aac cgt caa tcc gca gca cgg 1248
Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg
405 410 415

tca aag gag agg aag atg cgg tac ata gta gaa ttg gaa cac aaa gtg 1296
Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val
420 425 430

cag act ctt cag acc gag gct acc aca ttg tct gct cag ctc aca ctt 1344
Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu
435 440 445

ttg cag cgc gat atg atg ggg ttg aca aat cag aac aat gag ctt aag 1392
Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys
450 455 460

ttc cgg ctt caa gca atg gag caa caa gcg cgt ctt cgc gat gct ctg 1440
Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu
465 470 475 480

aac gaa gca ctg aat gga gaa gtc cag cga ctg aaa ctg gca atc ggt 1488
Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly
485 490 495

gag agc agt cag aac gaa tca gag aga tca aag atg caa tca ctc aac 1536
Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn
500 505 510

gct gag atg ttc cag caa ctc aac atc agc cag tta aga cag cag cca 1584
Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro
515 520 525

caa cag atg cag caa cag tct cat cag cag aac cac cag aat gga acc 1632
Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr
530 535 540

atg gca aca aaa tct gaa tca aat gaa tag 1662
Met Ala Thr Lys Ser Glu Ser Asn Glu *
545 550

<210> 116
<211> 553
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (249)...(297)

<223> Conserved domain

<400> 116
Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His
1   5   10   15
Ser Ser Phe Gly Thr Thr Ser Ser Ser Ile Pro Lys Asn Pro Ile Ser
            20   25   30
Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe
        35   40   45
Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser
    50   55   60
His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr
65   70   75   80
Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His
                85   90   95
Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu
            100   105   110
Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu
        115   120   125
Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser
    130   135   140
Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Ser Leu Arg Val Gly
145   150   155   160
Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile
                165   170   175
Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu
            180   185   190
Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro
        195   200   205
Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg
    210   215   220
Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile
225   230   235   240
Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu
                245   250   255
Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn
            260   265   270
Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn
        275   280   285
Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg
    290   295   300
Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val
305   310   315   320
Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser
                325   330   335
Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro
            340   345   350
Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe
        355   360   365
Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn
    370   375   380
Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg
385   390   395   400
Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg
                405   410   415
Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val
            420   425   430

Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu
435 440 445
Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys
450 455 460
Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu
465 470 475 480
Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly
485 490 495
Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn
500 505 510
Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro
515 520 525
Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr
530 535 540
Met Ala Thr Lys Ser Glu Ser Asn Glu
545 550

<210> 117
<211> 1218
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1218)

<400> 117
atg gat tct tgg agc tac ggg aga agc gtt ttc atg tca aat gaa act 48
Met Asp Ser Trp Ser Tyr Gly Arg Ser Val Phe Met Ser Asn Glu Thr
1 5 10 15

ctt tta cct tgt gat act ttt gct aag aat aga aga ttt gaa cag aga 96
Leu Leu Pro Cys Asp Thr Phe Ala Lys Asn Arg Arg Phe Glu Gln Arg
20 25 30

ctc tct aat aat gat gat gtg ttg att tct gac atg gct ggt aac tcc 144
Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser
35 40 45

aat gga ttc agt gct gtt tct att act aaa gtt gtt cct gaa gag gaa 192
Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu
50 55 60

gat gag gag aac ata tct tct tct tca aag ttc tct agt cag gaa ttg 240
Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu
65 70 75 80

aat agg ata gat ttc aaa ctt agg agc ttt ttg gat tta gga aat gat 288
Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp
85 90 95

gat gat gat aca tcc tct aga ggt ttt gct ctg cca tct aaa aag tct 336
Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser
100 105 110

cga gct tca aac ttg tgc tct cag aat ccc ttg tgt caa gtt tat ggg 384

Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly
115 120 125

tgt agt aag gat ctg agc tct tcg aaa gat tac cac aaa agg cat aga 432
Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg
130 135 140

gtt tgc gag gct cat tcg aaa act tct gtg gtc ata gtt aat ggt ctt 480
Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu
145 150 155 160

gaa cag agg ttt tgt caa cag tgc agc agg ttt cat ttc ctc tca gag 528
Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu
165 170 175

ttt gat gat ggc aaa aga agt tgc aga agg cga tta gcc ggt cac aat 576
Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn
180 185 190

gaa cga aga agg aaa cct gca ttc tat ttc cta ccg ggt aag cgc cat 624
Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His
195 200 205

aag ctt ctt cgc acc tct caa gat gta gta ggc aac aag ttt ctg gag 672
Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu
210 215 220

aat tca tca ttg gta ttg cca gag tca ttt cct ggt agt ctc tta tac 720
Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr
225 230 235 240

aga gta ata gat gaa gac gac cac cgt aca agt aga ctc gtg agt ttc 768
Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe
245 250 255

aaa gat gaa cct act tgt tcc atg ttt cct act aat gag caa aac agc 816
Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser
260 265 270

agc aga act tat gaa tct aaa cca gca att tat tcc acg gaa gta tcc 864
Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser
275 280 285

tcc att tgg gac tta cat gag acg gcg gca tca cgc tct act cgt gct 912
Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala
290 295 300

ctc tct ctt ctg tca gct cag tcc caa caa cac ttg tct aag ttt cca 960
Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro
305 310 315 320

aac aca acg ttc tca atc acc caa ccc aac caa aat ctc aat cac tca 1008
Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser
325 330 335

tca tca act gac tat cat cag atg gaa caa ccg ttg tgg atc gat cct 1056
Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro

```
            340                 345                 350

ggc aag acc aat tct gct ggt tct agt tct tgt aaa gga aaa gga aca     1104
Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr
        355                 360                 365

tcc acg gtt gat cta ctg caa ctg tca tca cat ctt caa aga atc gag     1152
Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu
    370                 375                 380

caa cag agg aat tac act ggt gat gtg aag cag gaa tat aat gag ctt     1200
Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu
385                 390                 395                 400

tat ttc cct ggc tcc taa                                             1218
Tyr Phe Pro Gly Ser  *
                405
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<210> 118
<211> 405
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (108)...(233)
<223> Conserved domain

<400> 118

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 1               5                  10                  15
Leu Leu Pro Cys Asp Thr Phe Ala Lys Asn Arg Arg Phe Glu Gln Arg
            20                  25                  30
Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser
        35                  40                  45
Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu
    50                  55                  60
Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu
65                  70                  75                  80
Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp
                85                  90                  95
Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser
            100                 105                 110
Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly
        115                 120                 125
Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg
    130                 135                 140
Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu
145                 150                 155                 160
Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu
                165                 170                 175
Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn
            180                 185                 190
Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His
        195                 200                 205
Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu
```

210 215 220
Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr
225 230 235 240
Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe
245 250 255
Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser
260 265 270
Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser
275 280 285
Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala
290 295 300
Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro
305 310 315 320
Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser
325 330 335
Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro
340 345 350
Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr
355 360 365
Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu
370 375 380
Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu
385 390 395 400
Tyr Phe Pro Gly Ser
405

<210> 119
<211> 1913
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (259)...(1593)

<400> 119
ggcaagaaga accttagcct ctctttcttc tttctctctc tctctctctg tggtactgtt 60
ctgtttcaac tttactccct cagtttcaga acaattccct atctagaaga gagataaaac 120
cgagaaggtt ttggagatag aatcttttgt tcttcttttg tccctccttg ctcgattttt 180
gttacgtgtg aagcaataaa aaaaaactga tatagctaaa tcttccatcc attcagaggc 240
ttctaaatct gatctgac atg gaa caa gtg ttt gct gat tgg aat ttt gaa 291
Met Glu Gln Val Phe Ala Asp Trp Asn Phe Glu
1 5 10

gat aat ttt cac atg tcc act aat aaa aga tca atc aga cca gaa gat 339
Asp Asn Phe His Met Ser Thr Asn Lys Arg Ser Ile Arg Pro Glu Asp
15 20 25

gaa tta gtg gag cta ttg tgg aga gat ggt caa gtg gtt tta caa agc 387
Glu Leu Val Glu Leu Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser
30 35 40

caa gct cgt aga gaa ccg tca gtc caa gtc caa acc cac aaa caa gaa 435
Gln Ala Arg Arg Glu Pro Ser Val Gln Val Gln Thr His Lys Gln Glu
45 50 55

```
acc cta aga aaa ccc aac aat att ttt ctt gac aac caa gaa aca gta    483
Thr Leu Arg Lys Pro Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val
 60                 65                  70                  75

caa aag cct aac tac gct gct cta gat gat caa gaa acc gtc tcc tgg    531
Gln Lys Pro Asn Tyr Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp
                80                  85                  90

ata caa tac cct ccg gat gac gtc atc gac cct ttc gaa tcc gag ttc    579
Ile Gln Tyr Pro Pro Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe
            95                 100                 105

tcc tct cat ttc ttc tct tcg atc gat cac ctc gga ggt cct gag aag    627
Ser Ser His Phe Phe Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys
        110                 115                 120

cca cga acg atc gaa gag aca gtt aag cat gag gct caa gcc atg gct    675
Pro Arg Thr Ile Glu Glu Thr Val Lys His Glu Ala Gln Ala Met Ala
    125                 130                 135

cct cct aag ttt aga tcc tcg gtt ata aca gtc gga ccg agt cat tgc    723
Pro Pro Lys Phe Arg Ser Ser Val Ile Thr Val Gly Pro Ser His Cys
140                 145                 150                 155

ggc agc aac cag tca aca aat att cat cag gcc act aca ctt ccg gtt    771
Gly Ser Asn Gln Ser Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val
                160                 165                 170

tct atg agt gat aga agc aag aac gtc gaa gaa aga ctt gac act tcg    819
Ser Met Ser Asp Arg Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser
            175                 180                 185

tca ggt ggc tcc tcc ggt tgc agc tat gga agg aac aac aaa gaa acc    867
Ser Gly Gly Ser Ser Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr
        190                 195                 200

gtt agt gga aca agt gta acc att gac cgt aaa aga aaa cat gtt atg    915
Val Ser Gly Thr Ser Val Thr Ile Asp Arg Lys Arg Lys His Val Met
    205                 210                 215

gat gct gat caa gaa tct gtg tct caa tca gat ata ggt ttg acc tca    963
Asp Ala Asp Gln Glu Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser
220                 225                 230                 235

acc gat gat caa acc atg ggt aac aaa tcg agc caa cgg tca gga tct   1011
Thr Asp Asp Gln Thr Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser
                240                 245                 250

act cga aga agc cgt gca gct gaa gtt cat aat ctc tca gaa agg agg   1059
Thr Arg Arg Ser Arg Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg
            255                 260                 265

agg aga gat cgg atc aat gaa aga atg aaa gct ctt caa gaa ctc ata   1107
Arg Arg Asp Arg Ile Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile
        270                 275                 280

cct cac tgc agc aga aca gat aaa gct tcg ata ttg gat gaa gca att   1155
```

```
Pro His Cys Ser Arg Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile
    285                 290                 295

gat tac tta aaa tca ctt caa atg caa ctc caa gtg atg tgg atg gga     1203
Asp Tyr Leu Lys Ser Leu Gln Met Gln Leu Gln Val Met Trp Met Gly
300                 305                 310                 315

agt gga atg gcg gcg gcg gca gca gca gca gca agt ccg atg atg ttt     1251
Ser Gly Met Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Met Met Phe
                320                 325                 330

ccc ggg gta caa tca tct cca tac att aat cag atg gct atg caa agt     1299
Pro Gly Val Gln Ser Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser
            335                 340                 345

cag atg caa ttg tct caa ttc ccg gtt atg aac cgg tcc gct ccg cag     1347
Gln Met Gln Leu Ser Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln
        350                 355                 360

aac cat ccc ggt tta gta tgt caa aac ccg gta cag ttg cag ctc caa     1395
Asn His Pro Gly Leu Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln
    365                 370                 375

gca cag aac caa atc tta tcg gag cag ctc gct agg tac atg ggc ggg     1443
Ala Gln Asn Gln Ile Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly
380                 385                 390                 395

att ccc cag atg ccg ccg gcg gga aat cag atg cag acc gtg caa caa     1491
Ile Pro Gln Met Pro Pro Ala Gly Asn Gln Met Gln Thr Val Gln Gln
                400                 405                 410

caa cca gcg gac atg ttg gga ttt gga tct ccg gcg gga ccg caa agt     1539
Gln Pro Ala Asp Met Leu Gly Phe Gly Ser Pro Ala Gly Pro Gln Ser
            415                 420                 425

caa ctg tcg gca ccg gcg acc acc gac agt ctt cat atg ggt aaa ata     1587
Gln Leu Ser Ala Pro Ala Thr Thr Asp Ser Leu His Met Gly Lys Ile
        430                 435                 440

ggc tga cttggcatat agttttcctc cgaaattatt cttcttacag ttggtgattg      1643
Gly  *


ttatttattt ttggtcgcct aagcaagcat aaaagctaag tcaaatgtat tatagagatc 1703
taataagtta gtctcatact tataacttat ttttaaacag ttgaattata gtatcaatca 1763
agtgttggga acctaaagat catacatgtg tcaatacttt tatatttgtt ctcaaggttc 1823
atcagaaaaa caaaataaaa aggatagact aggcctgcat ttgacattat catgggcttt 1883
tttgggtcta tgaatatgaa cattaacccc                                  1913
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<210> 120
<211> 444
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (253)...(313)

<223> Conserved domain

<400> 120
Met Glu Gln Val Phe Ala Asp Trp Asn Phe Glu Asp Asn Phe His Met
1   5   10   15
Ser Thr Asn Lys Arg Ser Ile Arg Pro Glu Asp Glu Leu Val Glu Leu
            20   25   30
Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser Gln Ala Arg Arg Glu
        35   40   45
Pro Ser Val Gln Val Gln Thr His Lys Gln Glu Thr Leu Arg Lys Pro
    50   55   60
Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val Gln Lys Pro Asn Tyr
65   70   75   80
Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro
                85   90   95
Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe Ser Ser His Phe Phe
            100   105   110
Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys Pro Arg Thr Ile Glu
        115   120   125
Glu Thr Val Lys His Glu Ala Gln Ala Met Ala Pro Pro Lys Phe Arg
    130   135   140
Ser Ser Val Ile Thr Val Gly Pro Ser His Cys Gly Ser Asn Gln Ser
145   150   155   160
Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val Ser Met Ser Asp Arg
                165   170   175
Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser Ser Gly Gly Ser Ser
            180   185   190
Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr Val Ser Gly Thr Ser
        195   200   205
Val Thr Ile Asp Arg Lys Arg Lys His Val Met Asp Ala Asp Gln Glu
    210   215   220
Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser Thr Asp Asp Gln Thr
225   230   235   240
Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser Thr Arg Arg Ser Arg
                245   250   255
Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg Ile
            260   265   270
Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser Arg
        275   280   285
Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys Ser
    290   295   300
Leu Gln Met Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala Ala
305   310   315   320
Ala Ala Ala Ala Ala Ala Ser Pro Met Met Phe Pro Gly Val Gln Ser
                325   330   335
Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser Gln Met Gln Leu Ser
            340   345   350
Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln Asn His Pro Gly Leu
        355   360   365
Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln Ala Gln Asn Gln Ile
    370   375   380
Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly Ile Pro Gln Met Pro
385   390   395   400
Pro Ala Gly Asn Gln Met Gln Thr Val Gln Gln Gln Pro Ala Asp Met
                405   410   415
Leu Gly Phe Gly Ser Pro Ala Gly Pro Gln Ser Gln Leu Ser Ala Pro
            420   425   430

```
Ala Thr Thr Asp Ser Leu His Met Gly Lys Ile Gly
        435                 440


<210> 121
<211> 668
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (47)...(610)

<400> 121
ataacaagcc tagaacacta gaaacttcaa aaaagaaaaa aatctt atg gag aac      55
                                                   Met Glu Asn
                                                    1

aac aac ggc aac aac cag ctg cca ccg aaa ggt aac gag caa ctg aag     103
Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu Gln Leu Lys
     5                  10                  15

agt ttc tgg tca aaa gag atg gaa ggt aac tta gat ttc aaa aat cac     151
Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe Lys Asn His
 20                  25                  30                  35

gac ctt cct ata act cgt atc aag aag att atg aag tat gat ccg gat     199
Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr Asp Pro Asp
                 40                  45                  50

gtg act atg ata gct agt gag gct cca atc ctc ctc tcg aaa gca tgt     247
Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser Lys Ala Cys
             55                  60                  65

gag atg ttt atc atg gat ctc acg atg cgt tcg tgg ctc cat gct cag     295
Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu His Ala Gln
         70                  75                  80

gaa agc aaa cga gtc acg cta cag aaa tct aat gtc gat gcc gca gtg     343
Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp Ala Ala Val
     85                  90                  95

gct caa act gtt atc ttt gat ttc ttg ctt gat gat gac att gag gta     391
Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp Ile Glu Val
100                 105                 110                 115

aag aga gag tct gtt gcc gcc gct gct gat cct gtg gcc atg cca cct     439
Lys Arg Glu Ser Val Ala Ala Ala Ala Asp Pro Val Ala Met Pro Pro
                120                 125                 130

att gac gat gga gag ctg cct cca gga atg gta att gga act cct gtt     487
Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly Thr Pro Val
            135                 140                 145

tgt tgt agt ctt gga atc cac caa cca caa cca caa atg cag gca tgg     535
Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met Gln Ala Trp
        150                 155                 160
```

```
cct gga gct tgg acc tcg gtg tct ggt gag gag gaa gaa gcg cgt ggg    583
Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu Ala Arg Gly
    165                 170                 175

aaa aaa gga ggt gac gac gga aac taa taagtggaat acgttttagg          630
Lys Lys Gly Gly Asp Asp Gly Asn  *
180                 185

gtattttcaa gggaatatgt agtaaatagt catggatc                          668
```

<210> 122
<211> 187
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (30)...(164)
<223> Conserved domain

<400> 122

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Met Glu Asn Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu
 1               5                  10                  15
Gln Leu Lys Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe
            20                  25                  30
Lys Asn His Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr
        35                  40                  45
Asp Pro Asp Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser
    50                  55                  60
Lys Ala Cys Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu
65                  70                  75                  80
His Ala Gln Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp
                85                  90                  95
Ala Ala Val Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp
            100                 105                 110
Ile Glu Val Lys Arg Glu Ser Val Ala Ala Ala Ala Asp Pro Val Ala
        115                 120                 125
Met Pro Pro Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly
    130                 135                 140
Thr Pro Val Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met
145                 150                 155                 160
Gln Ala Trp Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu
                165                 170                 175
Ala Arg Gly Lys Lys Gly Gly Asp Asp Gly Asn
            180                 185
```

<210> 123
<211> 1501
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (111)...(1421)

<400> 123

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tcgacatcag atttctctca cggattccta atcattttta ttatatttgg atatttgcta 60
attcttcccg tgtataaatc tcatataaac acgcatcata catatatatt atg tgc    116
                                                       Met Cys
                                                        1

agc gtc ttt gag ttt caa gac atg gac aac ttc caa gga gat cta aca    164
Ser Val Phe Glu Phe Gln Asp Met Asp Asn Phe Gln Gly Asp Leu Thr
        5                   10                  15

gac gtc gta cga gga ata gga tca ggc cac gtg tca cca tct cct gga    212
Asp Val Val Arg Gly Ile Gly Ser Gly His Val Ser Pro Ser Pro Gly
    20                  25                  30

cca ccg gaa ggt cca tct ccg agc agc atg tct ccg ccg cca aca tca    260
Pro Pro Glu Gly Pro Ser Pro Ser Ser Met Ser Pro Pro Pro Thr Ser
35                  40                  45                  50

gat ctc cac gtg gaa ttc ccc tcc gcc gct act tct gcc agc tgt ctc    308
Asp Leu His Val Glu Phe Pro Ser Ala Ala Thr Ser Ala Ser Cys Leu
                55                  60                  65

gca aat ccc ttc gga gac ccg ttc gta agc atg aag gat cct ctc atc    356
Ala Asn Pro Phe Gly Asp Pro Phe Val Ser Met Lys Asp Pro Leu Ile
            70                  75                  80

cac ctc ccg gcc agc tac atc tcc ggc gcc ggt gat aat aaa agc aac    404
His Leu Pro Ala Ser Tyr Ile Ser Gly Ala Gly Asp Asn Lys Ser Asn
        85                  90                  95

aaa agt ttt gca atc ttt cca aag att ttt gag gat gat cat att aag    452
Lys Ser Phe Ala Ile Phe Pro Lys Ile Phe Glu Asp Asp His Ile Lys
    100                 105                 110

agt caa tgc agt gtc ttc cca aga att aag atc tcg caa agt aac aat    500
Ser Gln Cys Ser Val Phe Pro Arg Ile Lys Ile Ser Gln Ser Asn Asn
115                 120                 125                 130

atc cac gat gcc tcc acg tgt aat tct ccg gcc ata acc gtc tcc tct    548
Ile His Asp Ala Ser Thr Cys Asn Ser Pro Ala Ile Thr Val Ser Ser
                135                 140                 145

gcc gcc gta gca gct tcg ccg tgg ggc atg atc aac gtt aat acc act    596
Ala Ala Val Ala Ala Ser Pro Trp Gly Met Ile Asn Val Asn Thr Thr
            150                 155                 160

aac agt cca aga aac tgt tta ctt gtc gat aat aat aac aac acg tca    644
Asn Ser Pro Arg Asn Cys Leu Leu Val Asp Asn Asn Asn Asn Thr Ser
        165                 170                 175

tca tgc tca cag gtt cag atc tct tct tcc cct cgg aat ctc gga att    692
Ser Cys Ser Gln Val Gln Ile Ser Ser Ser Pro Arg Asn Leu Gly Ile
    180                 185                 190

aag aga agg aag agc cag gca aag aaa gtg gtg tgc ata ccg gct cca    740
Lys Arg Arg Lys Ser Gln Ala Lys Lys Val Val Cys Ile Pro Ala Pro
195                 200                 205                 210
```

```
gcc gct atg aac agc cgg tcc agt gga gaa gtt gtt ccg tct gat cta     788
Ala Ala Met Asn Ser Arg Ser Ser Gly Glu Val Val Pro Ser Asp Leu
                215                 220                 225

tgg gct tgg cga aag tac ggt caa aaa cct atc aaa ggt tct cct tat     836
Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro Tyr
            230                 235                 240

cca agg ggt tac tac aga tgt agc agc tca aaa ggt tgt tca gct agg     884
Pro Arg Gly Tyr Tyr Arg Cys Ser Ser Ser Lys Gly Cys Ser Ala Arg
        245                 250                 255

aaa caa gtc gaa cgt agc cgc act gat cca aac atg tta gtc att act     932
Lys Gln Val Glu Arg Ser Arg Thr Asp Pro Asn Met Leu Val Ile Thr
    260                 265                 270

tac acc tct gag cat aac cac cca tgg cct act caa cgc aac gct ctc     980
Tyr Thr Ser Glu His Asn His Pro Trp Pro Thr Gln Arg Asn Ala Leu
275                 280                 285                 290

gca ggt tcc act cgt tcc tct tcc tcc tcc tct tta aac cct tct tcc     1028
Ala Gly Ser Thr Arg Ser Ser Ser Ser Ser Ser Leu Asn Pro Ser Ser
                295                 300                 305

aaa tcc tca acc gca gcc gcc act act tct ccc tca tcc aga gtt ttc     1076
Lys Ser Ser Thr Ala Ala Ala Thr Thr Ser Pro Ser Ser Arg Val Phe
            310                 315                 320

caa aac aac agc agc aaa gac gaa ccc aat aac tcc aac ttg cct tcc     1124
Gln Asn Asn Ser Ser Lys Asp Glu Pro Asn Asn Ser Asn Leu Pro Ser
        325                 330                 335

tct tcc act cat cct cct ttt gac gcc gcc gca att aag gag gag aac     1172
Ser Ser Thr His Pro Pro Phe Asp Ala Ala Ala Ile Lys Glu Glu Asn
    340                 345                 350

gtg gaa gag cgt cag gaa aag atg gag ttc gat tat aat gac gtt gaa     1220
Val Glu Glu Arg Gln Glu Lys Met Glu Phe Asp Tyr Asn Asp Val Glu
355                 360                 365                 370

aat acc tat aga ccg gag ttg ttg caa gag ttt caa cat cag ccg gag     1268
Asn Thr Tyr Arg Pro Glu Leu Leu Gln Glu Phe Gln His Gln Pro Glu
                375                 380                 385

gat ttc ttt gcc gat ctc gac gag ctt gag gga gat tct ttg act atg     1316
Asp Phe Phe Ala Asp Leu Asp Glu Leu Glu Gly Asp Ser Leu Thr Met
            390                 395                 400

ttg ctc tct cac agt agc ggc gga ggc aac atg gaa aac aaa acg acg     1364
Leu Leu Ser His Ser Ser Gly Gly Gly Asn Met Glu Asn Lys Thr Thr
        405                 410                 415

att cca gac gtt ttt agt gat ttc ttt gac gac gac gag tcc tca agg     1412
Ile Pro Asp Val Phe Ser Asp Phe Phe Asp Asp Asp Glu Ser Ser Arg
    420                 425                 430
```

```
tcg tta taa atattgttgt taatgtatac atagaaatga aattattcat          1461
Ser Leu  *
435

gtaattcgtt ttgtgttaaa tgacggtatt tgcctttgca                      1501

<210> 124
<211> 436
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (223)...(283)
<223> Conserved domain

<400> 124
Met Cys Ser Val Phe Glu Phe Gln Asp Met Asp Asn Phe Gln Gly Asp
 1               5                  10                  15
Leu Thr Asp Val Val Arg Gly Ile Gly Ser Gly His Val Ser Pro Ser
            20                  25                  30
Pro Gly Pro Pro Glu Gly Pro Ser Pro Ser Ser Met Ser Pro Pro Pro
        35                  40                  45
Thr Ser Asp Leu His Val Glu Phe Pro Ser Ala Ala Thr Ser Ala Ser
    50                  55                  60
Cys Leu Ala Asn Pro Phe Gly Asp Pro Phe Val Ser Met Lys Asp Pro
65                  70                  75                  80
Leu Ile His Leu Pro Ala Ser Tyr Ile Ser Gly Ala Gly Asp Asn Lys
                85                  90                  95
Ser Asn Lys Ser Phe Ala Ile Phe Pro Lys Ile Phe Glu Asp Asp His
            100                 105                 110
Ile Lys Ser Gln Cys Ser Val Phe Pro Arg Ile Lys Ile Ser Gln Ser
        115                 120                 125
Asn Asn Ile His Asp Ala Ser Thr Cys Asn Ser Pro Ala Ile Thr Val
    130                 135                 140
Ser Ser Ala Ala Val Ala Ala Ser Pro Trp Gly Met Ile Asn Val Asn
145                 150                 155                 160
Thr Thr Asn Ser Pro Arg Asn Cys Leu Leu Val Asp Asn Asn Asn Asn
                165                 170                 175
Thr Ser Ser Cys Ser Gln Val Gln Ile Ser Ser Ser Pro Arg Asn Leu
            180                 185                 190
Gly Ile Lys Arg Arg Lys Ser Gln Ala Lys Lys Val Val Cys Ile Pro
        195                 200                 205
Ala Pro Ala Ala Met Asn Ser Arg Ser Ser Gly Glu Val Val Pro Ser
    210                 215                 220
Asp Leu Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser
225                 230                 235                 240
Pro Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser Ser Ser Lys Gly Cys Ser
                245                 250                 255
Ala Arg Lys Gln Val Glu Arg Ser Arg Thr Asp Pro Asn Met Leu Val
            260                 265                 270
Ile Thr Tyr Thr Ser Glu His Asn His Pro Trp Pro Thr Gln Arg Asn
        275                 280                 285
Ala Leu Ala Gly Ser Thr Arg Ser Ser Ser Ser Ser Ser Leu Asn Pro
    290                 295                 300
Ser Ser Lys Ser Ser Thr Ala Ala Ala Thr Thr Ser Pro Ser Ser Arg
305                 310                 315                 320
```

```
Val Phe Gln Asn Asn Ser Ser Lys Asp Glu Pro Asn Asn Ser Asn Leu
                325                 330                 335
Pro Ser Ser Ser Thr His Pro Pro Phe Asp Ala Ala Ala Ile Lys Glu
            340                 345                 350
Glu Asn Val Glu Glu Arg Gln Glu Lys Met Glu Phe Asp Tyr Asn Asp
        355                 360                 365
Val Glu Asn Thr Tyr Arg Pro Glu Leu Leu Gln Glu Phe Gln His Gln
    370                 375                 380
Pro Glu Asp Phe Phe Ala Asp Leu Asp Glu Leu Glu Gly Asp Ser Leu
385                 390                 395                 400
Thr Met Leu Leu Ser His Ser Ser Gly Gly Gly Asn Met Glu Asn Lys
                405                 410                 415
Thr Thr Ile Pro Asp Val Phe Ser Asp Phe Phe Asp Asp Asp Glu Ser
            420                 425                 430
Ser Arg Ser Leu
        435


<210> 125
<211> 1828
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (36)...(1622)

<400> 125
gagagctaat aaaaaattta tcaaagaaga ctaat atg gag aag gac gat ttc      53
                                       Met Glu Lys Asp Asp Phe
                                        1               5

ttg agg agt ggt cat gga aga gaa gaa agc cat gat gag atg aga aaa    101
Leu Arg Ser Gly His Gly Arg Glu Glu Ser His Asp Glu Met Arg Lys
            10                  15                  20

ctt gat tca tct cac gat gat tct cat caa gaa cac gac cat att ata    149
Leu Asp Ser Ser His Asp Asp Ser His Gln Glu His Asp His Ile Ile
        25                  30                  35

aga tcc aag ttg gac tca act aaa gtc gaa atg gat gag gct aaa gag    197
Arg Ser Lys Leu Asp Ser Thr Lys Val Glu Met Asp Glu Ala Lys Glu
    40                  45                  50

gaa aat cga aga cta aag tca tca ttg agt aaa atc aag aaa gat ttt    245
Glu Asn Arg Arg Leu Lys Ser Ser Leu Ser Lys Ile Lys Lys Asp Phe
55                  60                  65                  70

gac atc ctt caa aca caa tac aac caa tta atg gcc aaa cat aac gaa    293
Asp Ile Leu Gln Thr Gln Tyr Asn Gln Leu Met Ala Lys His Asn Glu
                75                  80                  85

cca acc aag ttc caa tca aaa ggg cat cat caa gac aaa ggc gaa gat    341
Pro Thr Lys Phe Gln Ser Lys Gly His His Gln Asp Lys Gly Glu Asp
            90                  95                  100

gaa gac aga gaa aaa gtt aac gaa cgt gaa gaa ctt gtc tcg ttg agc    389
```

```
Glu Asp Arg Glu Lys Val Asn Glu Arg Glu Glu Leu Val Ser Leu Ser
        105                 110                 115

cta ggc aga cgg tta aat tca gag gtt cca agt ggt tcg aat aaa gaa      437
Leu Gly Arg Arg Leu Asn Ser Glu Val Pro Ser Gly Ser Asn Lys Glu
    120                 125                 130

gaa aaa aat aaa gat gtt gaa gaa gcg gaa ggt gac aga aat tat gat      485
Glu Lys Asn Lys Asp Val Glu Glu Ala Glu Gly Asp Arg Asn Tyr Asp
135                 140                 145                 150

gat aat gaa aaa agc agt att caa ggg ttg agt atg ggg att gaa tac      533
Asp Asn Glu Lys Ser Ser Ile Gln Gly Leu Ser Met Gly Ile Glu Tyr
                155                 160                 165

aag gct ttg agt aat cct aat gag aag tta gag att gat cat aat caa      581
Lys Ala Leu Ser Asn Pro Asn Glu Lys Leu Glu Ile Asp His Asn Gln
            170                 175                 180

gaa acc atg tcg ttg gag att agt aac aat aat aag atc aga tca caa      629
Glu Thr Met Ser Leu Glu Ile Ser Asn Asn Asn Lys Ile Arg Ser Gln
        185                 190                 195

aat agt ttt ggg ttt aag aat gat gga gat gat cat gaa gat gaa gat      677
Asn Ser Phe Gly Phe Lys Asn Asp Gly Asp Asp His Glu Asp Glu Asp
    200                 205                 210

gag att ttg cct caa aac ctt gtt aag aaa act agg gtt tcg gtg aga      725
Glu Ile Leu Pro Gln Asn Leu Val Lys Lys Thr Arg Val Ser Val Arg
215                 220                 225                 230

tca aga tgt gag aca cca acg atg aac gac gga tgt caa tgg agg aaa      773
Ser Arg Cys Glu Thr Pro Thr Met Asn Asp Gly Cys Gln Trp Arg Lys
                235                 240                 245

tat ggc cag aaa ata gct aaa ggc aat cca tgt ccc cga gct tac tat      821
Tyr Gly Gln Lys Ile Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr
            250                 255                 260

cgt tgc acc att gca gct tct tgt cca gta aga aaa cag gtg caa aga      869
Arg Cys Thr Ile Ala Ala Ser Cys Pro Val Arg Lys Gln Val Gln Arg
        265                 270                 275

tgt tca gaa gat atg tct ata ctt atc tca acg tac gaa gga aca cat      917
Cys Ser Glu Asp Met Ser Ile Leu Ile Ser Thr Tyr Glu Gly Thr His
    280                 285                 290

aac cat cca ctt ccc atg tca gca act gcc atg gcc tct gcc act tcc      965
Asn His Pro Leu Pro Met Ser Ala Thr Ala Met Ala Ser Ala Thr Ser
295                 300                 305                 310

gct gcc gcc tcc atg ctt ctc tcc ggc gcc tcc tcc tcc tca tcc gcc      1013
Ala Ala Ala Ser Met Leu Leu Ser Gly Ala Ser Ser Ser Ser Ser Ala
                315                 320                 325

gca gct gat ctt cat ggc ctt aac ttc tct ctt tcc ggc aac aac atc      1061
Ala Ala Asp Leu His Gly Leu Asn Phe Ser Leu Ser Gly Asn Asn Ile
```

```
            330                           335                           340

act cca aaa cct aaa act cat ttc ctc caa tcc cct tct tct tct ggc     1109
Thr Pro Lys Pro Lys Thr His Phe Leu Gln Ser Pro Ser Ser Ser Gly
        345                 350                 355

cat ccg acc gtc act ctc gac ctc aca acc tcc tcc tcg tcg cag caa     1157
His Pro Thr Val Thr Leu Asp Leu Thr Thr Ser Ser Ser Ser Gln Gln
    360                 365                 370

ccg ttc tta tca atg ctc aat aga ttc agc tct cct cca agt aat gtc     1205
Pro Phe Leu Ser Met Leu Asn Arg Phe Ser Ser Pro Pro Ser Asn Val
375                 380                 385                 390

tca cga tct aat agt tat cct tca acc aat ctc aac ttt tca aac aac     1253
Ser Arg Ser Asn Ser Tyr Pro Ser Thr Asn Leu Asn Phe Ser Asn Asn
                395                 400                 405

acc aac aca ttg atg aat tgg ggt ggt ggt ggt aat ccc agt gat caa     1301
Thr Asn Thr Leu Met Asn Trp Gly Gly Gly Gly Asn Pro Ser Asp Gln
            410                 415                 420

tac cgt gca gct tac ggc aac att aac acc cat cag caa tca cct tac     1349
Tyr Arg Ala Ala Tyr Gly Asn Ile Asn Thr His Gln Gln Ser Pro Tyr
        425                 430                 435

cac aaa atc att caa acc cga acc gcc ggg tca tct ttc gat ccg ttt     1397
His Lys Ile Ile Gln Thr Arg Thr Ala Gly Ser Ser Phe Asp Pro Phe
    440                 445                 450

gga aga tca tct tca tca cat tct cca caa ata aat ctt gat cat atc     1445
Gly Arg Ser Ser Ser Ser His Ser Pro Gln Ile Asn Leu Asp His Ile
455                 460                 465                 470

gga atc aag aac atc atc agt cac caa gtg cca tct tta ccg gct gaa     1493
Gly Ile Lys Asn Ile Ile Ser His Gln Val Pro Ser Leu Pro Ala Glu
                475                 480                 485

aca atc aag gca atc acg aca gat cca agt ttc caa tcg gct ttg gcg     1541
Thr Ile Lys Ala Ile Thr Thr Asp Pro Ser Phe Gln Ser Ala Leu Ala
            490                 495                 500

aca gct cta tct tcc atc atg ggc ggc gat tta aag att gat cac aat     1589
Thr Ala Leu Ser Ser Ile Met Gly Gly Asp Leu Lys Ile Asp His Asn
        505                 510                 515

gtg act aga aat gaa gct gag aag agc cct taa agagaattgt tatatatatg 1642
Val Thr Arg Asn Glu Ala Glu Lys Ser Pro  *
    520                 525

ttcttatata ctcagtacat tggtaaatgg gtttagactt tcactagttt cctagttcat 1702
ctatatattg gttgtttaat cacaagttta ttttgttgtt ggagtttatg gaactaatgt 1762
gtacatatga aactttagaa cgaataaata aaacttggaa ttccttttta aaaaaaaaaa 1822
aaaaaa                                                            1828

<210> 126
<211> 528
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<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (239)...(298)
<223> Conserved domain

<400> 126
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Met Glu Lys Asp Asp Phe Leu Arg Ser Gly His Gly Arg Glu Glu Ser
 1               5                  10                  15
His Asp Glu Met Arg Lys Leu Asp Ser Ser His Asp Asp Ser His Gln
            20                  25                  30
Glu His Asp His Ile Ile Arg Ser Lys Leu Asp Ser Thr Lys Val Glu
        35                  40                  45
Met Asp Glu Ala Lys Glu Glu Asn Arg Arg Leu Lys Ser Ser Leu Ser
    50                  55                  60
Lys Ile Lys Lys Asp Phe Asp Ile Leu Gln Thr Gln Tyr Asn Gln Leu
65                  70                  75                  80
Met Ala Lys His Asn Glu Pro Thr Lys Phe Gln Ser Lys Gly His His
                85                  90                  95
Gln Asp Lys Gly Glu Asp Glu Asp Arg Glu Lys Val Asn Glu Arg Glu
            100                 105                 110
Glu Leu Val Ser Leu Ser Leu Gly Arg Arg Leu Asn Ser Glu Val Pro
        115                 120                 125
Ser Gly Ser Asn Lys Glu Glu Lys Asn Lys Asp Val Glu Glu Ala Glu
    130                 135                 140
Gly Asp Arg Asn Tyr Asp Asp Asn Glu Lys Ser Ser Ile Gln Gly Leu
145                 150                 155                 160
Ser Met Gly Ile Glu Tyr Lys Ala Leu Ser Asn Pro Asn Glu Lys Leu
                165                 170                 175
Glu Ile Asp His Asn Gln Glu Thr Met Ser Leu Glu Ile Ser Asn Asn
            180                 185                 190
Asn Lys Ile Arg Ser Gln Asn Ser Phe Gly Phe Lys Asn Asp Gly Asp
        195                 200                 205
Asp His Glu Asp Glu Asp Glu Ile Leu Pro Gln Asn Leu Val Lys Lys
    210                 215                 220
Thr Arg Val Ser Val Arg Ser Arg Cys Glu Thr Pro Thr Met Asn Asp
225                 230                 235                 240
Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Ile Ala Lys Gly Asn Pro
                245                 250                 255
Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Ile Ala Ala Ser Cys Pro Val
            260                 265                 270
Arg Lys Gln Val Gln Arg Cys Ser Glu Asp Met Ser Ile Leu Ile Ser
        275                 280                 285
Thr Tyr Glu Gly Thr His Asn His Pro Leu Pro Met Ser Ala Thr Ala
    290                 295                 300
Met Ala Ser Ala Thr Ser Ala Ala Ala Ser Met Leu Leu Ser Gly Ala
305                 310                 315                 320
Ser Ser Ser Ser Ser Ala Ala Ala Asp Leu His Gly Leu Asn Phe Ser
                325                 330                 335
Leu Ser Gly Asn Asn Ile Thr Pro Lys Pro Lys Thr His Phe Leu Gln
            340                 345                 350
Ser Pro Ser Ser Ser Gly His Pro Thr Val Thr Leu Asp Leu Thr Thr
        355                 360                 365
Ser Ser Ser Ser Gln Gln Pro Phe Leu Ser Met Leu Asn Arg Phe Ser
    370                 375                 380
```

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Ser Pro Pro Ser Asn Val Ser Arg Ser Asn Ser Tyr Pro Ser Thr Asn
385                 390                 395                 400
Leu Asn Phe Ser Asn Asn Thr Asn Thr Leu Met Asn Trp Gly Gly Gly
                405                 410                 415
Gly Asn Pro Ser Asp Gln Tyr Arg Ala Ala Tyr Gly Asn Ile Asn Thr
            420                 425                 430
His Gln Gln Ser Pro Tyr His Lys Ile Ile Gln Thr Arg Thr Ala Gly
        435                 440                 445
Ser Ser Phe Asp Pro Phe Gly Arg Ser Ser Ser Ser His Ser Pro Gln
    450                 455                 460
Ile Asn Leu Asp His Ile Gly Ile Lys Asn Ile Ile Ser His Gln Val
465                 470                 475                 480
Pro Ser Leu Pro Ala Glu Thr Ile Lys Ala Ile Thr Thr Asp Pro Ser
                485                 490                 495
Phe Gln Ser Ala Leu Ala Thr Ala Leu Ser Ser Ile Met Gly Gly Asp
            500                 505                 510
Leu Lys Ile Asp His Asn Val Thr Arg Asn Glu Ala Glu Lys Ser Pro
        515                 520                 525
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<210> 127
<211> 913
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (81)...(761)

<400> 127

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agaaaacatc tctcactctc taaaatacac actctcatca aaaaccttct cttcggttca 60
gaagcattca agaatccatt atg agc tca tct gat tcc gtt aat aac ggc gtt 113
                      Met Ser Ser Ser Asp Ser Val Asn Asn Gly Val
                       1               5                  10

aac tca cgg atg tac ttc cgt aac ccg agt ttc agc aac gtt atc tta   161
Asn Ser Arg Met Tyr Phe Arg Asn Pro Ser Phe Ser Asn Val Ile Leu
            15                  20                  25

aac gat aac tgg agc gac ttg ccg tta agt gtc gac gat tct caa gac   209
Asn Asp Asn Trp Ser Asp Leu Pro Leu Ser Val Asp Asp Ser Gln Asp
        30                  35                  40

atg gct att tac aac act ctc cgt gat gcc gtt agc tcc ggc tgg aca   257
Met Ala Ile Tyr Asn Thr Leu Arg Asp Ala Val Ser Ser Gly Trp Thr
    45                  50                  55

ccc tcc gtt cct ccc gtt acc tct ccg gcg gag gaa aat aag cct ccg   305
Pro Ser Val Pro Pro Val Thr Ser Pro Ala Glu Glu Asn Lys Pro Pro
60                  65                  70                  75

gcg acg aag gcg agt ggc tca cac gcg ccg agg cag aag ggg atg cag   353
Ala Thr Lys Ala Ser Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln
                80                  85                  90

tac aga gga gtg agg agg agg ccg tgg ggg aaa ttc gcg gcg gag att   401
Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile
```

```
            95                  100                 105

agg gat ccg aag aag aac gga gct agg gtt tgg ctc ggg act tac gag    449
Arg Asp Pro Lys Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu
        110                 115                 120

acg ccg gag gac gcg gcg gtg gcg tac gac cga gcg gcg ttt cag ctc    497
Thr Pro Glu Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu
    125                 130                 135

aga gga tcg aaa gct aag ctg aat ttt ccg cat ttg att ggt tct tgt    545
Arg Gly Ser Lys Ala Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys
140                 145                 150                 155

aag tat gag ccg gtt agg att agg cct cgc cgt cgc tcg ccg gaa ccg    593
Lys Tyr Glu Pro Val Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro
                160                 165                 170

tca gtc tcc gat cag tta acg tcg gag cag aag agg gaa agc cac gtg    641
Ser Val Ser Asp Gln Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val
            175                 180                 185

gat gac ggc gag tct agt ttg gtt gta ccg gag ttg gat ttc acg gtg    689
Asp Asp Gly Glu Ser Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val
        190                 195                 200

gat cag ttt tac ttc gat ggt agt tta tta atg gac caa tca gaa tgt    737
Asp Gln Phe Tyr Phe Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys
    205                 210                 215

tct tat tct gat aat cgg ata taa ttagttttaa gattaagcaa aatttgtcca   791
Ser Tyr Ser Asp Asn Arg Ile  *
220                 225

acgagttttg ctgtatgaaa tatctatcga tgactcaaca ggttttgatc atgatcatat 851
gtaatgtgat ggaaattaaa tattgacgtt tgttttttg ttgtaaaaaa aaaaaaaaaa 911
aa                                                                913

<210> 128
<211> 226
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (89)...(157)
<223> Conserved domain

<400> 128
Met Ser Ser Ser Asp Ser Val Asn Asn Gly Val Asn Ser Arg Met Tyr
 1               5                  10                  15
Phe Arg Asn Pro Ser Phe Ser Asn Val Ile Leu Asn Asp Asn Trp Ser
            20                  25                  30
Asp Leu Pro Leu Ser Val Asp Asp Ser Gln Asp Met Ala Ile Tyr Asn
        35                  40                  45
Thr Leu Arg Asp Ala Val Ser Ser Gly Trp Thr Pro Ser Val Pro Pro
    50                  55                  60
```

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Val Thr Ser Pro Ala Glu Glu Asn Lys Pro Pro Ala Thr Lys Ala Ser
65                  70                  75                  80
Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln Tyr Arg Gly Val Arg
                85                  90                  95
Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys Lys
            100                 105                 110
Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu Thr Pro Glu Asp Ala
        115                 120                 125
Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu Arg Gly Ser Lys Ala
    130                 135                 140
Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys Lys Tyr Glu Pro Val
145                 150                 155                 160
Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro Ser Val Ser Asp Gln
                165                 170                 175
Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val Asp Asp Gly Glu Ser
            180                 185                 190
Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val Asp Gln Phe Tyr Phe
        195                 200                 205
Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys Ser Tyr Ser Asp Asn
    210                 215                 220
Arg Ile
225


<210> 129
<211> 1338
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1338)

<400> 129
atg tcg ttt cga ggc att gtt caa gat ttg aga gat ggg ttt ggg agc      48
Met Ser Phe Arg Gly Ile Val Gln Asp Leu Arg Asp Gly Phe Gly Ser
 1               5                  10                  15

ttg tca agg agg agt ttc gat ttt agg ctc tcg agt ctt cat aaa ggg      96
Leu Ser Arg Arg Ser Phe Asp Phe Arg Leu Ser Ser Leu His Lys Gly
            20                  25                  30

aaa gct cag ggt tct tcg ttc cgt gag tat tcg tca tcc cgt gat ctc     144
Lys Ala Gln Gly Ser Ser Phe Arg Glu Tyr Ser Ser Ser Arg Asp Leu
        35                  40                  45

ttg tcg cct gtg ata gtt cag aca agt aga tgg gct aat ctt cct cca     192
Leu Ser Pro Val Ile Val Gln Thr Ser Arg Trp Ala Asn Leu Pro Pro
    50                  55                  60

gag tta ctc ttt gat gtg atc aaa aga tta gag gaa agt gag agt aat     240
Glu Leu Leu Phe Asp Val Ile Lys Arg Leu Glu Glu Ser Glu Ser Asn
65                  70                  75                  80

tgg cct gca aga aaa cat gtt gtg gct tgt gct tcg gtt tgt cgg tct     288
Trp Pro Ala Arg Lys His Val Val Ala Cys Ala Ser Val Cys Arg Ser
                85                  90                  95
```

```
tgg aga gct atg tgc caa gag att gtt ttg ggg cct gaa atc tgt ggg      336
Trp Arg Ala Met Cys Gln Glu Ile Val Leu Gly Pro Glu Ile Cys Gly
            100                 105                 110

aaa ctc act ttc cct gtt tcc ctc aaa cag cca ggg cct cgt gat gca      384
Lys Leu Thr Phe Pro Val Ser Leu Lys Gln Pro Gly Pro Arg Asp Ala
        115                 120                 125

atg att cag tgt ttc atc aaa agg gat aaa tca aag cta aca ttt cac      432
Met Ile Gln Cys Phe Ile Lys Arg Asp Lys Ser Lys Leu Thr Phe His
    130                 135                 140

ctt ttt ctt tgt tta agt ccc gct cta tta gtg gag aat ggg aaa ttt      480
Leu Phe Leu Cys Leu Ser Pro Ala Leu Leu Val Glu Asn Gly Lys Phe
145                 150                 155                 160

ctt ctt tca gct aaa aga act cgt aga act act cga acc gag tac att      528
Leu Leu Ser Ala Lys Arg Thr Arg Arg Thr Thr Arg Thr Glu Tyr Ile
                165                 170                 175

atc tcc atg gat gct gat aac atc tca aga tcc agc aac tct tac ctc      576
Ile Ser Met Asp Ala Asp Asn Ile Ser Arg Ser Ser Asn Ser Tyr Leu
            180                 185                 190

gga aag ctc aga tca aac ttc ctt ggg aca aag ttc ttg gtg tac gac      624
Gly Lys Leu Arg Ser Asn Phe Leu Gly Thr Lys Phe Leu Val Tyr Asp
        195                 200                 205

acg caa cca cca cca aac aca tct tcg agc gca ctt atc act gat cga      672
Thr Gln Pro Pro Pro Asn Thr Ser Ser Ser Ala Leu Ile Thr Asp Arg
    210                 215                 220

aca agc cga agc agg ttt cac tcc aga cga gtt tct cct aaa gta cca      720
Thr Ser Arg Ser Arg Phe His Ser Arg Arg Val Ser Pro Lys Val Pro
225                 230                 235                 240

tcc gga agc tac aac att gct caa atc acc tat gag ctc aac gtg ttg      768
Ser Gly Ser Tyr Asn Ile Ala Gln Ile Thr Tyr Glu Leu Asn Val Leu
                245                 250                 255

ggc aca cgc ggg cca cga cga atg cac tgc atc atg aac tcc atc cca      816
Gly Thr Arg Gly Pro Arg Arg Met His Cys Ile Met Asn Ser Ile Pro
            260                 265                 270

att tca tcg ctc gaa cca ggc ggt tca gtc cct aac caa ccc gag aaa      864
Ile Ser Ser Leu Glu Pro Gly Gly Ser Val Pro Asn Gln Pro Glu Lys
        275                 280                 285

ctc gtc cct gca cca tac tct ctc gac gac tca ttc cgc agt aac atc      912
Leu Val Pro Ala Pro Tyr Ser Leu Asp Asp Ser Phe Arg Ser Asn Ile
    290                 295                 300

tcc ttc tcc aaa tca tca ttt gac cac cgc tcc ctc gat ttc agc agt      960
Ser Phe Ser Lys Ser Ser Phe Asp His Arg Ser Leu Asp Phe Ser Ser
305                 310                 315                 320
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tct aga ttc tcc gaa atg gga ata tcc tgc gac gac aac gaa gaa gaa     1008
Ser Arg Phe Ser Glu Met Gly Ile Ser Cys Asp Asp Asn Glu Glu Glu
                325                 330                 335

gcg agt ttc aga ccg ttg att cta aag aac aag cag cca agg tgg cac     1056
Ala Ser Phe Arg Pro Leu Ile Leu Lys Asn Lys Gln Pro Arg Trp His
            340                 345                 350

gag cag ttg caa tgc tgg tgt ttg aat ttc cgc gga cgt gtg aca gtt     1104
Glu Gln Leu Gln Cys Trp Cys Leu Asn Phe Arg Gly Arg Val Thr Val
        355                 360                 365

gca tcg gtt aag aat ttc cag ctt gta gca gca aga cag ccg cag cct     1152
Ala Ser Val Lys Asn Phe Gln Leu Val Ala Ala Arg Gln Pro Gln Pro
    370                 375                 380

caa ggg aca ggt gca gca gca gca cca aca agt gca cct gct cac cct     1200
Gln Gly Thr Gly Ala Ala Ala Ala Pro Thr Ser Ala Pro Ala His Pro
385                 390                 395                 400

gag caa gac aag gtg att ctc cag ttt ggt aaa gta ggg aaa gat atg     1248
Glu Gln Asp Lys Val Ile Leu Gln Phe Gly Lys Val Gly Lys Asp Met
                405                 410                 415

ttc aca atg gac tat agg tat cca tta tcg gcg ttt cag gcg ttt gcg     1296
Phe Thr Met Asp Tyr Arg Tyr Pro Leu Ser Ala Phe Gln Ala Phe Ala
            420                 425                 430

ata tgc tta agc agc ttt gac acc aag ctt gct tgt gaa tag             1338
Ile Cys Leu Ser Ser Phe Asp Thr Lys Leu Ala Cys Glu  *
        435                 440                 445


<210> 130
<211> 445
<212> PRT
<213> Arabidopsis thaliana

<400> 130
Met Ser Phe Arg Gly Ile Val Gln Asp Leu Arg Asp Gly Phe Gly Ser
 1               5                  10                  15
Leu Ser Arg Arg Ser Phe Asp Phe Arg Leu Ser Ser Leu His Lys Gly
            20                  25                  30
Lys Ala Gln Gly Ser Ser Phe Arg Glu Tyr Ser Ser Ser Arg Asp Leu
        35                  40                  45
Leu Ser Pro Val Ile Val Gln Thr Ser Arg Trp Ala Asn Leu Pro Pro
    50                  55                  60
Glu Leu Leu Phe Asp Val Ile Lys Arg Leu Glu Glu Ser Glu Ser Asn
65                  70                  75                  80
Trp Pro Ala Arg Lys His Val Val Ala Cys Ala Ser Val Cys Arg Ser
                85                  90                  95
Trp Arg Ala Met Cys Gln Glu Ile Val Leu Gly Pro Glu Ile Cys Gly
            100                 105                 110
Lys Leu Thr Phe Pro Val Ser Leu Lys Gln Pro Gly Pro Arg Asp Ala
        115                 120                 125
Met Ile Gln Cys Phe Ile Lys Arg Asp Lys Ser Lys Leu Thr Phe His
```

130 135 140
Leu Phe Leu Cys Leu Ser Pro Ala Leu Leu Val Glu Asn Gly Lys Phe
145 150 155 160
Leu Leu Ser Ala Lys Arg Thr Arg Arg Thr Thr Arg Thr Glu Tyr Ile
165 170 175
Ile Ser Met Asp Ala Asp Asn Ile Ser Arg Ser Ser Asn Ser Tyr Leu
180 185 190
Gly Lys Leu Arg Ser Asn Phe Leu Gly Thr Lys Phe Leu Val Tyr Asp
195 200 205
Thr Gln Pro Pro Pro Asn Thr Ser Ser Ser Ala Leu Ile Thr Asp Arg
210 215 220
Thr Ser Arg Ser Arg Phe His Ser Arg Arg Val Ser Pro Lys Val Pro
225 230 235 240
Ser Gly Ser Tyr Asn Ile Ala Gln Ile Thr Tyr Glu Leu Asn Val Leu
245 250 255
Gly Thr Arg Gly Pro Arg Arg Met His Cys Ile Met Asn Ser Ile Pro
260 265 270
Ile Ser Ser Leu Glu Pro Gly Gly Ser Val Pro Asn Gln Pro Glu Lys
275 280 285
Leu Val Pro Ala Pro Tyr Ser Leu Asp Asp Ser Phe Arg Ser Asn Ile
290 295 300
Ser Phe Ser Lys Ser Ser Phe Asp His Arg Ser Leu Asp Phe Ser Ser
305 310 315 320
Ser Arg Phe Ser Glu Met Gly Ile Ser Cys Asp Asp Asn Glu Glu Glu
325 330 335
Ala Ser Phe Arg Pro Leu Ile Leu Lys Asn Lys Gln Pro Arg Trp His
340 345 350
Glu Gln Leu Gln Cys Trp Cys Leu Asn Phe Arg Gly Arg Val Thr Val
355 360 365
Ala Ser Val Lys Asn Phe Gln Leu Val Ala Ala Arg Gln Pro Gln Pro
370 375 380
Gln Gly Thr Gly Ala Ala Ala Ala Pro Thr Ser Ala Pro Ala His Pro
385 390 395 400
Glu Gln Asp Lys Val Ile Leu Gln Phe Gly Lys Val Gly Lys Asp Met
405 410 415
Phe Thr Met Asp Tyr Arg Tyr Pro Leu Ser Ala Phe Gln Ala Phe Ala
420 425 430
Ile Cys Leu Ser Ser Phe Asp Thr Lys Leu Ala Cys Glu
435 440 445

<210> 131
<211> 1755
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1755)

<400> 131
atg gct tac atg tgc act gat agt ggc aat cta atg gct att gct caa 48
Met Ala Tyr Met Cys Thr Asp Ser Gly Asn Leu Met Ala Ile Ala Gln
1 5 10 15

caa gtc atc aaa cag aag cag caa caa gaa caa caa cag cag caa cat 96
Gln Val Ile Lys Gln Lys Gln Gln Gln Glu Gln Gln Gln Gln Gln His

```
            20                  25                  30

cat caa gac cat cag att ttt ggt att aat cct ttg tct ctt aac cca      144
His Gln Asp His Gln Ile Phe Gly Ile Asn Pro Leu Ser Leu Asn Pro
        35                  40                  45

tgg ccc aat act tcc ctc ggg ttt ggg ctt tca ggt tcg gct ttt ccc      192
Trp Pro Asn Thr Ser Leu Gly Phe Gly Leu Ser Gly Ser Ala Phe Pro
    50                  55                  60

gac ccg ttt caa gtt acc ggc ggc gga gat tcc aac gat cct ggc ttt      240
Asp Pro Phe Gln Val Thr Gly Gly Gly Asp Ser Asn Asp Pro Gly Phe
65                  70                  75                  80

cct ttt cct aac tta gac cac cac cac gcc aca acc acc ggc ggt ggg      288
Pro Phe Pro Asn Leu Asp His His His Ala Thr Thr Thr Gly Gly Gly
                85                  90                  95

ttc agg tta tct gat ttc ggc ggt gga acc ggc ggc ggc gag ttt gag      336
Phe Arg Leu Ser Asp Phe Gly Gly Gly Thr Gly Gly Gly Glu Phe Glu
            100                 105                 110

tcc gac gag tgg atg gag act ctt atc agc ggt gga gac tcc gtt gca      384
Ser Asp Glu Trp Met Glu Thr Leu Ile Ser Gly Gly Asp Ser Val Ala
        115                 120                 125

gac ggt cct gat tgt gac acc tgg cat gat aat ccc gat tac gta atc      432
Asp Gly Pro Asp Cys Asp Thr Trp His Asp Asn Pro Asp Tyr Val Ile
    130                 135                 140

tac ggt cct gat cca ttc gat act tac ccg agt cga ctc agt gtc caa      480
Tyr Gly Pro Asp Pro Phe Asp Thr Tyr Pro Ser Arg Leu Ser Val Gln
145                 150                 155                 160

ccg tca gat cta aac cga gtc att gac acg tcg agt ccg ctt cct ccg      528
Pro Ser Asp Leu Asn Arg Val Ile Asp Thr Ser Ser Pro Leu Pro Pro
                165                 170                 175

ccg acc ttg tgg cct cct tct tcg cca tta tcg att cct ccg ctt act      576
Pro Thr Leu Trp Pro Pro Ser Ser Pro Leu Ser Ile Pro Pro Leu Thr
            180                 185                 190

cat gag tca cca acc aaa gaa gat cca gag act aac gac tcc gaa gac      624
His Glu Ser Pro Thr Lys Glu Asp Pro Glu Thr Asn Asp Ser Glu Asp
        195                 200                 205

gat gac ttc gac cta gaa cca cct ctc ctc aaa gct ata tac gac tgt      672
Asp Asp Phe Asp Leu Glu Pro Pro Leu Leu Lys Ala Ile Tyr Asp Cys
    210                 215                 220

gca cgg atc tca gac tct gac cct aac gaa gct tcc aag acg ctt ctt      720
Ala Arg Ile Ser Asp Ser Asp Pro Asn Glu Ala Ser Lys Thr Leu Leu
225                 230                 235                 240

cag atc cga gaa tct gta tcg gag cta ggt gat ccg acg gag cga gtt      768
Gln Ile Arg Glu Ser Val Ser Glu Leu Gly Asp Pro Thr Glu Arg Val
                245                 250                 255
```

```
gca ttt tac ttc acg gaa gct ctc tcc aac aga ctg tct cct aat tcg    816
Ala Phe Tyr Phe Thr Glu Ala Leu Ser Asn Arg Leu Ser Pro Asn Ser
            260                 265                 270

ccg gcg acg tcg tct tct tct tca tct acg gag gat tta atc tta tct    864
Pro Ala Thr Ser Ser Ser Ser Ser Ser Thr Glu Asp Leu Ile Leu Ser
        275                 280                 285

tat aaa acc cta aac gac gct tgt cct tac tcc aaa ttc gca cat ttg    912
Tyr Lys Thr Leu Asn Asp Ala Cys Pro Tyr Ser Lys Phe Ala His Leu
    290                 295                 300

acg gcg aat caa gcg att cta gaa gcg acg gag aag tcg aac aag att    960
Thr Ala Asn Gln Ala Ile Leu Glu Ala Thr Glu Lys Ser Asn Lys Ile
305                 310                 315                 320

cac atc gtc gat ttt gga atc gtt caa ggt ata caa tgg cct gct ctt    1008
His Ile Val Asp Phe Gly Ile Val Gln Gly Ile Gln Trp Pro Ala Leu
                325                 330                 335

ctt caa gct cta gct act cgt act tct ggt aaa ccc act caa atc cgg    1056
Leu Gln Ala Leu Ala Thr Arg Thr Ser Gly Lys Pro Thr Gln Ile Arg
            340                 345                 350

gtc tcg ggt ata ccc gct cca tct ctc ggt gaa tct ccg gaa ccg tcg    1104
Val Ser Gly Ile Pro Ala Pro Ser Leu Gly Glu Ser Pro Glu Pro Ser
        355                 360                 365

tta atc gcc acc gga aac cgc ctc cgt gat ttc gcc aag gtt ctg gat    1152
Leu Ile Ala Thr Gly Asn Arg Leu Arg Asp Phe Ala Lys Val Leu Asp
    370                 375                 380

ctg aat ttc gat ttc atc cca att ctc act ccc ata cat tta ctt aac    1200
Leu Asn Phe Asp Phe Ile Pro Ile Leu Thr Pro Ile His Leu Leu Asn
385                 390                 395                 400

ggg tca agt ttc cgg gtc gac ccg gat gaa gta ctg gcc gtg aat ttc    1248
Gly Ser Ser Phe Arg Val Asp Pro Asp Glu Val Leu Ala Val Asn Phe
                405                 410                 415

atg ctc cag ctc tac aaa tta ctc gac gag acg ccg acg ata gtt gac    1296
Met Leu Gln Leu Tyr Lys Leu Leu Asp Glu Thr Pro Thr Ile Val Asp
            420                 425                 430

acc gca cta cgg ctc gcc aaa tcg ttg aac ccg agg gtc gtc act ctc    1344
Thr Ala Leu Arg Leu Ala Lys Ser Leu Asn Pro Arg Val Val Thr Leu
        435                 440                 445

gga gaa tac gaa gtg agc tta aac cgg gtc ggt ttc gct aac cgg gta    1392
Gly Glu Tyr Glu Val Ser Leu Asn Arg Val Gly Phe Ala Asn Arg Val
    450                 455                 460

aag aac gcg ctt caa ttc tat tcc gcg gtt ttc gaa tcc ctt gaa ccg    1440
Lys Asn Ala Leu Gln Phe Tyr Ser Ala Val Phe Glu Ser Leu Glu Pro
465                 470                 475                 480
```

aac ttg ggg cgt gat tcg gag gag aga gtg aga gtt gag cga gag ttg 1488
Asn Leu Gly Arg Asp Ser Glu Glu Arg Val Arg Val Glu Arg Glu Leu
485 490 495

ttc ggc cgg aga atc tcg ggt ttg att gga ccg gag aaa acc gga att 1536
Phe Gly Arg Arg Ile Ser Gly Leu Ile Gly Pro Glu Lys Thr Gly Ile
500 505 510

cat aga gaa aga atg gaa gag aaa gag caa tgg cgg gta tta atg gag 1584
His Arg Glu Arg Met Glu Glu Lys Glu Gln Trp Arg Val Leu Met Glu
515 520 525

aat gcc ggt ttt gaa tcg gtt aag ctg agt aat tac gca gtg agc caa 1632
Asn Ala Gly Phe Glu Ser Val Lys Leu Ser Asn Tyr Ala Val Ser Gln
530 535 540

gcg aag att cta ttg tgg aat tac aat tac agc aat ttg tat tca att 1680
Ala Lys Ile Leu Leu Trp Asn Tyr Asn Tyr Ser Asn Leu Tyr Ser Ile
545 550 555 560

gtt gaa tct aag cct ggc ttc atc tct ttg gcc tgg aac gat tta cct 1728
Val Glu Ser Lys Pro Gly Phe Ile Ser Leu Ala Trp Asn Asp Leu Pro
565 570 575

ctc ctc act ctt tct tcc tgg cga taa 1755
Leu Leu Thr Leu Ser Ser Trp Arg *
580

<210> 132
<211> 584
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (320)...(336)
<223> Conserved domain

<400> 132
Met Ala Tyr Met Cys Thr Asp Ser Gly Asn Leu Met Ala Ile Ala Gln
1 5 10 15
Gln Val Ile Lys Gln Lys Gln Gln Gln Glu Gln Gln Gln Gln Gln His
20 25 30
His Gln Asp His Gln Ile Phe Gly Ile Asn Pro Leu Ser Leu Asn Pro
35 40 45
Trp Pro Asn Thr Ser Leu Gly Phe Gly Leu Ser Gly Ser Ala Phe Pro
50 55 60
Asp Pro Phe Gln Val Thr Gly Gly Gly Asp Ser Asn Asp Pro Gly Phe
65 70 75 80
Pro Phe Pro Asn Leu Asp His His His Ala Thr Thr Thr Gly Gly Gly
85 90 95
Phe Arg Leu Ser Asp Phe Gly Gly Gly Thr Gly Gly Gly Glu Phe Glu
100 105 110
Ser Asp Glu Trp Met Glu Thr Leu Ile Ser Gly Gly Asp Ser Val Ala
115 120 125
Asp Gly Pro Asp Cys Asp Thr Trp His Asp Asn Pro Asp Tyr Val Ile

```
    130                 135                 140
Tyr Gly Pro Asp Pro Phe Asp Thr Tyr Pro Ser Arg Leu Ser Val Gln
145                 150                 155                 160
Pro Ser Asp Leu Asn Arg Val Ile Asp Thr Ser Ser Pro Leu Pro Pro
                165                 170                 175
Pro Thr Leu Trp Pro Pro Ser Ser Pro Leu Ser Ile Pro Pro Leu Thr
            180                 185                 190
His Glu Ser Pro Thr Lys Glu Asp Pro Glu Thr Asn Asp Ser Glu Asp
        195                 200                 205
Asp Asp Phe Asp Leu Glu Pro Pro Leu Leu Lys Ala Ile Tyr Asp Cys
    210                 215                 220
Ala Arg Ile Ser Asp Ser Asp Pro Asn Glu Ala Ser Lys Thr Leu Leu
225                 230                 235                 240
Gln Ile Arg Glu Ser Val Ser Glu Leu Gly Asp Pro Thr Glu Arg Val
                245                 250                 255
Ala Phe Tyr Phe Thr Glu Ala Leu Ser Asn Arg Leu Ser Pro Asn Ser
            260                 265                 270
Pro Ala Thr Ser Ser Ser Ser Ser Ser Thr Glu Asp Leu Ile Leu Ser
        275                 280                 285
Tyr Lys Thr Leu Asn Asp Ala Cys Pro Tyr Ser Lys Phe Ala His Leu
    290                 295                 300
Thr Ala Asn Gln Ala Ile Leu Glu Ala Thr Glu Lys Ser Asn Lys Ile
305                 310                 315                 320
His Ile Val Asp Phe Gly Ile Val Gln Gly Ile Gln Trp Pro Ala Leu
                325                 330                 335
Leu Gln Ala Leu Ala Thr Arg Thr Ser Gly Lys Pro Thr Gln Ile Arg
            340                 345                 350
Val Ser Gly Ile Pro Ala Pro Ser Leu Gly Glu Ser Pro Glu Pro Ser
        355                 360                 365
Leu Ile Ala Thr Gly Asn Arg Leu Arg Asp Phe Ala Lys Val Leu Asp
    370                 375                 380
Leu Asn Phe Asp Phe Ile Pro Ile Leu Thr Pro Ile His Leu Leu Asn
385                 390                 395                 400
Gly Ser Ser Phe Arg Val Asp Pro Asp Glu Val Leu Ala Val Asn Phe
                405                 410                 415
Met Leu Gln Leu Tyr Lys Leu Leu Asp Glu Thr Pro Thr Ile Val Asp
            420                 425                 430
Thr Ala Leu Arg Leu Ala Lys Ser Leu Asn Pro Arg Val Val Thr Leu
        435                 440                 445
Gly Glu Tyr Glu Val Ser Leu Asn Arg Val Gly Phe Ala Asn Arg Val
    450                 455                 460
Lys Asn Ala Leu Gln Phe Tyr Ser Ala Val Phe Glu Ser Leu Glu Pro
465                 470                 475                 480
Asn Leu Gly Arg Asp Ser Glu Glu Arg Val Arg Val Glu Arg Glu Leu
                485                 490                 495
Phe Gly Arg Arg Ile Ser Gly Leu Ile Gly Pro Glu Lys Thr Gly Ile
            500                 505                 510
His Arg Glu Arg Met Glu Glu Lys Glu Gln Trp Arg Val Leu Met Glu
        515                 520                 525
Asn Ala Gly Phe Glu Ser Val Lys Leu Ser Asn Tyr Ala Val Ser Gln
    530                 535                 540
Ala Lys Ile Leu Leu Trp Asn Tyr Asn Tyr Ser Asn Leu Tyr Ser Ile
545                 550                 555                 560
Val Glu Ser Lys Pro Gly Phe Ile Ser Leu Ala Trp Asn Asp Leu Pro
                565                 570                 575
Leu Leu Thr Leu Ser Ser Trp Arg
            580
```

<210> 133
<211> 1065
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (188)...(760)

<400> 133
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tcgacccacg cgtccggaca cttaacaatt cacaccttct ctttttactc ttcctaaaac 60
cctaaatttc ctcgcttcag tcttcccact caagtcaacc accaattgaa ttcgatttcg 120
aatcattgat ggaaatgatt tgaaaaaaga gtaaagttta ttttttttatt ccttgtaatt 180
ttcagaa atg ggg gat tcc gac agg gat tcc ggt gga ggg caa aac ggg   229
        Met Gly Asp Ser Asp Arg Asp Ser Gly Gly Gly Gln Asn Gly
         1               5                  10

aac aac cag aac gga cag tcc tcc ttg tct cca aga gag caa gac agg   277
Asn Asn Gln Asn Gly Gln Ser Ser Leu Ser Pro Arg Glu Gln Asp Arg
 15                  20                  25                  30

ttc ttg ccg atc gct aac gtc agc cgg atc atg aag aag gcc ttg ccc   325
Phe Leu Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro
                 35                  40                  45

gcc aac gcc aag atc tct aaa gat gcc aaa gag acg atg cag gag tgt   373
Ala Asn Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys
             50                  55                  60

gtc tcc gag ttc atc agc ttc gtc acc gga gaa gca tct gat aag tgt   421
Val Ser Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys
         65                  70                  75

cag aag gag aag agg aag acg atc aac gga gac gat ttg ctc tgg gct   469
Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala
     80                  85                  90

atg act act cta ggt ttt gag gat tat gtt gag cca ttg aaa gtt tac   517
Met Thr Thr Leu Gly Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr
 95                 100                 105                 110

ttg cag agg ttt agg gag atc gaa ggg gag agg act gga cta ggg agg   565
Leu Gln Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg
                115                 120                 125

cca cag act ggt ggt gag gtc gga gag cat cag aga gat gct gtc gga   613
Pro Gln Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly
            130                 135                 140

gat ggc ggt ggg ttc tac ggt ggt ggt ggt ggg atg cag tat cac caa   661
Asp Gly Gly Gly Phe Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln
        145                 150                 155

cat cat cag ttt ctt cac cag cag aac cat atg tat gga gcc aca ggt   709
His His Gln Phe Leu His Gln Gln Asn His Met Tyr Gly Ala Thr Gly
```

```
    160                 165                 170

ggc ggt agc gac agt gga ggt gga gct gcc tcc ggt agg aca agg act    757
Gly Gly Ser Asp Ser Gly Gly Gly Ala Ala Ser Gly Arg Thr Arg Thr
175                 180                 185                 190

taa caaagattgg tgaagtggat ctctctctgt atatagatac ataaatacat        810
 *

gtatacacat gcctattttt acgacccata taaggtatct atcatgtgat agaacgaaca 870
ttggtgttgg tgatgtaaaa tcagatgtgc attaagggtt tagattttga ggctgtgtaa 930
aagaagatca agtgtgcttt gttggacaat aggattcact aacgaatctg cttcattgga 990
tcttgtatgt aactaaagcc attgtattga atgcaaatgt tttcatttgg gatgctttaa 1050
aaaaaaaaaa aaaaa                                                  1065

<210> 134
<211> 190
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (25)...(116)
<223> Conserved domain

<400> 134
Met Gly Asp Ser Asp Arg Asp Ser Gly Gly Gly Gln Asn Gly Asn Asn
 1               5                  10                  15
Gln Asn Gly Gln Ser Ser Leu Ser Pro Arg Glu Gln Asp Arg Phe Leu
            20                  25                  30
Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
        35                  40                  45
Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys Val Ser
    50                  55                  60
Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys
65                  70                  75                  80
Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
                85                  90                  95
Thr Leu Gly Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln
            100                 105                 110
Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln
        115                 120                 125
Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly
    130                 135                 140
Gly Gly Phe Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln His His
145                 150                 155                 160
Gln Phe Leu His Gln Gln Asn His Met Tyr Gly Ala Thr Gly Gly Gly
                165                 170                 175
Ser Asp Ser Gly Gly Gly Ala Ala Ser Gly Arg Thr Arg Thr
            180                 185                 190

<210> 135
<211> 1009
<212> DNA
<213> Arabidopsis thaliana
```

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<220>
<221> CDS
<222> (27)...(746)

<400> 135
gatagtgata acgaaatcct aattcc atg gcc gac aac gac gga gca gtg agt  53
                             Met Ala Asp Asn Asp Gly Ala Val Ser
                              1               5

aac ggc atc ata gtc gag cag acg tca aac aaa gga cct ctt aac gcc   101
Asn Gly Ile Ile Val Glu Gln Thr Ser Asn Lys Gly Pro Leu Asn Ala
 10                  15                  20                  25

gtt aag aaa cca ccg tct aaa gat cga cac agc aaa gtt gac gga aga   149
Val Lys Lys Pro Pro Ser Lys Asp Arg His Ser Lys Val Asp Gly Arg
                 30                  35                  40

gga aga agg att cgt atg cca atc att tgc gca gct cga gtt ttt caa   197
Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe Gln
             45                  50                  55

ttg acc aga gag tta ggt cac aag tcc gat ggt caa acc ata gag tgg   245
Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu Trp
         60                  65                  70

ctt ctc cgt caa gct gag cct tct atc ata gcc gcc act gga act ggc   293
Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly
     75                  80                  85

act act ccg gcg agt ttc tcc act gct tct ctc tcc act tct tct ccg   341
Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Leu Ser Thr Ser Ser Pro
 90                  95                 100                 105

ttt act ctc ggg aaa cgt gtc gtc aga gcg gag gaa gga gaa tcc ggc   389
Phe Thr Leu Gly Lys Arg Val Val Arg Ala Glu Glu Gly Glu Ser Gly
                110                 115                 120

ggc gga gga gga gga ggg tta aca gtg gga cac aca atg ggg act tcg   437
Gly Gly Gly Gly Gly Gly Leu Thr Val Gly His Thr Met Gly Thr Ser
            125                 130                 135

tta atg ggt ggt ggt ggt tct ggt ggg ttt tgg gct gtt ccg gcg agg   485
Leu Met Gly Gly Gly Gly Ser Gly Gly Phe Trp Ala Val Pro Ala Arg
        140                 145                 150

ccg gat ttc gga caa gtc tgg agc ttt gca acc gga gct cca ccg gaa   533
Pro Asp Phe Gly Gln Val Trp Ser Phe Ala Thr Gly Ala Pro Pro Glu
    155                 160                 165

atg gtt ttt gcg cag cag cag caa cca gct aca ctc ttc gtc cgc cac   581
Met Val Phe Ala Gln Gln Gln Gln Pro Ala Thr Leu Phe Val Arg His
170                 175                 180                 185

cag cag caa cag caa gct tcc gcc gcc gca gca gct gca atg ggt gag   629
Gln Gln Gln Gln Gln Ala Ser Ala Ala Ala Ala Ala Ala Met Gly Glu
                190                 195                 200
```

gct tca gca gct aga gtt ggg aat tat ctt ccg ggt cat cat ctc aat 677
Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His His Leu Asn
205 210 215

ttg ctt gct tct ttg tct ggt gga gct aac ggg tcg ggt cgg agg gaa 725
Leu Leu Ala Ser Leu Ser Gly Gly Ala Asn Gly Ser Gly Arg Arg Glu
220 225 230

gac gac cac gaa cca cgt tga gaaatggtat tgtctttttg gtaatgtata 776
Asp Asp His Glu Pro Arg *
235

gaaaaattcc tatgttttat gtcatcgaaa gtgtttagaa agtacctcta atttgcggtt 836
tcttttgctc ctttttttact taatttaagc ttattgcttg tttgattagg gttttagggt 896
ttaagaatat ttggtctcgt taatttgttt cggagagtga tagaaagaga gagagattga 956
ttgattgttg tacctaaaac gctataaaag ctctgttttt actagcgaaa aaa 1009

<210> 136
<211> 239
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (32)...(93)
<223> Conserved domain

<400> 136
Met Ala Asp Asn Asp Gly Ala Val Ser Asn Gly Ile Ile Val Glu Gln
1 5 10 15
Thr Ser Asn Lys Gly Pro Leu Asn Ala Val Lys Lys Pro Pro Ser Lys
20 25 30
Asp Arg His Ser Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met Pro
35 40 45
Ile Ile Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu Gly His
50 55 60
Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu Pro
65 70 75 80
Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe Ser
85 90 95
Thr Ala Ser Leu Ser Thr Ser Ser Pro Phe Thr Leu Gly Lys Arg Val
100 105 110
Val Arg Ala Glu Glu Gly Glu Ser Gly Gly Gly Gly Gly Gly Gly Leu
115 120 125
Thr Val Gly His Thr Met Gly Thr Ser Leu Met Gly Gly Gly Gly Ser
130 135 140
Gly Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp
145 150 155 160
Ser Phe Ala Thr Gly Ala Pro Pro Glu Met Val Phe Ala Gln Gln Gln
165 170 175
Gln Pro Ala Thr Leu Phe Val Arg His Gln Gln Gln Gln Gln Ala Ser
180 185 190
Ala Ala Ala Ala Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly
195 200 205
Asn Tyr Leu Pro Gly His His Leu Asn Leu Leu Ala Ser Leu Ser Gly
210 215 220

```
Gly Ala Asn Gly Ser Gly Arg Arg Glu Asp Asp His Glu Pro Arg
225                 230                 235


<210> 137
<211> 1281
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (64)...(1098)

<400> 137
cacaacacaa acacatttct gttttctcca ttgtttcaaa ccataaaaaa aaacacagat 60
taa atg gaa tcg agt agc gtt gat gag agt act aca agt aca ggt tcc   108
    Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser
     1               5                  10                  15

atc tgt gaa acc ccg gcg ata act ccg gcg aaa aag tcg tcg gta ggt   156
Ile Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly
                20                  25                  30

aac tta tac agg atg gga agc gga tca agc gtt gtg tta gat tca gag   204
Asn Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu
            35                  40                  45

aac ggc gta gaa gct gaa tct agg aag ctt ccg tcg tca aaa tac aaa   252
Asn Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys
        50                  55                  60

ggt gtg gtg cca caa cca aac gga aga tgg gga gct cag att tac gag   300
Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu
    65                  70                  75

aaa cac cag cgc gtg tgg ctc ggg aca ttc aac gaa gaa gac gaa gcc   348
Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala
80                  85                  90                  95

gct cgt gcc tac gac gtc gcg gtt cac agg ttc cgt cgc cgt gac gcc   396
Ala Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala
                100                 105                 110

gtc aca aat ttc aaa gac gtg aag atg gac gaa gac gag gtc gat ttc   444
Val Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe
            115                 120                 125

ttg aat tct cat tcg aaa tct gag atc gtt gat atg ttg agg aaa cat   492
Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His
        130                 135                 140

act tat aac gaa gag tta gag cag agt aaa cgg cgt cgt aat ggt aac   540
Thr Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn
    145                 150                 155

gga aac atg act agg acg ttg tta acg tcg ggg ttg agt aat gat ggt   588
Gly Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly
```

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160                 165                 170                 175

gtt tct acg acg ggg ttt aga tcg gcg gag gca ctg ttt gag aaa gcg     636
Val Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala
                180                 185                 190

gta acg cca agc gac gtt ggg aag cta aac cgt ttg gtt ata ccg aaa     684
Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
            195                 200                 205

cat cac gca gag aaa cat ttt ccg tta ccg tca agt aac gtt tcc gtg     732
His His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val
        210                 215                 220

aaa gga gtg ttg ttg aac ttt gag gac gtt aac ggg aaa gtg tgg agg     780
Lys Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg
    225                 230                 235

ttc cgt tac tcg tat tgg aac agt agt cag agt tat gtt ttg act aaa     828
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
240                 245                 250                 255

ggt tgg agc agg ttc gtt aag gag aag aat cta cgt gct ggt gac gtg     876
Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val
                260                 265                 270

gtt agt ttc agt aga tct aac ggt cag gat caa cag ttg tac att ggg     924
Val Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly
            275                 280                 285

tgg aag tcg aga tcc ggg tca gat tta gat gcg ggt cgg gtt ttg aga     972
Trp Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg
        290                 295                 300

ttg ttc gga gtt aac att tca ccg gag agt tca aga aac gac gtc gta     1020
Leu Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val
    305                 310                 315

gga aac aaa aga gtg aac gat act gag atg tta tcg ttg gtg tgt agc     1068
Gly Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser
320                 325                 330                 335

aag aag caa cgc atc ttt cac gcc tcg taa caactcttct tcttttttt      1118
Lys Lys Gln Arg Ile Phe His Ala Ser  *
                340

tcttttgttg ttttaataat ttttaaaaac tccattttcg ttttctttat ttgcatcggt 1178
ttctttcttc ttgtttacca aaggttcatg agttgttttt gttgtattga tgaactgtaa 1238
attttattta taggataaat tttaaaaaaa aaaaaaaaaa aaa                   1281
```

<210> 138
<211> 344
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN

<222> (59)...(124)
<223> Conserved domain

<400> 138
Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser Ile
1 5 10 15
Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly Asn
20 25 30
Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu Asn
35 40 45
Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly
50 55 60
Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65 70 75 80
His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
85 90 95
Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala Val
100 105 110
Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe Leu
115 120 125
Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr
130 135 140
Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn Gly
145 150 155 160
Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly Val
165 170 175
Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala Val
180 185 190
Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His
195 200 205
His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val Lys
210 215 220
Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe
225 230 235 240
Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
245 250 255
Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
260 265 270
Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly Trp
275 280 285
Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg Leu
290 295 300
Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val Gly
305 310 315 320
Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser Lys
325 330 335
Lys Gln Arg Ile Phe His Ala Ser
340

<210> 139
<211> 1879
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS

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<222> (31)...(1575)

<400> 139
ttttttttg tttgttaatt ttggggatcg atg tcg gaa aag gaa gaa gct ccg  54
                                Met Ser Glu Lys Glu Glu Ala Pro
                                 1               5

tcg aca tcg aag tcc acc gga gct ccg tcg cgt ccg act tta tct ctt  102
Ser Thr Ser Lys Ser Thr Gly Ala Pro Ser Arg Pro Thr Leu Ser Leu
     10                  15                  20

cct cca cgg ccg ttt agt gag atg ttc ttt aac ggt ggc gtt gga ttc  150
Pro Pro Arg Pro Phe Ser Glu Met Phe Phe Asn Gly Gly Val Gly Phe
 25                  30                  35                  40

agt cct ggt ccg atg act ctg gtc tct aat atg ttc cct gat tcc gat  198
Ser Pro Gly Pro Met Thr Leu Val Ser Asn Met Phe Pro Asp Ser Asp
                 45                  50                  55

gag ttt agg tct ttc tct cag ctt ctc gct gga gcc atg tct tct cca  246
Glu Phe Arg Ser Phe Ser Gln Leu Leu Ala Gly Ala Met Ser Ser Pro
             60                  65                  70

gcg act gca gct gct gct gct gct gct gcg acg gct agt gat tac cag  294
Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Thr Ala Ser Asp Tyr Gln
         75                  80                  85

aga ctt ggt gaa ggg act aat agc tct agt ggt gat gtt gac ccg aga  342
Arg Leu Gly Glu Gly Thr Asn Ser Ser Ser Gly Asp Val Asp Pro Arg
     90                  95                 100

ttc aag caa aac aga cca acc ggt ttg atg att tct caa tct caa tcg  390
Phe Lys Gln Asn Arg Pro Thr Gly Leu Met Ile Ser Gln Ser Gln Ser
105                 110                 115                 120

ccg tcg atg ttc acc gta ccg cct ggt tta agt cca gct atg ttg ctc  438
Pro Ser Met Phe Thr Val Pro Pro Gly Leu Ser Pro Ala Met Leu Leu
                125                 130                 135

gat tca cca agc ttt ttg ggt ctt ttc tct ccc gtt cag gga tca tat  486
Asp Ser Pro Ser Phe Leu Gly Leu Phe Ser Pro Val Gln Gly Ser Tyr
            140                 145                 150

gga atg aca cat cag caa gct cta gct caa gtc act gct caa gca gtt  534
Gly Met Thr His Gln Gln Ala Leu Ala Gln Val Thr Ala Gln Ala Val
        155                 160                 165

caa gcc aat gcc aat atg caa cca caa aca gag tac cct cct ccc tct  582
Gln Ala Asn Ala Asn Met Gln Pro Gln Thr Glu Tyr Pro Pro Pro Ser
    170                 175                 180

caa gtt caa tca ttt tca tcg ggt caa gcg cag atc ccg acc tcg gct  630
Gln Val Gln Ser Phe Ser Ser Gly Gln Ala Gln Ile Pro Thr Ser Ala
185                 190                 195                 200

cca cta cca gct caa aga gaa acc tca gat gta acc atc ata gag cac  678
Pro Leu Pro Ala Gln Arg Glu Thr Ser Asp Val Thr Ile Ile Glu His
```

```
                205                     210                     215

agg tca caa cag cct cta aat gtt gac aaa cca gct gat gat ggc tat     726
Arg Ser Gln Gln Pro Leu Asn Val Asp Lys Pro Ala Asp Asp Gly Tyr
            220                 225                 230

aac tgg cga aaa tat ggg caa aag caa gtt aaa ggt agc gag ttt cca     774
Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Phe Pro
        235                 240                 245

cga agc tat tac aag tgt act aat cca gga tgt cct gtc aag aag aag     822
Arg Ser Tyr Tyr Lys Cys Thr Asn Pro Gly Cys Pro Val Lys Lys Lys
    250                 255                 260

gtt gag aga tct ctt gat gga caa gta acg gag att atc tac aaa ggt     870
Val Glu Arg Ser Leu Asp Gly Gln Val Thr Glu Ile Ile Tyr Lys Gly
265                 270                 275                 280

cag cac aat cat gaa cct cct caa aac act aag cga ggt aac aaa gat     918
Gln His Asn His Glu Pro Pro Gln Asn Thr Lys Arg Gly Asn Lys Asp
                285                 290                 295

aac acc gcg aat ata aat ggg agt tcg ata aat aac aat cgc ggg agt     966
Asn Thr Ala Asn Ile Asn Gly Ser Ser Ile Asn Asn Asn Arg Gly Ser
            300                 305                 310

tct gaa ttg ggg gca tca cag ttt caa act aat agc tcc aac aag act     1014
Ser Glu Leu Gly Ala Ser Gln Phe Gln Thr Asn Ser Ser Asn Lys Thr
        315                 320                 325

aag aga gag caa cat gaa gca gta agt caa gct acg aca aca gag cac     1062
Lys Arg Glu Gln His Glu Ala Val Ser Gln Ala Thr Thr Thr Glu His
    330                 335                 340

ttg tct gag gca agt gac ggt gaa gaa gtt ggt aat gga gaa act gat     1110
Leu Ser Glu Ala Ser Asp Gly Glu Glu Val Gly Asn Gly Glu Thr Asp
345                 350                 355                 360

gtg aga gag aaa gat gag aat gag cct gat ccc aag aga aga agt aca     1158
Val Arg Glu Lys Asp Glu Asn Glu Pro Asp Pro Lys Arg Arg Ser Thr
                365                 370                 375

gaa gtt cgg att tca gaa cca gct cct gct gct tca cat aga act gtg     1206
Glu Val Arg Ile Ser Glu Pro Ala Pro Ala Ala Ser His Arg Thr Val
            380                 385                 390

aca gag cct aga att att gtc caa acg acg agt gaa gtt gat ctt cta     1254
Thr Glu Pro Arg Ile Ile Val Gln Thr Thr Ser Glu Val Asp Leu Leu
        395                 400                 405

gat gat gga tat agg tgg cgt aaa tat gga cag aaa gtt gtc aaa ggg     1302
Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly
    410                 415                 420

aat cct tat ccg agg agc tac tac aag tgc aca aca cca gga tgt ggt     1350
Asn Pro Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Pro Gly Cys Gly
425                 430                 435                 440
```

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gtg agg aaa cat gta gag aga gca gca aca gat cca aaa gct gta gta    1398
Val Arg Lys His Val Glu Arg Ala Ala Thr Asp Pro Lys Ala Val Val
                445                 450                 455

aca aca tat gaa gga aaa cat aac cat gac ctt ccc gct gct aaa tca    1446
Thr Thr Tyr Glu Gly Lys His Asn His Asp Leu Pro Ala Ala Lys Ser
            460                 465                 470

agc agc cat gcc gct gca gcg gca cag tta agg cca gat aat cga cct    1494
Ser Ser His Ala Ala Ala Ala Ala Gln Leu Arg Pro Asp Asn Arg Pro
        475                 480                 485

ggc ggt ttg gct aac tta aat caa cag cag cag caa cag ccc gtt gcg    1542
Gly Gly Leu Ala Asn Leu Asn Gln Gln Gln Gln Gln Gln Pro Val Ala
    490                 495                 500

cgg cta agg ctt aaa gaa gag caa aca act tga gagaagaaaa ctcttgaccg 1595
Arg Leu Arg Leu Lys Glu Glu Gln Thr Thr  *
505                 510

tttttcatta caaaagcttt caaattccac tcacacactt gtctgaaaaa tctagcagtt 1655
tgcaggaaag aaacagcttc aagaggttgt agttcttcta tgttctggtg taaaacttaa 1715
aagcttttta gggttttcag atttctgttt actaatactg tatgtgaatt cttttgtaca 1775
tgaggaagaa aattacaggg ggatattttg tgttgtatct tttgtgttat tgtttcagta 1835
aaagataggt cttacatttt gtgtaaaaaa aaaaaaaaaa aaaa                  1879

<210> 140
<211> 514
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (227)...(285)
<223> Conserved domain

<221> DOMAIN
<222> (407)...(465)
<223> Conserved domain

<400> 140
Met Ser Glu Lys Glu Glu Ala Pro Ser Thr Ser Lys Ser Thr Gly Ala
 1               5                  10                  15
Pro Ser Arg Pro Thr Leu Ser Leu Pro Pro Arg Pro Phe Ser Glu Met
            20                  25                  30
Phe Phe Asn Gly Gly Val Gly Phe Ser Pro Gly Pro Met Thr Leu Val
        35                  40                  45
Ser Asn Met Phe Pro Asp Ser Asp Glu Phe Arg Ser Phe Ser Gln Leu
    50                  55                  60
Leu Ala Gly Ala Met Ser Ser Pro Ala Thr Ala Ala Ala Ala Ala Ala
65                  70                  75                  80
Ala Ala Thr Ala Ser Asp Tyr Gln Arg Leu Gly Glu Gly Thr Asn Ser
                85                  90                  95
Ser Ser Gly Asp Val Asp Pro Arg Phe Lys Gln Asn Arg Pro Thr Gly
            100                 105                 110
Leu Met Ile Ser Gln Ser Gln Ser Pro Ser Met Phe Thr Val Pro Pro
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115 120 125
Gly Leu Ser Pro Ala Met Leu Leu Asp Ser Pro Ser Phe Leu Gly Leu
130 135 140
Phe Ser Pro Val Gln Gly Ser Tyr Gly Met Thr His Gln Gln Ala Leu
145 150 155 160
Ala Gln Val Thr Ala Gln Ala Val Gln Ala Asn Ala Asn Met Gln Pro
165 170 175
Gln Thr Glu Tyr Pro Pro Pro Ser Gln Val Gln Ser Phe Ser Ser Gly
180 185 190
Gln Ala Gln Ile Pro Thr Ser Ala Pro Leu Pro Ala Gln Arg Glu Thr
195 200 205
Ser Asp Val Thr Ile Ile Glu His Arg Ser Gln Gln Pro Leu Asn Val
210 215 220
Asp Lys Pro Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys
225 230 235 240
Gln Val Lys Gly Ser Glu Phe Pro Arg Ser Tyr Tyr Lys Cys Thr Asn
245 250 255
Pro Gly Cys Pro Val Lys Lys Lys Val Glu Arg Ser Leu Asp Gly Gln
260 265 270
Val Thr Glu Ile Ile Tyr Lys Gly Gln His Asn His Glu Pro Pro Gln
275 280 285
Asn Thr Lys Arg Gly Asn Lys Asp Asn Thr Ala Asn Ile Asn Gly Ser
290 295 300
Ser Ile Asn Asn Asn Arg Gly Ser Ser Glu Leu Gly Ala Ser Gln Phe
305 310 315 320
Gln Thr Asn Ser Ser Asn Lys Thr Lys Arg Glu Gln His Glu Ala Val
325 330 335
Ser Gln Ala Thr Thr Thr Glu His Leu Ser Glu Ala Ser Asp Gly Glu
340 345 350
Glu Val Gly Asn Gly Glu Thr Asp Val Arg Glu Lys Asp Glu Asn Glu
355 360 365
Pro Asp Pro Lys Arg Arg Ser Thr Glu Val Arg Ile Ser Glu Pro Ala
370 375 380
Pro Ala Ala Ser His Arg Thr Val Thr Glu Pro Arg Ile Ile Val Gln
385 390 395 400
Thr Thr Ser Glu Val Asp Leu Leu Asp Asp Gly Tyr Arg Trp Arg Lys
405 410 415
Tyr Gly Gln Lys Val Val Lys Gly Asn Pro Tyr Pro Arg Ser Tyr Tyr
420 425 430
Lys Cys Thr Thr Pro Gly Cys Gly Val Arg Lys His Val Glu Arg Ala
435 440 445
Ala Thr Asp Pro Lys Ala Val Val Thr Thr Tyr Glu Gly Lys His Asn
450 455 460
His Asp Leu Pro Ala Ala Lys Ser Ser Ser His Ala Ala Ala Ala Ala
465 470 475 480
Gln Leu Arg Pro Asp Asn Arg Pro Gly Gly Leu Ala Asn Leu Asn Gln
485 490 495
Gln Gln Gln Gln Gln Pro Val Ala Arg Leu Arg Leu Lys Glu Glu Gln
500 505 510
Thr Thr

<210> 141
<211> 485
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (26)...(457)

<400> 141
atctcatctt catccaccca aaaac atg gat tca aga gac acc gga gaa act    52
                            Met Asp Ser Arg Asp Thr Gly Glu Thr
                             1               5

gac cag agc aag tac aaa ggt atc cgt cgt cgg aaa tgg gga aaa tgg   100
Asp Gln Ser Lys Tyr Lys Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp
 10                  15                  20                  25

gta tca gag att cgt gtc ccg gga act cgt caa cgt ctc tgg tta ggc   148
Val Ser Glu Ile Arg Val Pro Gly Thr Arg Gln Arg Leu Trp Leu Gly
                 30                  35                  40

tct ttc tcc acc gca gaa ggc gct gcc gta gcc cac gac gtc gct ttt   196
Ser Phe Ser Thr Ala Glu Gly Ala Ala Val Ala His Asp Val Ala Phe
             45                  50                  55

tac tgc ttg cac cga cca tct tcc ctc gac gac gaa tct ttt aac ttc   244
Tyr Cys Leu His Arg Pro Ser Ser Leu Asp Asp Glu Ser Phe Asn Phe
         60                  65                  70

cct cac tta ctt aca acc tcc ctc gcc tcc aat ata tct cct aag tcc   292
Pro His Leu Leu Thr Thr Ser Leu Ala Ser Asn Ile Ser Pro Lys Ser
     75                  80                  85

atc caa aaa gct gct tcc gac gcc ggc atg gcc gtg gac gcc gga ttc   340
Ile Gln Lys Ala Ala Ser Asp Ala Gly Met Ala Val Asp Ala Gly Phe
 90                  95                 100                 105

cat ggt gct gtg tct ggg agt ggt ggt tgt gaa gag aga tct tcc atg   388
His Gly Ala Val Ser Gly Ser Gly Gly Cys Glu Glu Arg Ser Ser Met
                110                 115                 120

gcg aat atg gag gag gag gac aaa ctt agt atc tcc gtg tat gat tat   436
Ala Asn Met Glu Glu Glu Asp Lys Leu Ser Ile Ser Val Tyr Asp Tyr
            125                 130                 135

ctt gaa gac gat ctc gtt tga tctatacgag tacgttttta gcagttaa        485
Leu Glu Asp Asp Leu Val  *
        140


<210> 142
<211> 143
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (11)...(83)
<223> Conserved domain
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<400> 142
Met Asp Ser Arg Asp Thr Gly Glu Thr Asp Gln Ser Lys Tyr Lys Gly
1 5 10 15
Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
20 25 30
Gly Thr Arg Gln Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35 40 45
Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Arg Pro Ser
50 55 60
Ser Leu Asp Asp Glu Ser Phe Asn Phe Pro His Leu Leu Thr Thr Ser
65 70 75 80
Leu Ala Ser Asn Ile Ser Pro Lys Ser Ile Gln Lys Ala Ala Ser Asp
85 90 95
Ala Gly Met Ala Val Asp Ala Gly Phe His Gly Ala Val Ser Gly Ser
100 105 110
Gly Gly Cys Glu Glu Arg Ser Ser Met Ala Asn Met Glu Glu Glu Asp
115 120 125
Lys Leu Ser Ile Ser Val Tyr Asp Tyr Leu Glu Asp Asp Leu Val
130 135 140

<210> 143
<211> 931
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (66)...(899)

<400> 143
tcctcactct ctctcttttt ctctaaccat aaaatctctt tgatctcttt ctctgtgttt 60
tgata atg gaa aat gtt ggt gtt ggg atg ccg ttt tac gat tta ggg caa 110
Met Glu Asn Val Gly Val Gly Met Pro Phe Tyr Asp Leu Gly Gln
1 5 10 15

aca agg gtt tac cca ctc ttg tct gat ttc cac gat tta tcg gcg gag 158
Thr Arg Val Tyr Pro Leu Leu Ser Asp Phe His Asp Leu Ser Ala Glu
20 25 30

agg tat ccg gta ggg ttc atg gat tta ctg ggt gtt cat cgt cat aca 206
Arg Tyr Pro Val Gly Phe Met Asp Leu Leu Gly Val His Arg His Thr
35 40 45

ccc acc cat acg ccg ttg atg cat ttt ccg acc aca cct aac tcg tcc 254
Pro Thr His Thr Pro Leu Met His Phe Pro Thr Thr Pro Asn Ser Ser
50 55 60

tcg agc gaa gct gtg aat gga gat gac gaa gaa gaa gaa gat gga gaa 302
Ser Ser Glu Ala Val Asn Gly Asp Asp Glu Glu Glu Glu Asp Gly Glu
65 70 75

gaa cag cag cat aag aca aag aag cgg ttt aaa ttc act aaa atg agt 350
Glu Gln Gln His Lys Thr Lys Lys Arg Phe Lys Phe Thr Lys Met Ser
80 85 90 95

aga aag cag acg aag aag aag gtg cca aaa gtg tca ttc atc acg agg 398

Arg Lys Gln Thr Lys Lys Lys Val Pro Lys Val Ser Phe Ile Thr Arg
100 105 110

agt gag gtt ctt cat cta gat gat ggt tat aag tgg aga aaa tac ggt 446
Ser Glu Val Leu His Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly
115 120 125

caa aaa cct gtc aaa gac agc cct ttt cca aga aat tat tac cgt tgc 494
Gln Lys Pro Val Lys Asp Ser Pro Phe Pro Arg Asn Tyr Tyr Arg Cys
130 135 140

aca aca act tgg tgt gac gtg aag aag aga gta gag aga tca ttc agt 542
Thr Thr Thr Trp Cys Asp Val Lys Lys Arg Val Glu Arg Ser Phe Ser
145 150 155

gat cca agc agt gta atc acc act tac gaa ggt caa cat act cat cct 590
Asp Pro Ser Ser Val Ile Thr Thr Tyr Glu Gly Gln His Thr His Pro
160 165 170 175

cgt cca cta ctc atc atg ccc aaa gaa ggc agc tct cca tcc aat ggc 638
Arg Pro Leu Leu Ile Met Pro Lys Glu Gly Ser Ser Pro Ser Asn Gly
180 185 190

tca gct tct agg gcc cac att ggc ctc cct aca ctc cct cct cag ctt 686
Ser Ala Ser Arg Ala His Ile Gly Leu Pro Thr Leu Pro Pro Gln Leu
195 200 205

tta gat tac aac aac caa caa caa caa gcg ccg tct tct ttt gga acc 734
Leu Asp Tyr Asn Asn Gln Gln Gln Gln Ala Pro Ser Ser Phe Gly Thr
210 215 220

gag tac att aac agg caa gaa aaa gga att aat cat gat gat gat gac 782
Glu Tyr Ile Asn Arg Gln Glu Lys Gly Ile Asn His Asp Asp Asp Asp
225 230 235

gat cat gtt gtg aag aag agt cga act cgg gat ctg ctg gat gga gct 830
Asp His Val Val Lys Lys Ser Arg Thr Arg Asp Leu Leu Asp Gly Ala
240 245 250 255

ggt tta gtc aaa gat cat ggc ctt ctt cag gat gtt gtt ccc tct cat 878
Gly Leu Val Lys Asp His Gly Leu Leu Gln Asp Val Val Pro Ser His
260 265 270

atc att aag gaa gag tat tag ttaatcgcat aattatgtag ctagctagct 929
Ile Ile Lys Glu Glu Tyr *
275

ag 931

<210> 144
<211> 277
<212> PRT
<213> Arabidopsis thaliana

<400> 144
Met Glu Asn Val Gly Val Gly Met Pro Phe Tyr Asp Leu Gly Gln Thr
1 5 10 15

Arg Val Tyr Pro Leu Leu Ser Asp Phe His Asp Leu Ser Ala Glu Arg
20 25 30
Tyr Pro Val Gly Phe Met Asp Leu Leu Gly Val His Arg His Thr Pro
35 40 45
Thr His Thr Pro Leu Met His Phe Pro Thr Thr Pro Asn Ser Ser Ser
50 55 60
Ser Glu Ala Val Asn Gly Asp Asp Glu Glu Glu Glu Asp Gly Glu Glu
65 70 75 80
Gln Gln His Lys Thr Lys Lys Arg Phe Lys Phe Thr Lys Met Ser Arg
85 90 95
Lys Gln Thr Lys Lys Lys Val Pro Lys Val Ser Phe Ile Thr Arg Ser
100 105 110
Glu Val Leu His Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln
115 120 125
Lys Pro Val Lys Asp Ser Pro Phe Pro Arg Asn Tyr Tyr Arg Cys Thr
130 135 140
Thr Thr Trp Cys Asp Val Lys Lys Arg Val Glu Arg Ser Phe Ser Asp
145 150 155 160
Pro Ser Ser Val Ile Thr Thr Tyr Glu Gly Gln His Thr His Pro Arg
165 170 175
Pro Leu Leu Ile Met Pro Lys Glu Gly Ser Ser Pro Ser Asn Gly Ser
180 185 190
Ala Ser Arg Ala His Ile Gly Leu Pro Thr Leu Pro Pro Gln Leu Leu
195 200 205
Asp Tyr Asn Asn Gln Gln Gln Gln Ala Pro Ser Ser Phe Gly Thr Glu
210 215 220
Tyr Ile Asn Arg Gln Glu Lys Gly Ile Asn His Asp Asp Asp Asp Asp
225 230 235 240
His Val Val Lys Lys Ser Arg Thr Arg Asp Leu Leu Asp Gly Ala Gly
245 250 255
Leu Val Lys Asp His Gly Leu Leu Gln Asp Val Val Pro Ser His Ile
260 265 270
Ile Lys Glu Glu Tyr
275

<210> 145
<211> 795
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(795)

<400> 145
atg gac gtc tat ggc tta tct tca cca gac tta ctt cga atc gac gac 48
Met Asp Val Tyr Gly Leu Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
1 5 10 15

ctt ctt gat ttc tcc aac gaa gac atc ttc tcc gct tct tct tcc ggt 96
Leu Leu Asp Phe Ser Asn Glu Asp Ile Phe Ser Ala Ser Ser Ser Gly
20 25 30

ggt tcc acc gcc gct act tcc tct tct tct ttc cct cct cct caa aac 144
Gly Ser Thr Ala Ala Thr Ser Ser Ser Ser Phe Pro Pro Pro Gln Asn
35 40 45

```
cct agt ttc cac cac cac cat ctc cct tcc tcc gcc gat cat cac tcc     192
Pro Ser Phe His His His His Leu Pro Ser Ser Ala Asp His His Ser
    50                  55                  60

ttc ctc cac gac att tgc gtt ccc agt gat gac gca gct cat ctt gaa     240
Phe Leu His Asp Ile Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu
65                  70                  75                  80

tgg ctt tcg caa ttc gtg gac gat tct ttc gct gat ttt ccg gcg aat     288
Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn
                85                  90                  95

cca tta gga gga act atg act tct gtc aaa act gaa act tcc ttt ccg     336
Pro Leu Gly Gly Thr Met Thr Ser Val Lys Thr Glu Thr Ser Phe Pro
            100                 105                 110

ggg aaa cca aga agc aaa cga tca aga gct cct gct cct ttc gcc gga     384
Gly Lys Pro Arg Ser Lys Arg Ser Arg Ala Pro Ala Pro Phe Ala Gly
        115                 120                 125

aca tgg tct ccg atg cca ctg gaa tcc gag cat cag cag ctt cac tcc     432
Thr Trp Ser Pro Met Pro Leu Glu Ser Glu His Gln Gln Leu His Ser
    130                 135                 140

gcc gcc aaa ttc aag cca aag aaa gaa caa tcc ggc gga gga gga gga     480
Ala Ala Lys Phe Lys Pro Lys Lys Glu Gln Ser Gly Gly Gly Gly Gly
145                 150                 155                 160

gga gga gga aga cat cag tca tcg tca tcg gag act acg gaa gga gga     528
Gly Gly Gly Arg His Gln Ser Ser Ser Ser Glu Thr Thr Glu Gly Gly
                165                 170                 175

gga atg agg aga tgt act cac tgt gca tcg gag aaa acg cca cag tgg     576
Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp
            180                 185                 190

agg aca gga cca ctt gga cct aaa aca cta tgt aac gct tgt gga gtc     624
Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val
        195                 200                 205

cgg ttt aaa tcc ggt aga ctt gta ccg gaa tat aga ccg gct tcg agt     672
Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser
    210                 215                 220

cct act ttt gtt ttg act cag cat tca aac tct cac cgg aaa gtg atg     720
Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met
225                 230                 235                 240

gag ctt cga cgg cag aaa gaa gtt atg aga caa cca caa caa gtt caa     768
Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln
                245                 250                 255

ctt cat cac cac cac cac ccg ttt tag                                 795
Leu His His His His His Pro Phe  *
            260
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<210> 146
<211> 264
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (178)...(214)
<223> Conserved domain

<400> 146
Met Asp Val Tyr Gly Leu Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
1 5 10 15
Leu Leu Asp Phe Ser Asn Glu Asp Ile Phe Ser Ala Ser Ser Ser Gly
20 25 30
Gly Ser Thr Ala Ala Thr Ser Ser Ser Ser Phe Pro Pro Pro Gln Asn
35 40 45
Pro Ser Phe His His His His Leu Pro Ser Ser Ala Asp His His Ser
50 55 60
Phe Leu His Asp Ile Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu
65 70 75 80
Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn
85 90 95
Pro Leu Gly Gly Thr Met Thr Ser Val Lys Thr Glu Thr Ser Phe Pro
100 105 110
Gly Lys Pro Arg Ser Lys Arg Ser Arg Ala Pro Ala Pro Phe Ala Gly
115 120 125
Thr Trp Ser Pro Met Pro Leu Glu Ser Glu His Gln Gln Leu His Ser
130 135 140
Ala Ala Lys Phe Lys Pro Lys Lys Glu Gln Ser Gly Gly Gly Gly Gly
145 150 155 160
Gly Gly Gly Arg His Gln Ser Ser Ser Ser Glu Thr Thr Glu Gly Gly
165 170 175
Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp
180 185 190
Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val
195 200 205
Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser
210 215 220
Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met
225 230 235 240
Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln
245 250 255
Leu His His His His His Pro Phe
260

<210> 147
<211> 2026
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (297)...(1781)

<400> 147
caaaaaaaaa gtttcaattt ttgaaagctc tgagaaatga aatctatcat tctctctctc 60
tatctctatc ttcctttca gatttcgctt cttcaattca tgaaatcctc gtgattctac 120
tttaatgctt ctctttttt acttttccaa gtctctgaat attcaaagta tatatctttt 180
gttttcaaac ttttgcagaa ttgtcttcaa gcttccaaat ttcagttaaa ggtctcaact 240
ttgcagaatt ttcctctaaa ggttcagact ttggggtaaa ggtgtcaact ttggcg atg 299
Met
1

ggt ctt gac gga aac aat ggt gga ggg gtt tgg tta aac ggt ggt ggt 347
Gly Leu Asp Gly Asn Asn Gly Gly Gly Val Trp Leu Asn Gly Gly Gly
5 10 15

gga gaa agg gaa gag aac gag gaa ggt tca tgg gga agg aat caa gaa 395
Gly Glu Arg Glu Glu Asn Glu Glu Gly Ser Trp Gly Arg Asn Gln Glu
20 25 30

gat ggt tct tct cag ttt aag cct atg ctt gaa ggt gat tgg ttt agt 443
Asp Gly Ser Ser Gln Phe Lys Pro Met Leu Glu Gly Asp Trp Phe Ser
35 40 45

agt aac caa cca cat cca caa gat ctt cag atg tta cag aat cag cca 491
Ser Asn Gln Pro His Pro Gln Asp Leu Gln Met Leu Gln Asn Gln Pro
50 55 60 65

gat ttc aga tac ttt ggt ggt ttt cct ttt aac cct aat gat aat ctt 539
Asp Phe Arg Tyr Phe Gly Gly Phe Pro Phe Asn Pro Asn Asp Asn Leu
70 75 80

ctt ctt caa cac tct att gat tct tct tct tct tgt tct cct tct caa 587
Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser Gln
85 90 95

gct ttt agt ctt gac cct tct cag caa aat cag ttc ttg tca act aac 635
Ala Phe Ser Leu Asp Pro Ser Gln Gln Asn Gln Phe Leu Ser Thr Asn
100 105 110

aac aac aag ggt tgt ctt ctc aat gtt cct tct tct gca aac cct ttt 683
Asn Asn Lys Gly Cys Leu Leu Asn Val Pro Ser Ser Ala Asn Pro Phe
115 120 125

gat aat gct ttt gag ttt ggc tct gaa tct ggt ttt ctt aac caa atc 731
Asp Asn Ala Phe Glu Phe Gly Ser Glu Ser Gly Phe Leu Asn Gln Ile
130 135 140 145

cat gct cct att tcg atg ggg ttt ggt tct ttg aca caa ttg ggg aac 779
His Ala Pro Ile Ser Met Gly Phe Gly Ser Leu Thr Gln Leu Gly Asn
150 155 160

agg gat ttg agt tct gtt cct gat ttc ttg tct gct cgg tca ctt ctt 827
Arg Asp Leu Ser Ser Val Pro Asp Phe Leu Ser Ala Arg Ser Leu Leu
165 170 175

gcg ccg gaa agc aac aac aac aac aca atg ttg tgt ggt ggt ttc aca 875
Ala Pro Glu Ser Asn Asn Asn Asn Thr Met Leu Cys Gly Gly Phe Thr
180 185 190

```
gct ccg ttg gag ttg gaa ggt ttt ggt agt cct gct aat ggt ggt ttt     923
Ala Pro Leu Glu Leu Glu Gly Phe Gly Ser Pro Ala Asn Gly Gly Phe
    195                 200                 205

gtt ggg aac aga gcg aaa gtt ctg aag cct tta gag gtg tta gca tcg     971
Val Gly Asn Arg Ala Lys Val Leu Lys Pro Leu Glu Val Leu Ala Ser
210                 215                 220                 225

tct ggt gca cag cct act ctg ttc cag aaa cgt gca gct atg cgt cag     1019
Ser Gly Ala Gln Pro Thr Leu Phe Gln Lys Arg Ala Ala Met Arg Gln
                230                 235                 240

agc tct gga agc aaa atg gga aat tcg gag agt tcg gga atg agg agg     1067
Ser Ser Gly Ser Lys Met Gly Asn Ser Glu Ser Ser Gly Met Arg Arg
            245                 250                 255

ttt agt gat gat gga gat atg gat gag act ggg att gag gtt tct ggg     1115
Phe Ser Asp Asp Gly Asp Met Asp Glu Thr Gly Ile Glu Val Ser Gly
        260                 265                 270

ttg aac tat gag tct gat gag ata aat gag agc ggt aaa gcg gct gag     1163
Leu Asn Tyr Glu Ser Asp Glu Ile Asn Glu Ser Gly Lys Ala Ala Glu
    275                 280                 285

agt gtt cag att gga gga gga gga aag ggt aag aag aaa ggt atg cct     1211
Ser Val Gln Ile Gly Gly Gly Gly Lys Gly Lys Lys Lys Gly Met Pro
290                 295                 300                 305

gct aag aat ctg atg gct gag agg aga agg agg aag aag ctt aat gat     1259
Ala Lys Asn Leu Met Ala Glu Arg Arg Arg Arg Lys Lys Leu Asn Asp
                310                 315                 320

agg ctt tat atg ctt aga tca gtt gtc ccc aag atc agc aaa atg gat     1307
Arg Leu Tyr Met Leu Arg Ser Val Val Pro Lys Ile Ser Lys Met Asp
            325                 330                 335

aga gca tca ata ctt gga gat gca att gat tat ctg aag gaa ctt cta     1355
Arg Ala Ser Ile Leu Gly Asp Ala Ile Asp Tyr Leu Lys Glu Leu Leu
        340                 345                 350

caa agg atc aat gat ctt cac aat gaa ctt gag tca act cct cct gga     1403
Gln Arg Ile Asn Asp Leu His Asn Glu Leu Glu Ser Thr Pro Pro Gly
    355                 360                 365

tct ttg cct cca act tca tca agc ttc cat ccg ttg aca cct aca ccg     1451
Ser Leu Pro Pro Thr Ser Ser Ser Phe His Pro Leu Thr Pro Thr Pro
370                 375                 380                 385

caa act ctt tct tgt cgt gtc aag gaa gag ttg tgt ccc tct tct tta     1499
Gln Thr Leu Ser Cys Arg Val Lys Glu Glu Leu Cys Pro Ser Ser Leu
                390                 395                 400

cca agt cct aaa ggc cag caa gct aga gtt gag gtt aga tta agg gaa     1547
Pro Ser Pro Lys Gly Gln Gln Ala Arg Val Glu Val Arg Leu Arg Glu
            405                 410                 415

gga aga gca gtg aac att cat atg ttc tgt ggt cgt aga ccg ggt ctg     1595
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Gly Arg Ala Val Asn Ile His Met Phe Cys Gly Arg Arg Pro Gly Leu
        420                 425                 430

ttg ctc gct acc atg aaa gct ttg gat aat ctt gga ttg gat gtt cag    1643
Leu Leu Ala Thr Met Lys Ala Leu Asp Asn Leu Gly Leu Asp Val Gln
    435                 440                 445

caa gct gtg atc agc tgt ttt aat ggg ttt gcc ttg gat gtt ttc cgc    1691
Gln Ala Val Ile Ser Cys Phe Asn Gly Phe Ala Leu Asp Val Phe Arg
450                 455                 460                 465

gct gag caa tgc caa gaa gga caa gag ata ctg cct gat caa atc aaa    1739
Ala Glu Gln Cys Gln Glu Gly Gln Glu Ile Leu Pro Asp Gln Ile Lys
                470                 475                 480

gca gtg ctt ttc gat aca gca ggg tat gct ggt atg atc tga            1781
Ala Val Leu Phe Asp Thr Ala Gly Tyr Ala Gly Met Ile  *
            485                 490

tctgatcctg acttcgagtc cattaagcat ctgttgaagc agagctagaa gaactaagtc 1841
cctttaaatc tgcaattttc ttctcaactt tttttcttat gtcataactt caatctaagc 1901
atgtaatgca attgcaaatg agagttgttt ttaaattaag cttttgagaa cttgaggttg 1961
ttgttgttgg atacataact tcaacctttt attagcaatg ttaacttcca tttatgtttc 2021
atctt                                                             2026

<210> 148
<211> 494
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (308)...(359)
<223> Conserved domain

<400> 148
Met Gly Leu Asp Gly Asn Asn Gly Gly Gly Val Trp Leu Asn Gly Gly
 1               5                  10                  15
Gly Gly Glu Arg Glu Glu Asn Glu Glu Gly Ser Trp Gly Arg Asn Gln
            20                  25                  30
Glu Asp Gly Ser Ser Gln Phe Lys Pro Met Leu Glu Gly Asp Trp Phe
        35                  40                  45
Ser Ser Asn Gln Pro His Pro Gln Asp Leu Gln Met Leu Gln Asn Gln
    50                  55                  60
Pro Asp Phe Arg Tyr Phe Gly Gly Phe Pro Phe Asn Pro Asn Asp Asn
65                  70                  75                  80
Leu Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser
                85                  90                  95
Gln Ala Phe Ser Leu Asp Pro Ser Gln Gln Asn Gln Phe Leu Ser Thr
            100                 105                 110
Asn Asn Asn Lys Gly Cys Leu Leu Asn Val Pro Ser Ser Ala Asn Pro
        115                 120                 125
Phe Asp Asn Ala Phe Glu Phe Gly Ser Glu Ser Gly Phe Leu Asn Gln
    130                 135                 140
Ile His Ala Pro Ile Ser Met Gly Phe Gly Ser Leu Thr Gln Leu Gly
145                 150                 155                 160
Asn Arg Asp Leu Ser Ser Val Pro Asp Phe Leu Ser Ala Arg Ser Leu
```

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                165                     170                     175
Leu Ala Pro Glu Ser Asn Asn Asn Asn Thr Met Leu Cys Gly Gly Phe
            180                     185                     190
Thr Ala Pro Leu Glu Leu Glu Gly Phe Gly Ser Pro Ala Asn Gly Gly
        195                     200                     205
Phe Val Gly Asn Arg Ala Lys Val Leu Lys Pro Leu Glu Val Leu Ala
    210                     215                     220
Ser Ser Gly Ala Gln Pro Thr Leu Phe Gln Lys Arg Ala Ala Met Arg
225                     230                     235                     240
Gln Ser Ser Gly Ser Lys Met Gly Asn Ser Glu Ser Ser Gly Met Arg
                245                     250                     255
Arg Phe Ser Asp Asp Gly Asp Met Asp Glu Thr Gly Ile Glu Val Ser
            260                     265                     270
Gly Leu Asn Tyr Glu Ser Asp Glu Ile Asn Glu Ser Gly Lys Ala Ala
        275                     280                     285
Glu Ser Val Gln Ile Gly Gly Gly Gly Lys Gly Lys Lys Lys Gly Met
    290                     295                     300
Pro Ala Lys Asn Leu Met Ala Glu Arg Arg Arg Arg Lys Lys Leu Asn
305                     310                     315                     320
Asp Arg Leu Tyr Met Leu Arg Ser Val Val Pro Lys Ile Ser Lys Met
                325                     330                     335
Asp Arg Ala Ser Ile Leu Gly Asp Ala Ile Asp Tyr Leu Lys Glu Leu
            340                     345                     350
Leu Gln Arg Ile Asn Asp Leu His Asn Glu Leu Glu Ser Thr Pro Pro
        355                     360                     365
Gly Ser Leu Pro Pro Thr Ser Ser Ser Phe His Pro Leu Thr Pro Thr
    370                     375                     380
Pro Gln Thr Leu Ser Cys Arg Val Lys Glu Glu Leu Cys Pro Ser Ser
385                     390                     395                     400
Leu Pro Ser Pro Lys Gly Gln Gln Ala Arg Val Glu Val Arg Leu Arg
                405                     410                     415
Glu Gly Arg Ala Val Asn Ile His Met Phe Cys Gly Arg Arg Pro Gly
            420                     425                     430
Leu Leu Leu Ala Thr Met Lys Ala Leu Asp Asn Leu Gly Leu Asp Val
        435                     440                     445
Gln Gln Ala Val Ile Ser Cys Phe Asn Gly Phe Ala Leu Asp Val Phe
    450                     455                     460
Arg Ala Glu Gln Cys Gln Glu Gly Gln Glu Ile Leu Pro Asp Gln Ile
465                     470                     475                     480
Lys Ala Val Leu Phe Asp Thr Ala Gly Tyr Ala Gly Met Ile
                485                     490
```

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<210> 149
<211> 1146
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1146)

<400> 149
atg gat cta aca gac cgt cgt aac cct ttt aac aat ctt gtt ttt ccg     48
Met Asp Leu Thr Asp Arg Arg Asn Pro Phe Asn Asn Leu Val Phe Pro
 1               5                  10                  15
```

ccg ccg cct ccg ccg cca tcc acg acc ttc aca agc cct ata ttc cca 96
Pro Pro Pro Pro Pro Pro Ser Thr Thr Phe Thr Ser Pro Ile Phe Pro
20 25 30

cga aca agc tct tcc ggc acc aat ttc ccc att ctg gcc atc gca gtg 144
Arg Thr Ser Ser Ser Gly Thr Asn Phe Pro Ile Leu Ala Ile Ala Val
35 40 45

att gga atc tta gcc act gcg ttc tta ctt gta agt tac tac atc ttc 192
Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe
50 55 60

gtg atc aaa tgc tgt ctt aat tgg cac caa atc gac atc ttt cgc cgc 240
Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg
65 70 75 80

cgc aga cga agc agt gac caa aac cct cta atg att tac tct cct cat 288
Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His
85 90 95

gag gta aac aga gga cta gac gaa tcc gcc att aga gct atc cca gtc 336
Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val
100 105 110

ttc aaa ttc aag aag aga gac gtt gtt gca gga gaa gaa gat cag agt 384
Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser
115 120 125

aag aac tct caa gaa tgc tct gtt tgt tta aac gag ttt caa gaa gac 432
Lys Asn Ser Gln Glu Cys Ser Val Cys Leu Asn Glu Phe Gln Glu Asp
130 135 140

gag aag cta agg att att cct aac tgc tgc cac gtg ttt cac att gat 480
Glu Lys Leu Arg Ile Ile Pro Asn Cys Cys His Val Phe His Ile Asp
145 150 155 160

tgc att gat atc tgg ctt cag ggc aac gca aat tgt ccc ttg tgc aga 528
Cys Ile Asp Ile Trp Leu Gln Gly Asn Ala Asn Cys Pro Leu Cys Arg
165 170 175

acc agc gtt tct tgc gaa gca agt ttc act ctt gac cta atc tct gca 576
Thr Ser Val Ser Cys Glu Ala Ser Phe Thr Leu Asp Leu Ile Ser Ala
180 185 190

ccg agc tct cct cgg gag aat agc cct cat tct cgg aac agg aat ctc 624
Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu
195 200 205

gaa ccc ggc ctg gtt cta gga ggc gat gat gac ttc gtc gtc ata gag 672
Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu
210 215 220

ctt ggg gcc agt aat ggt aac aac aga gaa agc gtg aga aac ata gac 720
Leu Gly Ala Ser Asn Gly Asn Asn Arg Glu Ser Val Arg Asn Ile Asp
225 230 235 240

ttc ctt acg gag caa gaa agg gtt acc tcg aat gag gtc tcg acc gga 768

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Phe Leu Thr Glu Gln Glu Arg Val Thr Ser Asn Glu Val Ser Thr Gly
                245                 250                 255

aac agc ccg aaa tcg gtg agt cct ttg cct ata aag ttt ggt aat cgg      816
Asn Ser Pro Lys Ser Val Ser Pro Leu Pro Ile Lys Phe Gly Asn Arg
            260                 265                 270

gga atg tat aag aaa gaa agg aaa ttt cac aaa gtg acg agt atg gga      864
Gly Met Tyr Lys Lys Glu Arg Lys Phe His Lys Val Thr Ser Met Gly
        275                 280                 285

gac gaa tgt atc gat act aga ggc aaa gat ggt cat ttt ggt gaa att      912
Asp Glu Cys Ile Asp Thr Arg Gly Lys Asp Gly His Phe Gly Glu Ile
    290                 295                 300

cag ccc ata aga aga tcg atc tcg atg gat tca tca gtg gat cgt cag      960
Gln Pro Ile Arg Arg Ser Ile Ser Met Asp Ser Ser Val Asp Arg Gln
305                 310                 315                 320

ctg tac ttg gcg gtc caa gag gaa atc agc cgg aga aac agg cag att      1008
Leu Tyr Leu Ala Val Gln Glu Glu Ile Ser Arg Arg Asn Arg Gln Ile
                325                 330                 335

ccg gta gct gga gac ggt gaa gat agt agc agt agt ggt ggt ggt aat      1056
Pro Val Ala Gly Asp Gly Glu Asp Ser Ser Ser Ser Gly Gly Gly Asn
            340                 345                 350

agc aga gtc atg aag aga tgt ttc ttc tct ttt gga agt agt aga act      1104
Ser Arg Val Met Lys Arg Cys Phe Phe Ser Phe Gly Ser Ser Arg Thr
        355                 360                 365

tca aaa agt tct tca ata tta cct gtt tat ttg gaa ccc taa              1146
Ser Lys Ser Ser Ser Ile Leu Pro Val Tyr Leu Glu Pro  *
    370                 375                 380


&lt;210&gt; 150
&lt;211&gt; 381
&lt;212&gt; PRT
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; DOMAIN
&lt;222&gt; (134)...(159)
&lt;223&gt; Conserved domain

&lt;400&gt; 150
Met Asp Leu Thr Asp Arg Arg Asn Pro Phe Asn Asn Leu Val Phe Pro
 1               5                  10                  15
Pro Pro Pro Pro Pro Pro Ser Thr Thr Phe Thr Ser Pro Ile Phe Pro
            20                  25                  30
Arg Thr Ser Ser Ser Gly Thr Asn Phe Pro Ile Leu Ala Ile Ala Val
        35                  40                  45
Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe
    50                  55                  60
Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg
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65                  70                  75                  80
Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His
                85                  90                  95
Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val
            100                 105                 110
Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser
        115                 120                 125
Lys Asn Ser Gln Glu Cys Ser Val Cys Leu Asn Glu Phe Gln Glu Asp
    130                 135                 140
Glu Lys Leu Arg Ile Ile Pro Asn Cys Cys His Val Phe His Ile Asp
145                 150                 155                 160
Cys Ile Asp Ile Trp Leu Gln Gly Asn Ala Asn Cys Pro Leu Cys Arg
                165                 170                 175
Thr Ser Val Ser Cys Glu Ala Ser Phe Thr Leu Asp Leu Ile Ser Ala
            180                 185                 190
Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu
        195                 200                 205
Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu
    210                 215                 220
Leu Gly Ala Ser Asn Gly Asn Asn Arg Glu Ser Val Arg Asn Ile Asp
225                 230                 235                 240
Phe Leu Thr Glu Gln Glu Arg Val Thr Ser Asn Glu Val Ser Thr Gly
                245                 250                 255
Asn Ser Pro Lys Ser Val Ser Pro Leu Pro Ile Lys Phe Gly Asn Arg
            260                 265                 270
Gly Met Tyr Lys Lys Glu Arg Lys Phe His Lys Val Thr Ser Met Gly
        275                 280                 285
Asp Glu Cys Ile Asp Thr Arg Gly Lys Asp Gly His Phe Gly Glu Ile
    290                 295                 300
Gln Pro Ile Arg Arg Ser Ile Ser Met Asp Ser Ser Val Asp Arg Gln
305                 310                 315                 320
Leu Tyr Leu Ala Val Gln Glu Glu Ile Ser Arg Arg Asn Arg Gln Ile
                325                 330                 335
Pro Val Ala Gly Asp Gly Glu Asp Ser Ser Ser Ser Gly Gly Gly Asn
            340                 345                 350
Ser Arg Val Met Lys Arg Cys Phe Phe Ser Phe Gly Ser Ser Arg Thr
        355                 360                 365
Ser Lys Ser Ser Ser Ile Leu Pro Val Tyr Leu Glu Pro
    370                 375                 380


<210> 151
<211> 1064
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (61)...(849)

<400> 151
taaagaaaga gaaaaaaagc tttcgtagtg tctattgaaa ccagagaaaa gccaaagggg 60
atg caa cca aca tcc gtc ggt agt agc ggc ggt ggt gac gac gga gga   108
Met Gln Pro Thr Ser Val Gly Ser Ser Gly Gly Gly Asp Asp Gly Gly
 1               5                  10                  15

ggc aga gga gga gga gga ggg cta agt aga agt gga cta tct cgg atc   156
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Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile
            20                      25                      30

cgt tca gct cca gcg act tgg ctt gaa gct tta ctt gag gaa gat gaa     204
Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu
        35                      40                      45

gaa gag tct ttg aaa cct aat ctt ggt ctc acc gat ttg ctt acc ggg     252
Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly
    50                      55                      60

aac tcg aac gat tta ccg aca agt cgc ggc tcg ttc gag ttc ccg att     300
Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile
65                      70                      75                      80

cct gtt gag caa ggg ttg tat caa caa ggt ggg ttt cac cga cag aat     348
Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn
                85                      90                      95

agt act ccg gcg gat ttt ctt agt ggt tct gat gga ttt atc caa agc     396
Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser
            100                     105                     110

ttt ggg att cag gcg aat tac gat tac tta tcg ggg aat atc gat gtt     444
Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val
        115                     120                     125

tct ccg gga agt aag cgg tct aga gaa atg gaa gca ctc ttc tct tct     492
Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser
    130                     135                     140

cct gag ttt act tct caa atg aaa gga gag caa agc agc ggt caa gtt     540
Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val
145                     150                     155                     160

cct acc gga gta tca agc atg tcg gat atg aac atg gag aac ctt atg     588
Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met
                165                     170                     175

gag gac tct gtt gct ttt agg gtt cgg gct aaa cgt ggt tgc gca act     636
Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr
            180                     185                     190

cat ccc cgc agc att gcc gag agg gta cga agg acg cgg att agt gat     684
His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp
        195                     200                     205

cgg ata agg aag cta caa gag ctt gta cct aac atg gac aag caa acc     732
Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr
    210                     215                     220

aac act gca gac atg tta gaa gaa gca gta gaa tac gtg aaa gtt ctt     780
Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu
225                     230                     235                     240

caa agg cag atc cag gag tta aca gaa gaa cag aag agg tgc aca tgc     828
Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys
```

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                245                 250                 255

ata cct aag gaa gaa caa taa ggtttgctcc tgatttgttt tatatttgct      879
Ile Pro Lys Glu Glu Gln  *
            260

taacggcaat gatctgatcg aaaaattcga aagatgatct tagcttgaat ttagatggat 939
gtcatgttga aaagtatatt atttgataaa tggatgtagg tgtaatataa aatttttgta 999
caataatgaa gaaagttaaa aagaattaat gaaaacatat attctttatg atataaaaaa 1059
aaaaa                                                             1064

<210> 152
<211> 262
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (198)...(247)
<223> Conserved domain

<400> 152
Met Gln Pro Thr Ser Val Gly Ser Ser Gly Gly Gly Asp Asp Gly Gly
 1               5                   10                  15
Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile
            20                  25                  30
Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu
        35                  40                  45
Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly
    50                  55                  60
Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile
65                  70                  75                  80
Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn
                85                  90                  95
Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser
            100                 105                 110
Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val
        115                 120                 125
Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser
    130                 135                 140
Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val
145                 150                 155                 160
Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met
                165                 170                 175
Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr
            180                 185                 190
His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp
        195                 200                 205
Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr
    210                 215                 220
Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu
225                 230                 235                 240
Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys
                245                 250                 255
Ile Pro Lys Glu Glu Gln
            260
```

<210> 153
<211> 831
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (201)...(791)

<400> 153
gtgtcggtga atttttgaa acttcttctc ttttgcggtt tcgtgttcca ctcctctctt 60
cttggcccac gtgttcatca atctctccct ccgcatgtaa tcgcttcgcc gtcaatatca 120
catctttctt cttctttatc tttaaaatct ctttagatcg attcttttgt ggattcttga 180
aatctccgga gaaaaccact atg gag acg gcg act gaa gtg gcc acg gtg gtg 233
Met Glu Thr Ala Thr Glu Val Ala Thr Val Val
1 5 10

tca act ccg gcg gtt acg gtt gcg gcg gtg gcg acg agg aag aga gat 281
Ser Thr Pro Ala Val Thr Val Ala Ala Val Ala Thr Arg Lys Arg Asp
15 20 25

aag ccg tat aaa ggg ata agg atg agg aag tgg ggg aag tgg gtg gcg 329
Lys Pro Tyr Lys Gly Ile Arg Met Arg Lys Trp Gly Lys Trp Val Ala
30 35 40

gag ata aga gag cct aat aaa agg tca agg atc tgg ctt ggc tct tac 377
Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Ile Trp Leu Gly Ser Tyr
45 50 55

tct act cct gaa gcg gcg gcg cgt gct tac gac acg gcg gtg ttt tat 425
Ser Thr Pro Glu Ala Ala Ala Arg Ala Tyr Asp Thr Ala Val Phe Tyr
60 65 70 75

ctc cga ggt cct tct gct cgg ctt aac ttc ccg gag ctt tta gcc gga 473
Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Glu Leu Leu Ala Gly
80 85 90

gtg acg gtg acg gga gga ggc gga gga gga gtg aac ggt ggt gga gat 521
Val Thr Val Thr Gly Gly Gly Gly Gly Gly Val Asn Gly Gly Gly Asp
95 100 105

atg tcg gcg gcg tat ata agg aga aaa gcg gcg gag gtt gga gca caa 569
Met Ser Ala Ala Tyr Ile Arg Arg Lys Ala Ala Glu Val Gly Ala Gln
110 115 120

gtg gat gcg tta gaa gcg gcg ggg gcg gga ggg aat cgt cat cat cat 617
Val Asp Ala Leu Glu Ala Ala Gly Ala Gly Gly Asn Arg His His His
125 130 135

cat cat caa cat caa cgt ggt aat cat gat tac gta gat aat cat agt 665
His His Gln His Gln Arg Gly Asn His Asp Tyr Val Asp Asn His Ser
140 145 150 155

gat tat cgt att aat gat gat ctt atg gag tgt agt agt aaa gaa ggg 713
Asp Tyr Arg Ile Asn Asp Asp Leu Met Glu Cys Ser Ser Lys Glu Gly
160 165 170

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ttt aag agg tgt aat gga tcg ttg gaa cgg gtt gat tta aac aaa tta   761
Phe Lys Arg Cys Asn Gly Ser Leu Glu Arg Val Asp Leu Asn Lys Leu
            175                 180                 185

ccc gat ccg gaa act tca gat gac gat tag gaaagcaaaa aatagaaaca     811
Pro Asp Pro Glu Thr Ser Asp Asp Asp  *
        190                 195

aaaaaaaaaa aaaaaaaaaa                                             831

<210> 154
<211> 196
<212> PRT
<213> Arabidopsis thaliana

<400> 154
Met Glu Thr Ala Thr Glu Val Ala Thr Val Val Ser Thr Pro Ala Val
 1               5                  10                  15
Thr Val Ala Ala Val Ala Thr Arg Lys Arg Asp Lys Pro Tyr Lys Gly
            20                  25                  30
Ile Arg Met Arg Lys Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
        35                  40                  45
Asn Lys Arg Ser Arg Ile Trp Leu Gly Ser Tyr Ser Thr Pro Glu Ala
    50                  55                  60
Ala Ala Arg Ala Tyr Asp Thr Ala Val Phe Tyr Leu Arg Gly Pro Ser
65                  70                  75                  80
Ala Arg Leu Asn Phe Pro Glu Leu Leu Ala Gly Val Thr Val Thr Gly
                85                  90                  95
Gly Gly Gly Gly Gly Val Asn Gly Gly Gly Asp Met Ser Ala Ala Tyr
            100                 105                 110
Ile Arg Arg Lys Ala Ala Glu Val Gly Ala Gln Val Asp Ala Leu Glu
        115                 120                 125
Ala Ala Gly Ala Gly Gly Asn Arg His His His His His Gln His Gln
    130                 135                 140
Arg Gly Asn His Asp Tyr Val Asp Asn His Ser Asp Tyr Arg Ile Asn
145                 150                 155                 160
Asp Asp Leu Met Glu Cys Ser Ser Lys Glu Gly Phe Lys Arg Cys Asn
                165                 170                 175
Gly Ser Leu Glu Arg Val Asp Leu Asn Lys Leu Pro Asp Pro Glu Thr
            180                 185                 190
Ser Asp Asp Asp
        195


<210> 155
<211> 981
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (36)...(959)

<400> 155
gtaccggcga cctctttgtg ggtcactctt catca atg ggt gac aaa gga agg    53
                                       Met Gly Asp Lys Gly Arg
```

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                                                1               5

agc tta aag atc aac aag aac atg gag gaa ttc acg aaa gtg gaa gaa    101
Ser Leu Lys Ile Asn Lys Asn Met Glu Glu Phe Thr Lys Val Glu Glu
            10                  15                  20

gaa atg gac gta agg aga ggt cca tgg aca gtt gag gaa gat tta gag    149
Glu Met Asp Val Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Glu
        25                  30                  35

ctc atc aat tac att gct agt cat ggt gaa ggt cga tgg aac tct ctc    197
Leu Ile Asn Tyr Ile Ala Ser His Gly Glu Gly Arg Trp Asn Ser Leu
    40                  45                  50

gct cgt tgc gcc gaa ctc aaa agg acc gga aaa agc tgc aga ctt cgg    245
Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg
55                  60                  65                  70

tgg ctg aac tat ctc cga cca gat gtg cgc cgt gga aac ata acc ctc    293
Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu
                75                  80                  85

gaa gaa caa ctc ttg att ctt gaa ctt cac aca cgt tgg ggc aat aga    341
Glu Glu Gln Leu Leu Ile Leu Glu Leu His Thr Arg Trp Gly Asn Arg
            90                  95                  100

tgg tct aag att gca caa tat tta cca gga aga acg gat aac gag atc    389
Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile
        105                 110                 115

aaa aac tat tgg aga aca cgt gtt caa aag cat gca aaa cag ctt aaa    437
Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys
    120                 125                 130

tgc gac gtg aac agt caa caa ttt aaa gac acc atg aag tat ctt tgg    485
Cys Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp
135                 140                 145                 150

atg cct cgg ctc gta gaa agg atc caa gcc gcg tcc atc ggg tct gtt    533
Met Pro Arg Leu Val Glu Arg Ile Gln Ala Ala Ser Ile Gly Ser Val
                155                 160                 165

tcc atg tca tct tgc gtc acc acc tcc tca gat cag ttc gtg atc aac    581
Ser Met Ser Ser Cys Val Thr Thr Ser Ser Asp Gln Phe Val Ile Asn
            170                 175                 180

aac aac aac acc aac aac gtg gat aat ttg gct tta atg agt aac cct    629
Asn Asn Asn Thr Asn Asn Val Asp Asn Leu Ala Leu Met Ser Asn Pro
        185                 190                 195

aat ggt tac atc acg ccg gat aat tcc agc gtg gca gta tct cct gta    677
Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser Val Ala Val Ser Pro Val
    200                 205                 210

tca gat ttg acg gag tgt caa gtg agt agt gaa gtg tgg aag att ggt    725
Ser Asp Leu Thr Glu Cys Gln Val Ser Ser Glu Val Trp Lys Ile Gly
215                 220                 225                 230
```

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cag gat gag aat ttg gtg gat cca aaa atg aca tcg ccg aat tat atg     773
Gln Asp Glu Asn Leu Val Asp Pro Lys Met Thr Ser Pro Asn Tyr Met
                235                 240                 245

gat aat agc agt gga cta tta aac gga gat ttt acg aag atg caa gat     821
Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp Phe Thr Lys Met Gln Asp
            250                 255                 260

caa agt gac ctt aat tgg ttt gaa aat att aat ggg atg gta cca aat     869
Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile Asn Gly Met Val Pro Asn
        265                 270                 275

tat tcg gac agt ttt tgg aac att gga aat gat gaa gac ttc tgg ctc     917
Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn Asp Glu Asp Phe Trp Leu
    280                 285                 290

tta caa caa cat caa caa gtc cac gac aat gga agc ttc tga             959
Leu Gln Gln His Gln Gln Val His Asp Asn Gly Ser Phe  *
295                 300                 305

atagacaaga agctatgcgg cc                                            981

<210> 156
<211> 307
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (28)...(134)
<223> Conserved domain

<400> 156
Met Gly Asp Lys Gly Arg Ser Leu Lys Ile Asn Lys Asn Met Glu Glu
 1               5                  10                  15
Phe Thr Lys Val Glu Glu Glu Met Asp Val Arg Arg Gly Pro Trp Thr
            20                  25                  30
Val Glu Glu Asp Leu Glu Leu Ile Asn Tyr Ile Ala Ser His Gly Glu
        35                  40                  45
Gly Arg Trp Asn Ser Leu Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly
    50                  55                  60
Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg
65                  70                  75                  80
Arg Gly Asn Ile Thr Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His
                85                  90                  95
Thr Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly
            100                 105                 110
Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys
        115                 120                 125
His Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Gln Gln Phe Lys Asp
    130                 135                 140
Thr Met Lys Tyr Leu Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala
145                 150                 155                 160
Ala Ser Ile Gly Ser Val Ser Met Ser Ser Cys Val Thr Thr Ser Ser
                165                 170                 175
Asp Gln Phe Val Ile Asn Asn Asn Asn Thr Asn Asn Val Asp Asn Leu
```

```
                180                     185                     190
Ala Leu Met Ser Asn Pro Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser
            195                     200                     205
Val Ala Val Ser Pro Val Ser Asp Leu Thr Glu Cys Gln Val Ser Ser
    210                     215                     220
Glu Val Trp Lys Ile Gly Gln Asp Glu Asn Leu Val Asp Pro Lys Met
225                     230                     235                     240
Thr Ser Pro Asn Tyr Met Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp
                245                     250                     255
Phe Thr Lys Met Gln Asp Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile
                260                     265                     270
Asn Gly Met Val Pro Asn Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn
            275                     280                     285
Asp Glu Asp Phe Trp Leu Leu Gln Gln His Gln Gln Val His Asp Asn
    290                     295                     300
Gly Ser Phe
305


<210> 157
<211> 1891
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (108)...(1664)

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aagattttta gagagagagc taccacgttt tcgtatctcc gggaacg atg gat gaa   116
                                                    Met Asp Glu
                                                     1

tca agt att att ccg gca gag aaa gtg gcc gga gct gag aaa aaa gag   164
Ser Ser Ile Ile Pro Ala Glu Lys Val Ala Gly Ala Glu Lys Lys Glu
    5                  10                  15

ctt caa ggg ctg ctt aag acg gcg gtt caa tct gtg gac tgg act tat   212
Leu Gln Gly Leu Leu Lys Thr Ala Val Gln Ser Val Asp Trp Thr Tyr
 20                  25                  30                  35

agt gtc ttc tgg caa ttt tgt cct caa caa cgg gtc ttg gtg tgg ggg   260
Ser Val Phe Trp Gln Phe Cys Pro Gln Gln Arg Val Leu Val Trp Gly
                40                  45                  50

aat gga tac tac aac ggt gca ata aag acg agg aag aca act caa cca   308
Asn Gly Tyr Tyr Asn Gly Ala Ile Lys Thr Arg Lys Thr Thr Gln Pro
            55                  60                  65

gcg gag gtg acg gca gaa gag gcg gcg tta gag agg agc caa cag ctc   356
Ala Glu Val Thr Ala Glu Glu Ala Ala Leu Glu Arg Ser Gln Gln Leu
        70                  75                  80

agg gag ctt tat gag aca ctt tta gcc gga gag tca acg tca gaa gca   404
Arg Glu Leu Tyr Glu Thr Leu Leu Ala Gly Glu Ser Thr Ser Glu Ala
    85                  90                  95
```

aga gca tgc acc gca ttg tca ccg gag gat ttg acg gag aca gaa tgg 452
Arg Ala Cys Thr Ala Leu Ser Pro Glu Asp Leu Thr Glu Thr Glu Trp
100 105 110 115

ttt tat cta atg tgc gtc tct ttc tct ttt cct cct cca tct ggg atg 500
Phe Tyr Leu Met Cys Val Ser Phe Ser Phe Pro Pro Pro Ser Gly Met
120 125 130

cca gga aaa gcg tat gca agg agg aag cac gta tgg cta agt ggt gca 548
Pro Gly Lys Ala Tyr Ala Arg Arg Lys His Val Trp Leu Ser Gly Ala
135 140 145

aat gaà gtt gac agt aaa act ttt tct aga gct att ctc gct aag agt 596
Asn Glu Val Asp Ser Lys Thr Phe Ser Arg Ala Ile Leu Ala Lys Ser
150 155 160

gct aaa att cag aca gtg gtt tgc att cca atg ctt gat ggt gtt gtg 644
Ala Lys Ile Gln Thr Val Val Cys Ile Pro Met Leu Asp Gly Val Val
165 170 175

gaa cta ggc aca acg aaa aag gta aga gaa gat gta gag ttt gtt gag 692
Glu Leu Gly Thr Thr Lys Lys Val Arg Glu Asp Val Glu Phe Val Glu
180 185 190 195

ctc aca aag agt ttc ttc tat gac cac tgc aag acg aac cca aag ccg 740
Leu Thr Lys Ser Phe Phe Tyr Asp His Cys Lys Thr Asn Pro Lys Pro
200 205 210

gct ctt tct gaa cac tcc acc tac gaa gtg cat gaa gaa gcc gaa gac 788
Ala Leu Ser Glu His Ser Thr Tyr Glu Val His Glu Glu Ala Glu Asp
215 220 225

gaa gaa gaa gta gaa gaa gag atg aca atg tca gag gaa atg agg ctt 836
Glu Glu Glu Val Glu Glu Glu Met Thr Met Ser Glu Glu Met Arg Leu
230 235 240

ggc tct cct gat gat gaa gat gtt tcc aat caa aat cta cac tct gat 884
Gly Ser Pro Asp Asp Glu Asp Val Ser Asn Gln Asn Leu His Ser Asp
245 250 255

ctt cat att gaa tca acc cat acg tta gac aca cat atg gac atg atg 932
Leu His Ile Glu Ser Thr His Thr Leu Asp Thr His Met Asp Met Met
260 265 270 275

aat cta atg gag gaa ggt gga aac tat tct cag aca gta aca aca ctt 980
Asn Leu Met Glu Glu Gly Gly Asn Tyr Ser Gln Thr Val Thr Thr Leu
280 285 290

ctc atg tca cac ccc aca agt ctt ctt tca gat tca gtt tcc aca tct 1028
Leu Met Ser His Pro Thr Ser Leu Leu Ser Asp Ser Val Ser Thr Ser
295 300 305

tct tac atc caa tca tcg ttt gcc acg tgg agg gtt gag aat ggc aaa 1076
Ser Tyr Ile Gln Ser Ser Phe Ala Thr Trp Arg Val Glu Asn Gly Lys
310 315 320

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gag cat cag caa gtg aaa acg gcg ccg tcg tca caa tgg gtg ctc aaa     1124
Glu His Gln Gln Val Lys Thr Ala Pro Ser Ser Gln Trp Val Leu Lys
    325                 330                 335

caa atg atc ttc aga gtt cct ttc ctc cat gac aac act aaa gat aag     1172
Gln Met Ile Phe Arg Val Pro Phe Leu His Asp Asn Thr Lys Asp Lys
340                 345                 350                 355

agg cta ccg cgg gaa gat ctg agc cac gta gta gca gag cga cgc agg     1220
Arg Leu Pro Arg Glu Asp Leu Ser His Val Val Ala Glu Arg Arg Arg
                360                 365                 370

agg gag aag ctg aac gag aaa ttc ata acg ttg aga tca atg gtt cca     1268
Arg Glu Lys Leu Asn Glu Lys Phe Ile Thr Leu Arg Ser Met Val Pro
            375                 380                 385

ttt gtg acc aag atg gat aaa gtc tca atc ctt gga gac acc att gcg     1316
Phe Val Thr Lys Met Asp Lys Val Ser Ile Leu Gly Asp Thr Ile Ala
        390                 395                 400

tac gta aat cat ctt cga aag agg gtc cat gag ctt gag aat act cat     1364
Tyr Val Asn His Leu Arg Lys Arg Val His Glu Leu Glu Asn Thr His
    405                 410                 415

cat gag caa cag cat aag cgg acg cgt act tgt aag aga aaa aca tcg     1412
His Glu Gln Gln His Lys Arg Thr Arg Thr Cys Lys Arg Lys Thr Ser
420                 425                 430                 435

gag gag gtg gag gtt tcc atc ata gag aat gat gtt ttg tta gag atg     1460
Glu Glu Val Glu Val Ser Ile Ile Glu Asn Asp Val Leu Leu Glu Met
                440                 445                 450

aga tgt gag tac cga gat ggt ttg ttg ctt gac att ctt cag gtt ctt     1508
Arg Cys Glu Tyr Arg Asp Gly Leu Leu Leu Asp Ile Leu Gln Val Leu
            455                 460                 465

cat gag ctt ggt ata gag act acg gca gtt cat acc tcg gtg aac gac     1556
His Glu Leu Gly Ile Glu Thr Thr Ala Val His Thr Ser Val Asn Asp
        470                 475                 480

cat gat ttc gag gcg gag ata agg gcg aaa gta aga ggg aag aaa gca     1604
His Asp Phe Glu Ala Glu Ile Arg Ala Lys Val Arg Gly Lys Lys Ala
    485                 490                 495

agc atc gct gag gtc aaa aga gcc atc cac caa gtc ata ata cat gat     1652
Ser Ile Ala Glu Val Lys Arg Ala Ile His Gln Val Ile Ile His Asp
500                 505                 510                 515

act aat cta tag accctaactt tattgatgcc aactctagag aaggataatt         1704
Thr Asn Leu  *

aagcgtattt ttgttttagc ctcacatgta ttaagacatc agttacatat atagccggat 1764
gcaacatata aatgaaaatg tactagatga tattgttcat ttgtccaatg tagtacttgt 1824
gtatgatgca attgcaacat ataaatgcaa atgtactaga tgacgatgtt gttcgttgtc 1884
caattta                                                           1891
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<210> 158
<211> 518
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (353)...(420)
<223> Conserved domain

<400> 158
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 1               5                  10                  15
Lys Lys Glu Leu Gln Gly Leu Leu Lys Thr Ala Val Gln Ser Val Asp
            20                  25                  30
Trp Thr Tyr Ser Val Phe Trp Gln Phe Cys Pro Gln Gln Arg Val Leu
        35                  40                  45
Val Trp Gly Asn Gly Tyr Tyr Asn Gly Ala Ile Lys Thr Arg Lys Thr
    50                  55                  60
Thr Gln Pro Ala Glu Val Thr Ala Glu Glu Ala Ala Leu Glu Arg Ser
65                  70                  75                  80
Gln Gln Leu Arg Glu Leu Tyr Glu Thr Leu Leu Ala Gly Glu Ser Thr
                85                  90                  95
Ser Glu Ala Arg Ala Cys Thr Ala Leu Ser Pro Glu Asp Leu Thr Glu
            100                 105                 110
Thr Glu Trp Phe Tyr Leu Met Cys Val Ser Phe Ser Phe Pro Pro Pro
        115                 120                 125
Ser Gly Met Pro Gly Lys Ala Tyr Ala Arg Arg Lys His Val Trp Leu
    130                 135                 140
Ser Gly Ala Asn Glu Val Asp Ser Lys Thr Phe Ser Arg Ala Ile Leu
145                 150                 155                 160
Ala Lys Ser Ala Lys Ile Gln Thr Val Val Cys Ile Pro Met Leu Asp
                165                 170                 175
Gly Val Val Glu Leu Gly Thr Thr Lys Lys Val Arg Glu Asp Val Glu
            180                 185                 190
Phe Val Glu Leu Thr Lys Ser Phe Phe Tyr Asp His Cys Lys Thr Asn
        195                 200                 205
Pro Lys Pro Ala Leu Ser Glu His Ser Thr Tyr Glu Val His Glu Glu
    210                 215                 220
Ala Glu Asp Glu Glu Glu Val Glu Glu Glu Met Thr Met Ser Glu Glu
225                 230                 235                 240
Met Arg Leu Gly Ser Pro Asp Asp Glu Asp Val Ser Asn Gln Asn Leu
                245                 250                 255
His Ser Asp Leu His Ile Glu Ser Thr His Thr Leu Asp Thr His Met
            260                 265                 270
Asp Met Met Asn Leu Met Glu Glu Gly Gly Asn Tyr Ser Gln Thr Val
        275                 280                 285
Thr Thr Leu Leu Met Ser His Pro Thr Ser Leu Leu Ser Asp Ser Val
    290                 295                 300
Ser Thr Ser Ser Tyr Ile Gln Ser Ser Phe Ala Thr Trp Arg Val Glu
305                 310                 315                 320
Asn Gly Lys Glu His Gln Gln Val Lys Thr Ala Pro Ser Ser Gln Trp
                325                 330                 335
Val Leu Lys Gln Met Ile Phe Arg Val Pro Phe Leu His Asp Asn Thr
            340                 345                 350
Lys Asp Lys Arg Leu Pro Arg Glu Asp Leu Ser His Val Val Ala Glu
        355                 360                 365
```

```
Arg Arg Arg Arg Glu Lys Leu Asn Glu Lys Phe Ile Thr Leu Arg Ser
    370                 375                 380
Met Val Pro Phe Val Thr Lys Met Asp Lys Val Ser Ile Leu Gly Asp
385                 390                 395                 400
Thr Ile Ala Tyr Val Asn His Leu Arg Lys Arg Val His Glu Leu Glu
                405                 410                 415
Asn Thr His His Glu Gln Gln His Lys Arg Thr Arg Thr Cys Lys Arg
            420                 425                 430
Lys Thr Ser Glu Glu Val Glu Val Ser Ile Ile Glu Asn Asp Val Leu
        435                 440                 445
Leu Glu Met Arg Cys Glu Tyr Arg Asp Gly Leu Leu Leu Asp Ile Leu
    450                 455                 460
Gln Val Leu His Glu Leu Gly Ile Glu Thr Thr Ala Val His Thr Ser
465                 470                 475                 480
Val Asn Asp His Asp Phe Glu Ala Glu Ile Arg Ala Lys Val Arg Gly
                485                 490                 495
Lys Lys Ala Ser Ile Ala Glu Val Lys Arg Ala Ile His Gln Val Ile
            500                 505                 510
Ile His Asp Thr Asn Leu
        515
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<210> 159
<211> 558
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(558)

<400> 159
atg act cga ccg tca aga tta ctt gag acg gcg gcg cca cca cca caa      48
Met Thr Arg Pro Ser Arg Leu Leu Glu Thr Ala Ala Pro Pro Pro Gln
 1               5                  10                  15

ccg tcg gag gag atg atc gca gcg gaa tcc gac atg gtg gtg atc ttg      96
Pro Ser Glu Glu Met Ile Ala Ala Glu Ser Asp Met Val Val Ile Leu
            20                  25                  30

tcg gct ctt ctt tgc gct ctt atc tgc gtt gct ggt ctc gcc gcc gtc     144
Ser Ala Leu Leu Cys Ala Leu Ile Cys Val Ala Gly Leu Ala Ala Val
        35                  40                  45

gta cga tgc gct tgg ctc cgg cgg ttt aca gcc gga gga gat tcg ccg     192
Val Arg Cys Ala Trp Leu Arg Arg Phe Thr Ala Gly Gly Asp Ser Pro
    50                  55                  60

tca ccg aac aaa ggc ttg aaa aag aaa gct ctt cag tct ctt cca aga     240
Ser Pro Asn Lys Gly Leu Lys Lys Lys Ala Leu Gln Ser Leu Pro Arg
 65                  70                  75                  80

tcc act ttc acc gcc gcg gaa tca acc tcc ggc gcc gcc gct gaa gag     288
Ser Thr Phe Thr Ala Ala Glu Ser Thr Ser Gly Ala Ala Ala Glu Glu
                85                  90                  95

gga gac tcg acg gaa tgt gct att tgc ctc act gac ttc gcc gac ggt     336
```

```
Gly Asp Ser Thr Glu Cys Ala Ile Cys Leu Thr Asp Phe Ala Asp Gly
            100                 105                 110

gaa gaa ata aga gtg ctt cct ctt tgt ggt cat tct ttc cac gtg gag    384
Glu Glu Ile Arg Val Leu Pro Leu Cys Gly His Ser Phe His Val Glu
        115                 120                 125

tgt att gac aaa tgg cta gtt tct agg tct tct tgt cct tct tgt cgc    432
Cys Ile Asp Lys Trp Leu Val Ser Arg Ser Ser Cys Pro Ser Cys Arg
    130                 135                 140

agg att ctt acg ccg gtg aga tgt gac cgg tgt ggt cat gct tct acg    480
Arg Ile Leu Thr Pro Val Arg Cys Asp Arg Cys Gly His Ala Ser Thr
145                 150                 155                 160

gcg gag atg aaa gat caa gct cat cgt cat caa cat cac caa cac tct    528
Ala Glu Met Lys Asp Gln Ala His Arg His Gln His His Gln His Ser
                165                 170                 175

tct act acc att cct acg ttt ctt cct taa                            558
Ser Thr Thr Ile Pro Thr Phe Leu Pro  *
            180                 185


<210> 160
<211> 185
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (114)...(155)
<223> Conserved domain

<400> 160
Met Thr Arg Pro Ser Arg Leu Leu Glu Thr Ala Ala Pro Pro Pro Gln
 1               5                  10                  15
Pro Ser Glu Glu Met Ile Ala Ala Glu Ser Asp Met Val Val Ile Leu
            20                  25                  30
Ser Ala Leu Leu Cys Ala Leu Ile Cys Val Ala Gly Leu Ala Ala Val
        35                  40                  45
Val Arg Cys Ala Trp Leu Arg Arg Phe Thr Ala Gly Gly Asp Ser Pro
    50                  55                  60
Ser Pro Asn Lys Gly Leu Lys Lys Lys Ala Leu Gln Ser Leu Pro Arg
65                  70                  75                  80
Ser Thr Phe Thr Ala Ala Glu Ser Thr Ser Gly Ala Ala Ala Glu Glu
                85                  90                  95
Gly Asp Ser Thr Glu Cys Ala Ile Cys Leu Thr Asp Phe Ala Asp Gly
            100                 105                 110
Glu Glu Ile Arg Val Leu Pro Leu Cys Gly His Ser Phe His Val Glu
        115                 120                 125
Cys Ile Asp Lys Trp Leu Val Ser Arg Ser Ser Cys Pro Ser Cys Arg
    130                 135                 140
Arg Ile Leu Thr Pro Val Arg Cys Asp Arg Cys Gly His Ala Ser Thr
145                 150                 155                 160
Ala Glu Met Lys Asp Gln Ala His Arg His Gln His His Gln His Ser
                165                 170                 175
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```
Ser Thr Thr Ile Pro Thr Phe Leu Pro
            180                 185


<210> 161
<211> 2001
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (175)...(1878)

<400> 161
tgcttaattc caatgccatc gtgatcgatt catctctctc tctctcttcc aattttccca 60
attctttttt aaaaccctaa tttttcagat atctgattat ctcttgtatt tcttctactc 120
gatttgctcc cataaaaacc cttactttct tcaagttctg gttttcaccg attg atg   177
                                                            Met
                                                             1

ggt cgt ggc tca gtg acg tcg ctt gct cct ggg ttc cgt ttt cac ccg   225
Gly Arg Gly Ser Val Thr Ser Leu Ala Pro Gly Phe Arg Phe His Pro
            5                   10                  15

acg gat gag gaa ctt gtt cgc tac tac ctt aag cgt aag gtc tgc aac   273
Thr Asp Glu Glu Leu Val Arg Tyr Tyr Leu Lys Arg Lys Val Cys Asn
        20                  25                  30

aaa ccc ttt aag ttc gat gct att tcc gtc acc gac ata tac aag tct   321
Lys Pro Phe Lys Phe Asp Ala Ile Ser Val Thr Asp Ile Tyr Lys Ser
    35                  40                  45

gag cct tgg gat cta cca gat aag tcg aag ctg aaa agt aga gac ttg   369
Glu Pro Trp Asp Leu Pro Asp Lys Ser Lys Leu Lys Ser Arg Asp Leu
 50                  55                  60                  65

gaa tgg tac ttc ttt agt atg ctg gat aag aag tac agt aat ggt tcc   417
Glu Trp Tyr Phe Phe Ser Met Leu Asp Lys Lys Tyr Ser Asn Gly Ser
                 70                  75                  80

aag acg aat cgt gct acg gag aaa ggg tat tgg aag acg act ggg aaa   465
Lys Thr Asn Arg Ala Thr Glu Lys Gly Tyr Trp Lys Thr Thr Gly Lys
             85                  90                  95

gat cgg gag att cgt aat ggt tca aga gtc gtt ggg atg aag aag aca   513
Asp Arg Glu Ile Arg Asn Gly Ser Arg Val Val Gly Met Lys Lys Thr
        100                 105                 110

ctt gtt tat cac aag ggt cga gct cct cgt ggt gaa agg acc aat tgg   561
Leu Val Tyr His Lys Gly Arg Ala Pro Arg Gly Glu Arg Thr Asn Trp
    115                 120                 125

gtt atg cat gag tat cgg ctt tct gat gag gac ttg aag aaa gct ggt   609
Val Met His Glu Tyr Arg Leu Ser Asp Glu Asp Leu Lys Lys Ala Gly
130                 135                 140                 145

gtg cca caa gaa gca tat gtg tta tgt agg ata ttc cag aaa agt ggt   657
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Val Pro Gln Glu Ala Tyr Val Leu Cys Arg Ile Phe Gln Lys Ser Gly
150 155 160

acg ggt cct aag aat ggg gag cag tat ggt gct cct tat ctt gag gag 705
Thr Gly Pro Lys Asn Gly Glu Gln Tyr Gly Ala Pro Tyr Leu Glu Glu
165 170 175

gag tgg gaa gaa gat gga atg act tat gta cct gct caa gat gct ttc 753
Glu Trp Glu Glu Asp Gly Met Thr Tyr Val Pro Ala Gln Asp Ala Phe
180 185 190

agt gaa gga ttg gct ttg aat gat gat gtt tat gtc gat att gat gac 801
Ser Glu Gly Leu Ala Leu Asn Asp Asp Val Tyr Val Asp Ile Asp Asp
195 200 205

att gac gag aag ccc gaa aat ctg gtg gtc tat gat gcc gtt cct att 849
Ile Asp Glu Lys Pro Glu Asn Leu Val Val Tyr Asp Ala Val Pro Ile
210 215 220 225

cta cct aac tat tgt cat ggg gaa tca agt aac aat gtt gaa tca ggc 897
Leu Pro Asn Tyr Cys His Gly Glu Ser Ser Asn Asn Val Glu Ser Gly
230 235 240

aat tac tca gac tct gga aat tac att caa cca gga aac aat gtt gtc 945
Asn Tyr Ser Asp Ser Gly Asn Tyr Ile Gln Pro Gly Asn Asn Val Val
245 250 255

gac tct ggt ggg tac ttt gaa caa cca att gaa act ttt gag gaa gat 993
Asp Ser Gly Gly Tyr Phe Glu Gln Pro Ile Glu Thr Phe Glu Glu Asp
260 265 270

cgg aag cct att ata cgg gag ggt agc att cag cct tgt tct ctg ttt 1041
Arg Lys Pro Ile Ile Arg Glu Gly Ser Ile Gln Pro Cys Ser Leu Phe
275 280 285

cca gag gaa caa att ggc tgt ggt gtg caa gac gaa aat gtg gtg aat 1089
Pro Glu Glu Gln Ile Gly Cys Gly Val Gln Asp Glu Asn Val Val Asn
290 295 300 305

ctg gaa tct tcc aac aat aat gtg ttt gta gct gat aca tgc tac agt 1137
Leu Glu Ser Ser Asn Asn Asn Val Phe Val Ala Asp Thr Cys Tyr Ser
310 315 320

gac att cct att gat cat aac tat tta ccc gat gag cca ttc atg gat 1185
Asp Ile Pro Ile Asp His Asn Tyr Leu Pro Asp Glu Pro Phe Met Asp
325 330 335

cct aat aac aat ctt cca ctc aac gat ggt ctg tac ctg gaa acg aat 1233
Pro Asn Asn Asn Leu Pro Leu Asn Asp Gly Leu Tyr Leu Glu Thr Asn
340 345 350

gat ctc agc tgt gct caa caa gat gat ttt aac ttc gaa gat tat ctc 1281
Asp Leu Ser Cys Ala Gln Gln Asp Asp Phe Asn Phe Glu Asp Tyr Leu
355 360 365

agc ttc ttt gat gat gag ggt ttg act ttt gac gat tct cta tta atg 1329
Ser Phe Phe Asp Asp Glu Gly Leu Thr Phe Asp Asp Ser Leu Leu Met

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370                 375                 380                 385

gga cct gaa gat ttt ctt ccc aac caa gaa gcc ctt gac cag aaa cct     1377
Gly Pro Glu Asp Phe Leu Pro Asn Gln Glu Ala Leu Asp Gln Lys Pro
                390                 395                 400

gcc cct aaa gaa ttg gag aag gag gtc gca gga ggc aaa gag gca gtg     1425
Ala Pro Lys Glu Leu Glu Lys Glu Val Ala Gly Gly Lys Glu Ala Val
            405                 410                 415

gag gaa aag gaa agt ggc gaa gga tct tct tca aaa caa gat aca gat     1473
Glu Glu Lys Glu Ser Gly Glu Gly Ser Ser Ser Lys Gln Asp Thr Asp
        420                 425                 430

ttc aag gac ttt gat tca gct ccg aag tac cca ttt ctc aaa aag acg     1521
Phe Lys Asp Phe Asp Ser Ala Pro Lys Tyr Pro Phe Leu Lys Lys Thr
    435                 440                 445

agc cac atg ctt gga gcc att cct act cca tct tca ttt gct tca cag     1569
Ser His Met Leu Gly Ala Ile Pro Thr Pro Ser Ser Phe Ala Ser Gln
450                 455                 460                 465

ttc caa aca aag gac gca atg cgt cta cac gca gca caa tct tct ggt     1617
Phe Gln Thr Lys Asp Ala Met Arg Leu His Ala Ala Gln Ser Ser Gly
                470                 475                 480

tca gtt cac gtg act gca ggt atg atg aga ata tca aac atg act cta     1665
Ser Val His Val Thr Ala Gly Met Met Arg Ile Ser Asn Met Thr Leu
            485                 490                 495

gca gcg gac agc ggt atg ggc tgg tca tat gac aag aac ggt aac ctc     1713
Ala Ala Asp Ser Gly Met Gly Trp Ser Tyr Asp Lys Asn Gly Asn Leu
        500                 505                 510

aac gta gtc ctt tca ttc ggg gta gtc caa cag gat gat gcg atg act     1761
Asn Val Val Leu Ser Phe Gly Val Val Gln Gln Asp Asp Ala Met Thr
    515                 520                 525

gcc tcg gga agc aag aca gga att acg gcg aca aga gct atg tta gtc     1809
Ala Ser Gly Ser Lys Thr Gly Ile Thr Ala Thr Arg Ala Met Leu Val
530                 535                 540                 545

ttc atg tgt tta tgg gtt ctc cta ctc tct gtt agc ttc aaa ata gta     1857
Phe Met Cys Leu Trp Val Leu Leu Leu Ser Val Ser Phe Lys Ile Val
                550                 555                 560

acc atg gtg tct gct cgg taa taggatcaaa gttgaatcgt ctcaaagact        1908
Thr Met Val Ser Ala Arg  *
            565

tttttggtg tttgtacctc tccaatcata tagcctttaa ctttggcagt gctttgctgc 1968
tcaatattta aattttaaaa aaaaaaaaaa aaa                              2001

<210> 162
<211> 567
<212> PRT
<213> Arabidopsis thaliana
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<220>
<221> DOMAIN
<222> (12)...(156)
<223> Conserved domain

<400> 162
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 1               5                  10                  15
Pro Thr Asp Glu Glu Leu Val Arg Tyr Tyr Leu Lys Arg Lys Val Cys
            20                  25                  30
Asn Lys Pro Phe Lys Phe Asp Ala Ile Ser Val Thr Asp Ile Tyr Lys
        35                  40                  45
Ser Glu Pro Trp Asp Leu Pro Asp Lys Ser Lys Leu Lys Ser Arg Asp
    50                  55                  60
Leu Glu Trp Tyr Phe Phe Ser Met Leu Asp Lys Lys Tyr Ser Asn Gly
65                  70                  75                  80
Ser Lys Thr Asn Arg Ala Thr Glu Lys Gly Tyr Trp Lys Thr Thr Gly
                85                  90                  95
Lys Asp Arg Glu Ile Arg Asn Gly Ser Arg Val Val Gly Met Lys Lys
            100                 105                 110
Thr Leu Val Tyr His Lys Gly Arg Ala Pro Arg Gly Glu Arg Thr Asn
        115                 120                 125
Trp Val Met His Glu Tyr Arg Leu Ser Asp Glu Asp Leu Lys Lys Ala
    130                 135                 140
Gly Val Pro Gln Glu Ala Tyr Val Leu Cys Arg Ile Phe Gln Lys Ser
145                 150                 155                 160
Gly Thr Gly Pro Lys Asn Gly Glu Gln Tyr Gly Ala Pro Tyr Leu Glu
                165                 170                 175
Glu Glu Trp Glu Glu Asp Gly Met Thr Tyr Val Pro Ala Gln Asp Ala
            180                 185                 190
Phe Ser Glu Gly Leu Ala Leu Asn Asp Asp Val Tyr Val Asp Ile Asp
        195                 200                 205
Asp Ile Asp Glu Lys Pro Glu Asn Leu Val Val Tyr Asp Ala Val Pro
    210                 215                 220
Ile Leu Pro Asn Tyr Cys His Gly Glu Ser Ser Asn Asn Val Glu Ser
225                 230                 235                 240
Gly Asn Tyr Ser Asp Ser Gly Asn Tyr Ile Gln Pro Gly Asn Asn Val
                245                 250                 255
Val Asp Ser Gly Gly Tyr Phe Glu Gln Pro Ile Glu Thr Phe Glu Glu
            260                 265                 270
Asp Arg Lys Pro Ile Ile Arg Glu Gly Ser Ile Gln Pro Cys Ser Leu
        275                 280                 285
Phe Pro Glu Glu Gln Ile Gly Cys Gly Val Gln Asp Glu Asn Val Val
    290                 295                 300
Asn Leu Glu Ser Ser Asn Asn Asn Val Phe Val Ala Asp Thr Cys Tyr
305                 310                 315                 320
Ser Asp Ile Pro Ile Asp His Asn Tyr Leu Pro Asp Glu Pro Phe Met
                325                 330                 335
Asp Pro Asn Asn Asn Leu Pro Leu Asn Asp Gly Leu Tyr Leu Glu Thr
            340                 345                 350
Asn Asp Leu Ser Cys Ala Gln Gln Asp Asp Phe Asn Phe Glu Asp Tyr
        355                 360                 365
Leu Ser Phe Phe Asp Asp Glu Gly Leu Thr Phe Asp Asp Ser Leu Leu
    370                 375                 380
Met Gly Pro Glu Asp Phe Leu Pro Asn Gln Glu Ala Leu Asp Gln Lys
385                 390                 395                 400
```

Pro Ala Pro Lys Glu Leu Glu Lys Glu Val Ala Gly Gly Lys Glu Ala
405 410 415
Val Glu Glu Lys Glu Ser Gly Glu Gly Ser Ser Ser Lys Gln Asp Thr
420 425 430
Asp Phe Lys Asp Phe Asp Ser Ala Pro Lys Tyr Pro Phe Leu Lys Lys
435 440 445
Thr Ser His Met Leu Gly Ala Ile Pro Thr Pro Ser Ser Phe Ala Ser
450 455 460
Gln Phe Gln Thr Lys Asp Ala Met Arg Leu His Ala Ala Gln Ser Ser
465 470 475 480
Gly Ser Val His Val Thr Ala Gly Met Met Arg Ile Ser Asn Met Thr
485 490 495
Leu Ala Ala Asp Ser Gly Met Gly Trp Ser Tyr Asp Lys Asn Gly Asn
500 505 510
Leu Asn Val Val Leu Ser Phe Gly Val Val Gln Gln Asp Asp Ala Met
515 520 525
Thr Ala Ser Gly Ser Lys Thr Gly Ile Thr Ala Thr Arg Ala Met Leu
530 535 540
Val Phe Met Cys Leu Trp Val Leu Leu Leu Ser Val Ser Phe Lys Ile
545 550 555 560
Val Thr Met Val Ser Ala Arg
565

<210> 163
<211> 890
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (108)...(806)

<400> 163
cattcaaaaa catcatatat atacacaaac acactttgat acaacaaaaa aaaacagaac 60
acaaacaaaa acacattgta acattagttt aagcattaag cttcttt atg tcg aat 116
Met Ser Asn
1

aat aat aat tct ccg acc acc gtg aat caa gaa acg acg acg tct cgt 164
Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr Thr Ser Arg
5 10 15

gaa gtc tca atc aca ttg cct act gat caa tct cct caa acc tca cca 212
Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln Thr Ser Pro
20 25 30 35

gga tca tct tct tct cct tca ccg aga cct tcc ggt gga tca ccg gcg 260
Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly Ser Pro Ala
40 45 50

aga aga acg gcg act gga tta tcc ggc aag cac tct att ttc agg ggg 308
Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile Phe Arg Gly
55 60 65

att cga cta cgt aac gga aaa tgg gta tcg gag att aga gag cca cgt 356
Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg

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        70                  75                  80

aaa acg aca aga att tgg ctc ggg act tat ccg gta ccg gag atg gct    404
Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro Glu Met Ala
     85                  90                  95

gcc gcc gct tac gac gtg gct gcg tta gct tta aaa gga ccc gac gcc    452
Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Pro Asp Ala
100                 105                 110                 115

gtt ttg aat ttt cct ggt tta gct ttg act tac gtg gct ccg gtt tca    500
Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala Pro Val Ser
                120                 125                 130

aac tct gct gcg gat ata aga gcg gct gct agt aga gca gcg gag atg    548
Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala Ala Glu Met
            135                 140                 145

aag caa ccg gat cag ggt ggg gat gag aag gta ttg gaa ccg gtt caa    596
Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val Gln
        150                 155                 160

ccc ggc aaa gag gaa gaa tta gaa gaa gtg tcg tgt aac tcg tgt tcg    644
Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn Ser Cys Ser
    165                 170                 175

ttg gag ttt atg gat gag gaa gcg atg ttg aat atg ccg act ttg ttg    692
Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu Leu
180                 185                 190                 195

acg gag atg gct gaa ggg atg ttg atg agt cca ccg aga atg atg ata    740
Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met Ile
                200                 205                 210

cat ccg acg atg gaa gat gat tcg ccg gag aat cat gaa gga gat aat    788
His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp Asn
            215                 220                 225

ctt tgg agt tat aaa tga atccattgaa gctgctctct tttttattgt            836
Leu Trp Ser Tyr Lys  *
        230

tttccggtcg aatgagattt tcccccttttt ttttttctt tttgggtcgc tgtt         890

<210> 164
<211> 232
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (62)...(128)
<223> Conserved domain

<400> 164
Met Ser Asn Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr
 1               5                  10                  15
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Thr Ser Arg Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln
            20                  25                  30
Thr Ser Pro Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly
        35                  40                  45
Ser Pro Ala Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile
    50                  55                  60
Phe Arg Gly Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg
65                  70                  75                  80
Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro
                85                  90                  95
Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly
            100                 105                 110
Pro Asp Ala Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala
        115                 120                 125
Pro Val Ser Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala
    130                 135                 140
Ala Glu Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu
145                 150                 155                 160
Pro Val Gln Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn
                165                 170                 175
Ser Cys Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro
            180                 185                 190
Thr Leu Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg
        195                 200                 205
Met Met Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu
    210                 215                 220
Gly Asp Asn Leu Trp Ser Tyr Lys
225                 230

<210> 165
<211> 1728
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (106)...(1575)

<400> 165
ctttattttt tttcccctct tgtcgaaaac atcacatata aataaaaaac caaaaaccct 60
aatttataaa atatatataa aatagttata gctccccact tatat atg caa aag cca 117
                                                  Met Gln Lys Pro
                                                   1

aca tca agt atc tta aat gtc ata atg gac ggt gga gac agc gtc gga    165
Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly Asp Ser Val Gly
 5                  10                  15                  20

gga gga gga gga gat gat cac cac cgt cac ctc cac cat cac cac cgc    213
Gly Gly Gly Gly Asp Asp His His Arg His Leu His His His His Arg
                25                  30                  35

cct act ttc cct ttt caa cta ctc gga aaa cac gac ccc gac gac aac    261
Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp Pro Asp Asp Asn
            40                  45                  50
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cat caa caa caa cct tcc cct tcc tcc tcc tcc tct cta ttt tct ctc    309
His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser Ser Leu Phe Ser Leu
        55                  60                  65

cat caa cac caa caa tta tct caa tcg caa cct caa tcg caa tcg caa    357
His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln Ser Gln Ser Gln
    70                  75                  80

aag tca caa ccg cag aca acg caa aaa gag tta tta caa acg caa gag    405
Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu Gln Thr Gln Glu
85                  90                  95                  100

gaa tct gcg gtg gtg gca gct aaa aag cca ccg ttg aaa cga gcg tcg    453
Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu Lys Arg Ala Ser
                105                 110                 115

acg aaa gac cga cac acg aaa gta gac gga aga ggg agg aga ata agg    501
Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly Arg Arg Ile Arg
            120                 125                 130

atg ccg gcg tta tgt gca gct agg gtt ttt cag cta acg cga gag cta    549
Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu
        135                 140                 145

ggt cat aaa tcc gac ggt gag aca ata gag tgg ctt ctt caa caa gct    597
Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala
    150                 155                 160

gaa cca tct gta atc gcc gcc acc gga acc gga aca atc ccg gcg aat    645
Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn
165                 170                 175                 180

ttc act tct tta aac atc tct ctc cgt tct tca ggc tct tcc atg tct    693
Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly Ser Ser Met Ser
                185                 190                 195

ctt cct tct cat ttc cgc tcc gcc gct tcc act ttt agc cct aat aac    741
Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe Ser Pro Asn Asn
            200                 205                 210

ata ttt tct ccg gcg atg ctt caa caa caa caa caa caa caa cgt ggt    789
Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln Gln Gln Arg Gly
        215                 220                 225

ggt ggt gtt ggg ttt cat cat ccc cat cta cag gga cgt gca cct acg    837
Gly Gly Val Gly Phe His His Pro His Leu Gln Gly Arg Ala Pro Thr
    230                 235                 240

tcg tct ttg ttt cct ggt att gat aac ttc aca cca acg acg tcg ttt    885
Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro Thr Thr Ser Phe
245                 250                 255                 260

ttg aac ttt cat aat cca aca aag caa gaa gga gat caa gat tct gaa    933
Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp Gln Asp Ser Glu
                265                 270                 275

gag tta aac tcg gag aag aaa aga aga atc caa acg acg tcg gat ttg    981
```

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Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr Thr Ser Asp Leu
            280                 285                 290

cat caa caa caa caa caa cac caa cat gat caa atc gga gga tat aca    1029
His Gln Gln Gln Gln Gln His Gln His Asp Gln Ile Gly Gly Tyr Thr
        295                 300                 305

ctt caa tct agc aac agt gga tct acg gcc acc gca gcc gcc gcg caa    1077
Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala Ala Ala Ala Gln
    310                 315                 320

caa ata ccg gga aat ttc tgg atg gtt gcg gcg gct gcg gct gca ggt    1125
Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala Ala Ala Ala Gly
325                 330                 335                 340

ggt ggt ggt ggt aat aac aac caa aca ggt ggt ctt atg aca gct tct    1173
Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu Met Thr Ala Ser
                345                 350                 355

att ggt act ggt ggc ggc ggt gga gag cct gtt tgg acg ttt cct tcc    1221
Ile Gly Thr Gly Gly Gly Gly Gly Glu Pro Val Trp Thr Phe Pro Ser
            360                 365                 370

att aac acg gca gcg gca gcg tta tat aga agt ggc gtt tcg ggc gtt    1269
Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly Val Ser Gly Val
        375                 380                 385

cca agc ggc gcg gtt tct agc ggt tta cat ttt atg aat ttc gca gcg    1317
Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met Asn Phe Ala Ala
    390                 395                 400

cca atg gca ttt ctt act gga caa caa cag cta gca aca act agt aat    1365
Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala Thr Thr Ser Asn
405                 410                 415                 420

cat gag att aat gaa gat agt aat aat aat gaa gga gga aga agt gac    1413
His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly Gly Arg Ser Asp
                425                 430                 435

ggt ggt ggt gat cat cat aat aca cag aga cat cat cat cat caa caa    1461
Gly Gly Gly Asp His His Asn Thr Gln Arg His His His His Gln Gln
            440                 445                 450

caa cat cat cat aat att ctc tcc ggc ttg aac cag tac gga cgg caa    1509
Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln Tyr Gly Arg Gln
        455                 460                 465

gtt tcc ggc gac tct caa gct agt gga tca ctt gga ggt ggt gat gag    1557
Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly Gly Gly Asp Glu
    470                 475                 480

gag gat cag caa gat tag acacacacaa aaacatttta atggtgggat          1605
Glu Asp Gln Gln Asp  *
485

tttctgccga cggcggtagc ggtgacggcg ttcggcggct gtgtaaaact tttgttttca 1665
ccgttaattt tttttatttt ctgtagtaat tttttttgct aagtaaaaaa aaaaaaaaaa 1725
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aaa 1728

<210> 166
<211> 489
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (116)...(179)
<223> Conserved domain

<400> 166
Met Gln Lys Pro Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly
1 5 10 15
Asp Ser Val Gly Gly Gly Gly Gly Asp Asp His His Arg His Leu His
20 25 30
His His His Arg Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp
35 40 45
Pro Asp Asp Asn His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser Ser
50 55 60
Leu Phe Ser Leu His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln
65 70 75 80
Ser Gln Ser Gln Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu
85 90 95
Gln Thr Gln Glu Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu
100 105 110
Lys Arg Ala Ser Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly
115 120 125
Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu
130 135 140
Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu
145 150 155 160
Leu Gln Gln Ala Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr
165 170 175
Ile Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly
180 185 190
Ser Ser Met Ser Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe
195 200 205
Ser Pro Asn Asn Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln
210 215 220
Gln Gln Arg Gly Gly Gly Val Gly Phe His His Pro His Leu Gln Gly
225 230 235 240
Arg Ala Pro Thr Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro
245 250 255
Thr Thr Ser Phe Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp
260 265 270
Gln Asp Ser Glu Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr
275 280 285
Thr Ser Asp Leu His Gln Gln Gln Gln Gln His Gln His Asp Gln Ile
290 295 300
Gly Gly Tyr Thr Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala
305 310 315 320
Ala Ala Ala Gln Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala
325 330 335
Ala Ala Ala Gly Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu
340 345 350

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Met Thr Ala Ser Ile Gly Thr Gly Gly Gly Gly Gly Glu Pro Val Trp
        355                 360                 365
Thr Phe Pro Ser Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly
    370                 375                 380
Val Ser Gly Val Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met
385                 390                 395                 400
Asn Phe Ala Ala Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala
                405                 410                 415
Thr Thr Ser Asn His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly
            420                 425                 430
Gly Arg Ser Asp Gly Gly Gly Asp His His Asn Thr Gln Arg His His
        435                 440                 445
His His Gln Gln Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln
    450                 455                 460
Tyr Gly Arg Gln Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly
465                 470                 475                 480
Gly Gly Asp Glu Glu Asp Gln Gln Asp
                485


<210> 167
<211> 2535
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(2535)

<400> 167
atg gga tgt tct cat tcc aag tta gat gat gaa gaa gca gtt cag atc      48
Met Gly Cys Ser His Ser Lys Leu Asp Asp Glu Glu Ala Val Gln Ile
 1               5                  10                  15

tgt aaa gac agg aaa cgt ttc atc aaa caa gct att gaa cat aga act      96
Cys Lys Asp Arg Lys Arg Phe Ile Lys Gln Ala Ile Glu His Arg Thr
            20                  25                  30

aag ttt gct tct ggt cac att gct tat att cac tct ctt aga aaa gtc     144
Lys Phe Ala Ser Gly His Ile Ala Tyr Ile His Ser Leu Arg Lys Val
        35                  40                  45

tct gat gct ctc cat gac ttt atc ctc caa gga gac aac aac aat gag     192
Ser Asp Ala Leu His Asp Phe Ile Leu Gln Gly Asp Asn Asn Asn Glu
    50                  55                  60

ttt gtt cct act ctc tgt caa gac tca ttc gtc act ccg gtc aag aga     240
Phe Val Pro Thr Leu Cys Gln Asp Ser Phe Val Thr Pro Val Lys Arg
65                  70                  75                  80

atg cca cag aga cgt cgt cga agc agc cgt agt aat agc ggt gag ttc     288
Met Pro Gln Arg Arg Arg Arg Ser Ser Arg Ser Asn Ser Gly Glu Phe
                85                  90                  95

atc tcc att tcg cct tct tcg att cct ccg aaa atg att caa ggt agg     336
Ile Ser Ile Ser Pro Ser Ser Ile Pro Pro Lys Met Ile Gln Gly Arg
            100                 105                 110
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cca aga tcg aat gtg aaa gcg aat tat ttg atg gct aat aga agt aga     384
Pro Arg Ser Asn Val Lys Ala Asn Tyr Leu Met Ala Asn Arg Ser Arg
        115                 120                 125

ccg gtt aga gtc gaa cag aga tct cct gaa acg ttt aga gtt gag aca     432
Pro Val Arg Val Glu Gln Arg Ser Pro Glu Thr Phe Arg Val Glu Thr
    130                 135                 140

ttt tct cca cct agt agt agt aac caa tat ggt gaa tca gat ggt ttc     480
Phe Ser Pro Pro Ser Ser Ser Asn Gln Tyr Gly Glu Ser Asp Gly Phe
145                 150                 155                 160

ttt gga atg aat atg aat atg aat act tct gcg tct act tca tct tcg     528
Phe Gly Met Asn Met Asn Met Asn Thr Ser Ala Ser Thr Ser Ser Ser
                165                 170                 175

ttt tgg aat ccg ttg agc tct cct gag caa agg tta agt agt cat aac     576
Phe Trp Asn Pro Leu Ser Ser Pro Glu Gln Arg Leu Ser Ser His Asn
            180                 185                 190

att cct cct cct tca ccg cag aat tcg cag tgg gat ttc ttc tgg aat     624
Ile Pro Pro Pro Ser Pro Gln Asn Ser Gln Trp Asp Phe Phe Trp Asn
        195                 200                 205

ccg ttt tct tcg ttg gat tat tat gga tac aat agt tat gac cga gga     672
Pro Phe Ser Ser Leu Asp Tyr Tyr Gly Tyr Asn Ser Tyr Asp Arg Gly
    210                 215                 220

agt gtt gat agt agg agt ggt ata gat gat gag att aga gga ttg aga     720
Ser Val Asp Ser Arg Ser Gly Ile Asp Asp Glu Ile Arg Gly Leu Arg
225                 230                 235                 240

cgt gtt aga gag gaa gaa ggg att cct gat ttg gaa gaa gat gat gaa     768
Arg Val Arg Glu Glu Glu Gly Ile Pro Asp Leu Glu Glu Asp Asp Glu
                245                 250                 255

cct cat aaa cct gaa cct gtc gtc aat gtg cgg ttt cag aat cat aat     816
Pro His Lys Pro Glu Pro Val Val Asn Val Arg Phe Gln Asn His Asn
            260                 265                 270

ccg aat ccg aaa gca acg gaa gag aat aga ggt aaa gtt gat aag agt     864
Pro Asn Pro Lys Ala Thr Glu Glu Asn Arg Gly Lys Val Asp Lys Ser
        275                 280                 285

tgt tgc aat gag gaa gtt aaa gtt gaa gat gtt gat gag gat gaa gac     912
Cys Cys Asn Glu Glu Val Lys Val Glu Asp Val Asp Glu Asp Glu Asp
    290                 295                 300

gag gat gga gat gag gat gat gat gag ttt acg gat agc ggg tgt gag     960
Glu Asp Gly Asp Glu Asp Asp Asp Glu Phe Thr Asp Ser Gly Cys Glu
305                 310                 315                 320

act gag aat gag gga gac gag aaa tgc gtt gct cct cca acg caa gaa    1008
Thr Glu Asn Glu Gly Asp Glu Lys Cys Val Ala Pro Pro Thr Gln Glu
                325                 330                 335
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cag cga aaa gct gag gtg tgt aga gga gga gaa gct aca ggg aat gtt     1056
Gln Arg Lys Ala Glu Val Cys Arg Gly Gly Glu Ala Thr Gly Asn Val
            340                 345                 350

gtt gga gta ggt aag gtt caa gag atg aag aat gtt gtt ggt gtt aga     1104
Val Gly Val Gly Lys Val Gln Glu Met Lys Asn Val Val Gly Val Arg
        355                 360                 365

gat gat gca aag acg acg ggg ttc acg gta tat gtg aac cgg aga cca     1152
Asp Asp Ala Lys Thr Thr Gly Phe Thr Val Tyr Val Asn Arg Arg Pro
    370                 375                 380

act agc atg gct gaa gta atc aaa gat ctt gaa gat cag ttc aca aca     1200
Thr Ser Met Ala Glu Val Ile Lys Asp Leu Glu Asp Gln Phe Thr Thr
385                 390                 395                 400

att tgt gat gcg gct aag gaa gtc tcg ggg cta ttg gaa gct ggt aga     1248
Ile Cys Asp Ala Ala Lys Glu Val Ser Gly Leu Leu Glu Ala Gly Arg
                405                 410                 415

gct caa tac aca tca tcc ttt aat gac cat agt ggt gag ttt atg aac     1296
Ala Gln Tyr Thr Ser Ser Phe Asn Asp His Ser Gly Glu Phe Met Asn
            420                 425                 430

aat gtt gca ata ttt ctc tcc agg aaa atg ctg aat cca gta gcg ttg     1344
Asn Val Ala Ile Phe Leu Ser Arg Lys Met Leu Asn Pro Val Ala Leu
        435                 440                 445

ttc cgc tcg ggt tca tca aga tct tcc tcg tca aga ttc ttg atc act     1392
Phe Arg Ser Gly Ser Ser Arg Ser Ser Ser Ser Arg Phe Leu Ile Thr
    450                 455                 460

tct tct ggt ggt tca aga gag agc ggg tct gaa agc aga agc gat gtt     1440
Ser Ser Gly Gly Ser Arg Glu Ser Gly Ser Glu Ser Arg Ser Asp Val
465                 470                 475                 480

tca gat gaa tct tgc atg att tca ggt agc cac caa aca aca ttg gac     1488
Ser Asp Glu Ser Cys Met Ile Ser Gly Ser His Gln Thr Thr Leu Asp
                485                 490                 495

aga ctt ttc gcg tgg gag aag aaa ctc tat gat gaa gtt agg gta agt     1536
Arg Leu Phe Ala Trp Glu Lys Lys Leu Tyr Asp Glu Val Arg Val Ser
            500                 505                 510

aac aag aga tat aag caa cta tct gga gaa cgt gtt cga aga gca tat     1584
Asn Lys Arg Tyr Lys Gln Leu Ser Gly Glu Arg Val Arg Arg Ala Tyr
        515                 520                 525

gaa aag aaa tgt atg cag ctg agg aat cag gac gtg aaa gga gat gat     1632
Glu Lys Lys Cys Met Gln Leu Arg Asn Gln Asp Val Lys Gly Asp Asp
    530                 535                 540

ccg ctt gcg gtt gat aaa act agg gct act atc aga gat cta gat aca     1680
Pro Leu Ala Val Asp Lys Thr Arg Ala Thr Ile Arg Asp Leu Asp Thr
545                 550                 555                 560

cag atc aag gtg tca ata cac tcc att gaa tcc atc tcc aaa aga atc     1728
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Gln Ile Lys Val Ser Ile His Ser Ile Glu Ser Ile Ser Lys Arg Ile
                565                 570                 575

gag act ctt cgt gac caa gaa ctg ttg cct cag ctt ctt gag ctc gtt      1776
Glu Thr Leu Arg Asp Gln Glu Leu Leu Pro Gln Leu Leu Glu Leu Val
            580                 585                 590

gaa gga ctg aca aat ggt aat cat gat cat aac aga tta aca agg atg      1824
Glu Gly Leu Thr Asn Gly Asn His Asp His Asn Arg Leu Thr Arg Met
        595                 600                 605

tgg aaa gta atg gcg gaa agt cac cag ata cag aaa cga aca cta gac      1872
Trp Lys Val Met Ala Glu Ser His Gln Ile Gln Lys Arg Thr Leu Asp
    610                 615                 620

gaa gcc aaa ctg tta ctt gca ggc aca ccg gtt tca aag cgt cac aag      1920
Glu Ala Lys Leu Leu Leu Ala Gly Thr Pro Val Ser Lys Arg His Lys
625                 630                 635                 640

aag aga caa cct cca ata atg cca gag gct att aac tct caa aga tta      1968
Lys Arg Gln Pro Pro Ile Met Pro Glu Ala Ile Asn Ser Gln Arg Leu
                645                 650                 655

gct caa tct gct ttg aat ctt gaa gct cag ctt cga aac tgg aga acc      2016
Ala Gln Ser Ala Leu Asn Leu Glu Ala Gln Leu Arg Asn Trp Arg Thr
            660                 665                 670

tgt ttt gaa ttc tgg atc acc tct cag aga tcc tac atg aaa gca tta      2064
Cys Phe Glu Phe Trp Ile Thr Ser Gln Arg Ser Tyr Met Lys Ala Leu
        675                 680                 685

tct ggt tgg ctt cta aga tgt ttc aga tgt gat cct gac ccc gaa aaa      2112
Ser Gly Trp Leu Leu Arg Cys Phe Arg Cys Asp Pro Asp Pro Glu Lys
    690                 695                 700

gtt aga tta tcc tca tgt ctt cac ccg ata tac cga gtc tgc att caa      2160
Val Arg Leu Ser Ser Cys Leu His Pro Ile Tyr Arg Val Cys Ile Gln
705                 710                 715                 720

tgg tca agg ttg ctt aac agc ttg aat gaa aaa cca gtt ttg gac aaa      2208
Trp Ser Arg Leu Leu Asn Ser Leu Asn Glu Lys Pro Val Leu Asp Lys
                725                 730                 735

ctt gag ttc ttt gcc tca ggg atg ggt tca ata tat gca agg caa gtt      2256
Leu Glu Phe Phe Ala Ser Gly Met Gly Ser Ile Tyr Ala Arg Gln Val
            740                 745                 750

agg gaa gat cca aac tgg agt gga agc ggg tca agg aga tac tcc ggg      2304
Arg Glu Asp Pro Asn Trp Ser Gly Ser Gly Ser Arg Arg Tyr Ser Gly
        755                 760                 765

tca gaa agc atg gag ctt gta gtg gct gat aag gga gaa gaa gat gtt      2352
Ser Glu Ser Met Glu Leu Val Val Ala Asp Lys Gly Glu Glu Asp Val
    770                 775                 780

gtg atg act gct gag aaa ctt gca gag gtt gct gtg aag gtt ctc tgc      2400
Val Met Thr Ala Glu Lys Leu Ala Glu Val Ala Val Lys Val Leu Cys
```

```
785                 790                 795                 800

cat gga atg tct gtt gca gtt agt tca cta gct gag ttt tcc atc aac     2448
His Gly Met Ser Val Ala Val Ser Ser Leu Ala Glu Phe Ser Ile Asn
                805                 810                 815

tcg gcc gat gaa cac tcg aag ctt gtt agc caa cca gca gac gat gcg     2496
Ser Ala Asp Glu His Ser Lys Leu Val Ser Gln Pro Ala Asp Asp Ala
            820                 825                 830

tcg gag cag cag ccc ccg gat gta aat ttc aat tcc tag                 2535
Ser Glu Gln Gln Pro Pro Asp Val Asn Phe Asn Ser  *
        835                 840
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<210> 168
<211> 844
<212> PRT
<213> Arabidopsis thaliana

<400> 168

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Met Gly Cys Ser His Ser Lys Leu Asp Asp Glu Glu Ala Val Gln Ile
1               5                   10                  15
Cys Lys Asp Arg Lys Arg Phe Ile Lys Gln Ala Ile Glu His Arg Thr
            20                  25                  30
Lys Phe Ala Ser Gly His Ile Ala Tyr Ile His Ser Leu Arg Lys Val
        35                  40                  45
Ser Asp Ala Leu His Asp Phe Ile Leu Gln Gly Asp Asn Asn Asn Glu
    50                  55                  60
Phe Val Pro Thr Leu Cys Gln Asp Ser Phe Val Thr Pro Val Lys Arg
65                  70                  75                  80
Met Pro Gln Arg Arg Arg Arg Ser Ser Arg Ser Asn Ser Gly Glu Phe
                85                  90                  95
Ile Ser Ile Ser Pro Ser Ser Ile Pro Pro Lys Met Ile Gln Gly Arg
            100                 105                 110
Pro Arg Ser Asn Val Lys Ala Asn Tyr Leu Met Ala Asn Arg Ser Arg
        115                 120                 125
Pro Val Arg Val Glu Gln Arg Ser Pro Glu Thr Phe Arg Val Glu Thr
    130                 135                 140
Phe Ser Pro Pro Ser Ser Ser Asn Gln Tyr Gly Glu Ser Asp Gly Phe
145                 150                 155                 160
Phe Gly Met Asn Met Asn Met Asn Thr Ser Ala Ser Thr Ser Ser Ser
                165                 170                 175
Phe Trp Asn Pro Leu Ser Ser Pro Glu Gln Arg Leu Ser Ser His Asn
            180                 185                 190
Ile Pro Pro Pro Ser Pro Gln Asn Ser Gln Trp Asp Phe Phe Trp Asn
        195                 200                 205
Pro Phe Ser Ser Leu Asp Tyr Tyr Gly Tyr Asn Ser Tyr Asp Arg Gly
    210                 215                 220
Ser Val Asp Ser Arg Ser Gly Ile Asp Asp Glu Ile Arg Gly Leu Arg
225                 230                 235                 240
Arg Val Arg Glu Glu Glu Gly Ile Pro Asp Leu Glu Glu Asp Asp Glu
                245                 250                 255
Pro His Lys Pro Glu Pro Val Val Asn Val Arg Phe Gln Asn His Asn
            260                 265                 270
Pro Asn Pro Lys Ala Thr Glu Glu Asn Arg Gly Lys Val Asp Lys Ser
        275                 280                 285
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Cys Cys Asn Glu Glu Val Lys Val Glu Asp Val Asp Glu Asp Glu Asp
290 295 300
Glu Asp Gly Asp Glu Asp Asp Asp Glu Phe Thr Asp Ser Gly Cys Glu
305 310 315 320
Thr Glu Asn Glu Gly Asp Glu Lys Cys Val Ala Pro Pro Thr Gln Glu
325 330 335
Gln Arg Lys Ala Glu Val Cys Arg Gly Gly Glu Ala Thr Gly Asn Val
340 345 350
Val Gly Val Gly Lys Val Gln Glu Met Lys Asn Val Val Gly Val Arg
355 360 365
Asp Asp Ala Lys Thr Thr Gly Phe Thr Val Tyr Val Asn Arg Arg Pro
370 375 380
Thr Ser Met Ala Glu Val Ile Lys Asp Leu Glu Asp Gln Phe Thr Thr
385 390 395 400
Ile Cys Asp Ala Ala Lys Glu Val Ser Gly Leu Leu Glu Ala Gly Arg
405 410 415
Ala Gln Tyr Thr Ser Ser Phe Asn Asp His Ser Gly Glu Phe Met Asn
420 425 430
Asn Val Ala Ile Phe Leu Ser Arg Lys Met Leu Asn Pro Val Ala Leu
435 440 445
Phe Arg Ser Gly Ser Ser Arg Ser Ser Ser Ser Arg Phe Leu Ile Thr
450 455 460
Ser Ser Gly Gly Ser Arg Glu Ser Gly Ser Glu Ser Arg Ser Asp Val
465 470 475 480
Ser Asp Glu Ser Cys Met Ile Ser Gly Ser His Gln Thr Thr Leu Asp
485 490 495
Arg Leu Phe Ala Trp Glu Lys Lys Leu Tyr Asp Glu Val Arg Val Ser
500 505 510
Asn Lys Arg Tyr Lys Gln Leu Ser Gly Glu Arg Val Arg Arg Ala Tyr
515 520 525
Glu Lys Lys Cys Met Gln Leu Arg Asn Gln Asp Val Lys Gly Asp Asp
530 535 540
Pro Leu Ala Val Asp Lys Thr Arg Ala Thr Ile Arg Asp Leu Asp Thr
545 550 555 560
Gln Ile Lys Val Ser Ile His Ser Ile Glu Ser Ile Ser Lys Arg Ile
565 570 575
Glu Thr Leu Arg Asp Gln Glu Leu Leu Pro Gln Leu Leu Glu Leu Val
580 585 590
Glu Gly Leu Thr Asn Gly Asn His Asp His Asn Arg Leu Thr Arg Met
595 600 605
Trp Lys Val Met Ala Glu Ser His Gln Ile Gln Lys Arg Thr Leu Asp
610 615 620
Glu Ala Lys Leu Leu Leu Ala Gly Thr Pro Val Ser Lys Arg His Lys
625 630 635 640
Lys Arg Gln Pro Pro Ile Met Pro Glu Ala Ile Asn Ser Gln Arg Leu
645 650 655
Ala Gln Ser Ala Leu Asn Leu Glu Ala Gln Leu Arg Asn Trp Arg Thr
660 665 670
Cys Phe Glu Phe Trp Ile Thr Ser Gln Arg Ser Tyr Met Lys Ala Leu
675 680 685
Ser Gly Trp Leu Leu Arg Cys Phe Arg Cys Asp Pro Asp Pro Glu Lys
690 695 700
Val Arg Leu Ser Ser Cys Leu His Pro Ile Tyr Arg Val Cys Ile Gln
705 710 715 720
Trp Ser Arg Leu Leu Asn Ser Leu Asn Glu Lys Pro Val Leu Asp Lys
725 730 735
Leu Glu Phe Phe Ala Ser Gly Met Gly Ser Ile Tyr Ala Arg Gln Val

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        740                     745                     750
Arg Glu Asp Pro Asn Trp Ser Gly Ser Gly Ser Arg Arg Tyr Ser Gly
        755                     760                     765
Ser Glu Ser Met Glu Leu Val Val Ala Asp Lys Gly Glu Glu Asp Val
    770                     775                     780
Val Met Thr Ala Glu Lys Leu Ala Glu Val Ala Val Lys Val Leu Cys
785                     790                     795                 800
His Gly Met Ser Val Ala Val Ser Ser Leu Ala Glu Phe Ser Ile Asn
                805                     810                     815
Ser Ala Asp Glu His Ser Lys Leu Val Ser Gln Pro Ala Asp Asp Ala
            820                     825                     830
Ser Glu Gln Gln Pro Pro Asp Val Asn Phe Asn Ser
        835                     840


<210> 169
<211> 2054
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (390)...(1793)

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aagactaccc atctattcag ttctttctct tatgatttaa gtttcattta gttttttttt 120
ctcatccgcc attttcgttg actttttgaa gcatttctcg aattgacttt gttcttcaca 180
ttgattcatt agaatgttct ttcataaagt ttggatcttt tcttcagggc ttgattaatt 240
tcatatctat gatcttctct gtattgtttt tgatccaatc acttctcaaa atttgatcct 300
tgtcattgga tttagattta gggtttttgt atccttgggg atttgaagat caaaaacaga 360
gtctttgagt gatacttctg gggaacaaa atg gct gca act gca ata gag cca   413
                                Met Ala Ala Thr Ala Ile Glu Pro
                                 1               5

tct tca tct ata agt ttc aca tct tct cac tta tca aac cct tct cct   461
Ser Ser Ser Ile Ser Phe Thr Ser Ser His Leu Ser Asn Pro Ser Pro
     10                  15                  20

gtt gtt act act tat cac tca gct gct aat ctt gaa gag ctc agc tct   509
Val Val Thr Thr Tyr His Ser Ala Ala Asn Leu Glu Glu Leu Ser Ser
 25                  30                  35                  40

aac ttg gag cag ctt ctc act aat cca gat tgc gat tac act gac gca   557
Asn Leu Glu Gln Leu Leu Thr Asn Pro Asp Cys Asp Tyr Thr Asp Ala
                 45                  50                  55

gag atc atc att gaa gaa gaa gct aac cct cgg aag ctt cgt aac tat   605
Glu Ile Ile Ile Glu Glu Glu Ala Asn Pro Arg Lys Leu Arg Asn Tyr
             60                  65                  70

gtt gag aag tca cta gta gag aat gtt ctt cct atc ctc tta gtt gcg   653
Val Glu Lys Ser Leu Val Glu Asn Val Leu Pro Ile Leu Leu Val Ala
         75                  80                  85

ttt cat tgt gat ttg aca cag ctt ctt gat caa tgc att gag aga gtg   701
Phe His Cys Asp Leu Thr Gln Leu Leu Asp Gln Cys Ile Glu Arg Val
```

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 90                  95                  100

gcg aga tca gac tta gac aga ttc tgt atc gaa aag gag ctt cct tta    749
Ala Arg Ser Asp Leu Asp Arg Phe Cys Ile Glu Lys Glu Leu Pro Leu
105                 110                 115                 120

gaa gta ttg gaa aaa atc aaa cag ctt cga gtt aag tcg gtg aac ata    797
Glu Val Leu Glu Lys Ile Lys Gln Leu Arg Val Lys Ser Val Asn Ile
                125                 130                 135

ccc gag gtg gag gat aaa tcg ata gag aga aca ggg aaa gta ctc aag    845
Pro Glu Val Glu Asp Lys Ser Ile Glu Arg Thr Gly Lys Val Leu Lys
            140                 145                 150

gca ttg gat tca gat gat gta gaa ctc gtg aag ctt ctt ttg act gag    893
Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu Leu Leu Thr Glu
        155                 160                 165

tca gat ata act cta gac caa gcc aat ggt cta cat tat gca gtg gca    941
Ser Asp Ile Thr Leu Asp Gln Ala Asn Gly Leu His Tyr Ala Val Ala
    170                 175                 180

tac agt gat ccg aaa gtt gtg aca cag gtt ctt gat cta gat atg gct    989
Tyr Ser Asp Pro Lys Val Val Thr Gln Val Leu Asp Leu Asp Met Ala
185                 190                 195                 200

gat gtt aat ttc aga aat tcc agg ggg tat acg gtt ctt cat att gct    1037
Asp Val Asn Phe Arg Asn Ser Arg Gly Tyr Thr Val Leu His Ile Ala
                205                 210                 215

gct atg cgt aga gag cca aca att atc ata cca ctt att caa aaa gga    1085
Ala Met Arg Arg Glu Pro Thr Ile Ile Ile Pro Leu Ile Gln Lys Gly
            220                 225                 230

gct aat gct tca gat ttc acg ttt gat gga cgc agt gcg gta aat ata    1133
Ala Asn Ala Ser Asp Phe Thr Phe Asp Gly Arg Ser Ala Val Asn Ile
        235                 240                 245

tgt agg aga ctc act agg ccg aaa gat tat cat acc aaa acc tca agg    1181
Cys Arg Arg Leu Thr Arg Pro Lys Asp Tyr His Thr Lys Thr Ser Arg
    250                 255                 260

aaa gaa cct agt aaa tac cgc tta tgc atc gat atc ttg gaa agg gaa    1229
Lys Glu Pro Ser Lys Tyr Arg Leu Cys Ile Asp Ile Leu Glu Arg Glu
265                 270                 275                 280

att aga agg aat cca ttg gtt agt ggg gat aca ccc act tgt tcc cat    1277
Ile Arg Arg Asn Pro Leu Val Ser Gly Asp Thr Pro Thr Cys Ser His
                285                 290                 295

tcg atg ccc gag gat ctc caa atg agg ttg tta tac tta gaa aag cga    1325
Ser Met Pro Glu Asp Leu Gln Met Arg Leu Leu Tyr Leu Glu Lys Arg
            300                 305                 310

gtg gga ctt gct cag ttg ttc ttc cca gca gaa gcc aat gtg gct atg    1373
Val Gly Leu Ala Gln Leu Phe Phe Pro Ala Glu Ala Asn Val Ala Met
        315                 320                 325
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gac gtt gct aat gtt gaa ggg aca agc gag tgc aca ggt ctt cta act    1421
Asp Val Ala Asn Val Glu Gly Thr Ser Glu Cys Thr Gly Leu Leu Thr
    330                 335                 340

cca cct cca tca aat gat aca act gaa aac ttg ggt aaa gtc gat tta    1469
Pro Pro Pro Ser Asn Asp Thr Thr Glu Asn Leu Gly Lys Val Asp Leu
345                 350                 355                 360

aat gaa acg cct tat gtg caa acg aaa aga atg ctt aca cgt atg aaa    1517
Asn Glu Thr Pro Tyr Val Gln Thr Lys Arg Met Leu Thr Arg Met Lys
                365                 370                 375

gcc ctc atg aaa aca gtt gag aca ggt cgg aga tac ttc cca tct tgt    1565
Ala Leu Met Lys Thr Val Glu Thr Gly Arg Arg Tyr Phe Pro Ser Cys
            380                 385                 390

tat gag gtt ctg gat aag tac atg gat cag tat atg gac gaa gaa atc    1613
Tyr Glu Val Leu Asp Lys Tyr Met Asp Gln Tyr Met Asp Glu Glu Ile
        395                 400                 405

cct gat atg tcg tat ccc gag aaa ggc act gtg aaa gag aga aga cag    1661
Pro Asp Met Ser Tyr Pro Glu Lys Gly Thr Val Lys Glu Arg Arg Gln
    410                 415                 420

aag agg atg aga tat aac gag ctg aag aac gac gtt aaa aaa gca tat    1709
Lys Arg Met Arg Tyr Asn Glu Leu Lys Asn Asp Val Lys Lys Ala Tyr
425                 430                 435                 440

agc aaa gac aaa gtc gcg cgg tct tgt ctt tct tct tca tca cca gct    1757
Ser Lys Asp Lys Val Ala Arg Ser Cys Leu Ser Ser Ser Ser Pro Ala
                445                 450                 455

tct tct ctt aga gaa gcc tta gag aat cca aca tga tcttgtccca         1803
Ser Ser Leu Arg Glu Ala Leu Glu Asn Pro Thr  *
            460                 465

gataagtaat gctactagag atagttcctt ggaagaaatt agctatttta taggttttgg 1863
tttagaaaac agtggagatc ccattttggt attcaggttt attacatggt ttaggtttga 1923
ttttgtatta aaggagatgg atttttgaaa tgtataaagc aaaacctttc ctttttgctt 1983
tgcttctttc tttaaaaaaa aaattgtaat atatggaagt gaaatcgaag caacgattga 2043
gcaaaaaaaa a                                                      2054

<210> 170
<211> 467
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (179)...(254)
<223> Conserved domain

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Met Ala Ala Thr Ala Ile Glu Pro Ser Ser Ser Ile Ser Phe Thr Ser
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Ser His Leu Ser Asn Pro Ser Pro Val Val Thr Thr Tyr His Ser Ala
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            20                  25                  30
Ala Asn Leu Glu Glu Leu Ser Ser Asn Leu Glu Gln Leu Leu Thr Asn
        35                  40                  45
Pro Asp Cys Asp Tyr Thr Asp Ala Glu Ile Ile Ile Glu Glu Glu Ala
    50                  55                  60
Asn Pro Arg Lys Leu Arg Asn Tyr Val Glu Lys Ser Leu Val Glu Asn
65                  70                  75                  80
Val Leu Pro Ile Leu Leu Val Ala Phe His Cys Asp Leu Thr Gln Leu
                85                  90                  95
Leu Asp Gln Cys Ile Glu Arg Val Ala Arg Ser Asp Leu Asp Arg Phe
            100                 105                 110
Cys Ile Glu Lys Glu Leu Pro Leu Glu Val Leu Glu Lys Ile Lys Gln
        115                 120                 125
Leu Arg Val Lys Ser Val Asn Ile Pro Glu Val Glu Asp Lys Ser Ile
    130                 135                 140
Glu Arg Thr Gly Lys Val Leu Lys Ala Leu Asp Ser Asp Asp Val Glu
145                 150                 155                 160
Leu Val Lys Leu Leu Leu Thr Glu Ser Asp Ile Thr Leu Asp Gln Ala
                165                 170                 175
Asn Gly Leu His Tyr Ala Val Ala Tyr Ser Asp Pro Lys Val Val Thr
            180                 185                 190
Gln Val Leu Asp Leu Asp Met Ala Asp Val Asn Phe Arg Asn Ser Arg
        195                 200                 205
Gly Tyr Thr Val Leu His Ile Ala Ala Met Arg Arg Glu Pro Thr Ile
    210                 215                 220
Ile Ile Pro Leu Ile Gln Lys Gly Ala Asn Ala Ser Asp Phe Thr Phe
225                 230                 235                 240
Asp Gly Arg Ser Ala Val Asn Ile Cys Arg Arg Leu Thr Arg Pro Lys
                245                 250                 255
Asp Tyr His Thr Lys Thr Ser Arg Lys Glu Pro Ser Lys Tyr Arg Leu
            260                 265                 270
Cys Ile Asp Ile Leu Glu Arg Glu Ile Arg Arg Asn Pro Leu Val Ser
        275                 280                 285
Gly Asp Thr Pro Thr Cys Ser His Ser Met Pro Glu Asp Leu Gln Met
    290                 295                 300
Arg Leu Leu Tyr Leu Glu Lys Arg Val Gly Leu Ala Gln Leu Phe Phe
305                 310                 315                 320
Pro Ala Glu Ala Asn Val Ala Met Asp Val Ala Asn Val Glu Gly Thr
                325                 330                 335
Ser Glu Cys Thr Gly Leu Leu Thr Pro Pro Pro Ser Asn Asp Thr Thr
            340                 345                 350
Glu Asn Leu Gly Lys Val Asp Leu Asn Glu Thr Pro Tyr Val Gln Thr
        355                 360                 365
Lys Arg Met Leu Thr Arg Met Lys Ala Leu Met Lys Thr Val Glu Thr
    370                 375                 380
Gly Arg Arg Tyr Phe Pro Ser Cys Tyr Glu Val Leu Asp Lys Tyr Met
385                 390                 395                 400
Asp Gln Tyr Met Asp Glu Glu Ile Pro Asp Met Ser Tyr Pro Glu Lys
                405                 410                 415
Gly Thr Val Lys Glu Arg Arg Gln Lys Arg Met Arg Tyr Asn Glu Leu
            420                 425                 430
Lys Asn Asp Val Lys Lys Ala Tyr Ser Lys Asp Lys Val Ala Arg Ser
        435                 440                 445
Cys Leu Ser Ser Ser Ser Pro Ala Ser Ser Leu Arg Glu Ala Leu Glu
    450                 455                 460
Asn Pro Thr
465
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<210> 171
<211> 1538
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (138)...(1388)

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taattgagat tgatctcaaa accaaagctc tcgtgctctt gtcgttgatg ttggttgtgt 120
agactttgta tacaatg atg aaa agt ttg gcg aat gct gtt gga gcg aag 170
Met Lys Ser Leu Ala Asn Ala Val Gly Ala Lys
1 5 10

acg gcg agg gct tgc gac agc tgc gtg aag aga cgt gca cgg tgg tac 218
Thr Ala Arg Ala Cys Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr
15 20 25

tgc gcg gcc gac gat gct ttt ctt tgc cag tct tgc gac agt ttg gtc 266
Cys Ala Ala Asp Asp Ala Phe Leu Cys Gln Ser Cys Asp Ser Leu Val
30 35 40

cat tca gca aac cct ctt gct cgc cgc cac gag aga gtc cgt ttg aag 314
His Ser Ala Asn Pro Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys
45 50 55

acg gct agc ccg gcg gtc gta aag cat agc aac cac tca tca gct tct 362
Thr Ala Ser Pro Ala Val Val Lys His Ser Asn His Ser Ser Ala Ser
60 65 70 75

cct cca cat gag gtc gcc acg tgg cat cac ggg ttt act cgt aaa gct 410
Pro Pro His Glu Val Ala Thr Trp His His Gly Phe Thr Arg Lys Ala
80 85 90

cga acg cca cgt ggc tct ggt aag aaa aac aat tcg tcg ata ttt cat 458
Arg Thr Pro Arg Gly Ser Gly Lys Lys Asn Asn Ser Ser Ile Phe His
95 100 105

gac ttg gtt cct gat att agt att gag gat cag aca gac aac tat gag 506
Asp Leu Val Pro Asp Ile Ser Ile Glu Asp Gln Thr Asp Asn Tyr Glu
110 115 120

ctt gaa gag cag ctg atc tgt caa gtg ccg gtt cta gat ccg ttg gtg 554
Leu Glu Glu Gln Leu Ile Cys Gln Val Pro Val Leu Asp Pro Leu Val
125 130 135

tct gag cag ttc ttg aac gat gtc gtt gag ccc aag atc gag ttt cct 602
Ser Glu Gln Phe Leu Asn Asp Val Val Glu Pro Lys Ile Glu Phe Pro
140 145 150 155

atg atc aga agt ggt ttg atg atc gag gag gag gaa gac aac gct gaa 650
Met Ile Arg Ser Gly Leu Met Ile Glu Glu Glu Glu Asp Asn Ala Glu
160 165 170

agt tgt ctt aat gga ttt ttc ccg acc gac atg gag ctt gag gag ttt 698
Ser Cys Leu Asn Gly Phe Phe Pro Thr Asp Met Glu Leu Glu Glu Phe
175 180 185

gct gct gac gtg gag act ctg ctc ggt cgc ggg tta gac acg gag tcg 746
Ala Ala Asp Val Glu Thr Leu Leu Gly Arg Gly Leu Asp Thr Glu Ser
190 195 200

tat gcc atg gag gag cta ggg tta tct aat tca gag atg ttc aaa atc 794
Tyr Ala Met Glu Glu Leu Gly Leu Ser Asn Ser Glu Met Phe Lys Ile
205 210 215

gaa aaa gat gag att gaa gaa gaa gta gaa gag ata aaa gcc atg agc 842
Glu Lys Asp Glu Ile Glu Glu Glu Val Glu Glu Ile Lys Ala Met Ser
220 225 230 235

atg gat ata ttt gat gat gat cga aaa gac gtg gat gga aca gta ccg 890
Met Asp Ile Phe Asp Asp Asp Arg Lys Asp Val Asp Gly Thr Val Pro
240 245 250

ttt gag cta agc ttt gat tac gag tcg tca cac aag acg tcc gaa gaa 938
Phe Glu Leu Ser Phe Asp Tyr Glu Ser Ser His Lys Thr Ser Glu Glu
255 260 265

gag gta atg aag aac gtt gaa agt agt ggt gaa tgt gtt gtt aag gtg 986
Glu Val Met Lys Asn Val Glu Ser Ser Gly Glu Cys Val Val Lys Val
270 275 280

aaa gag gaa gaa cat aag aat gtt ctg atg cta aga tta aac tat gac 1034
Lys Glu Glu Glu His Lys Asn Val Leu Met Leu Arg Leu Asn Tyr Asp
285 290 295

tcg gtg ata tcc act tgg gga ggt caa ggt cca ccg tgg agt tca gga 1082
Ser Val Ile Ser Thr Trp Gly Gly Gln Gly Pro Pro Trp Ser Ser Gly
300 305 310 315

gag cca ccg gaa cga gac atg gac atc agc ggt tgg cca gcc ttt tcc 1130
Glu Pro Pro Glu Arg Asp Met Asp Ile Ser Gly Trp Pro Ala Phe Ser
320 325 330

atg gtg gag aat gga gga gaa agt act cat cag aag caa tac gtt ggt 1178
Met Val Glu Asn Gly Gly Glu Ser Thr His Gln Lys Gln Tyr Val Gly
335 340 345

gga tgt tta cca tca agt ggg ttt gga gat gga ggt aga gaa gct aga 1226
Gly Cys Leu Pro Ser Ser Gly Phe Gly Asp Gly Gly Arg Glu Ala Arg
350 355 360

gtt tcg aga tac aga gag aag agg agg aca agg ttg ttt tct aag aag 1274
Val Ser Arg Tyr Arg Glu Lys Arg Arg Thr Arg Leu Phe Ser Lys Lys
365 370 375

ata cgg tac gag gta cgt aaa ttg aat gca gag aaa aga cca cga atg 1322
Ile Arg Tyr Glu Val Arg Lys Leu Asn Ala Glu Lys Arg Pro Arg Met
380 385 390 395

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aaa gga aga ttc gtg aag aga gcc tcg ctc gct gct gct gct tca cca    1370
Lys Gly Arg Phe Val Lys Arg Ala Ser Leu Ala Ala Ala Ala Ser Pro
                400                 405                 410

tta ggt gtt aat tac tga atagttaata tctattcatg ttatatctca           1418
Leu Gly Val Asn Tyr  *
            415

ctttacaaat ttcggtgaat ctttttttctt ctgaaacaac agaagttatt ttggcactta 1478
attgtgcttt gaggacttgt atgtacatag aagtaaccaa taataatgtg acttttacta 1538


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<211> 416
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (18)...(56)
<223> Conserved domain

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Met Lys Ser Leu Ala Asn Ala Val Gly Ala Lys Thr Ala Arg Ala Cys
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Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp Asp
            20                  25                  30
Ala Phe Leu Cys Gln Ser Cys Asp Ser Leu Val His Ser Ala Asn Pro
        35                  40                  45
Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Thr Ala Ser Pro Ala
    50                  55                  60
Val Val Lys His Ser Asn His Ser Ser Ala Ser Pro Pro His Glu Val
65                  70                  75                  80
Ala Thr Trp His His Gly Phe Thr Arg Lys Ala Arg Thr Pro Arg Gly
                85                  90                  95
Ser Gly Lys Lys Asn Asn Ser Ser Ile Phe His Asp Leu Val Pro Asp
            100                 105                 110
Ile Ser Ile Glu Asp Gln Thr Asp Asn Tyr Glu Leu Glu Glu Gln Leu
        115                 120                 125
Ile Cys Gln Val Pro Val Leu Asp Pro Leu Val Ser Glu Gln Phe Leu
    130                 135                 140
Asn Asp Val Val Glu Pro Lys Ile Glu Phe Pro Met Ile Arg Ser Gly
145                 150                 155                 160
Leu Met Ile Glu Glu Glu Glu Asp Asn Ala Glu Ser Cys Leu Asn Gly
                165                 170                 175
Phe Phe Pro Thr Asp Met Glu Leu Glu Glu Phe Ala Ala Asp Val Glu
            180                 185                 190
Thr Leu Leu Gly Arg Gly Leu Asp Thr Glu Ser Tyr Ala Met Glu Glu
        195                 200                 205
Leu Gly Leu Ser Asn Ser Glu Met Phe Lys Ile Glu Lys Asp Glu Ile
    210                 215                 220
Glu Glu Glu Val Glu Glu Ile Lys Ala Met Ser Met Asp Ile Phe Asp
225                 230                 235                 240
Asp Asp Arg Lys Asp Val Asp Gly Thr Val Pro Phe Glu Leu Ser Phe
                245                 250                 255
Asp Tyr Glu Ser Ser His Lys Thr Ser Glu Glu Glu Val Met Lys Asn
            260                 265                 270
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Val Glu Ser Ser Gly Glu Cys Val Val Lys Val Lys Glu Glu Glu His
        275                 280                 285
Lys Asn Val Leu Met Leu Arg Leu Asn Tyr Asp Ser Val Ile Ser Thr
    290                 295                 300
Trp Gly Gly Gln Gly Pro Pro Trp Ser Ser Gly Glu Pro Pro Glu Arg
305                 310                 315                 320
Asp Met Asp Ile Ser Gly Trp Pro Ala Phe Ser Met Val Glu Asn Gly
                325                 330                 335
Gly Glu Ser Thr His Gln Lys Gln Tyr Val Gly Gly Cys Leu Pro Ser
            340                 345                 350
Ser Gly Phe Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg
        355                 360                 365
Glu Lys Arg Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val
    370                 375                 380
Arg Lys Leu Asn Ala Glu Lys Arg Pro Arg Met Lys Gly Arg Phe Val
385                 390                 395                 400
Lys Arg Ala Ser Leu Ala Ala Ala Ala Ser Pro Leu Gly Val Asn Tyr
                405                 410                 415
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<210> 173
<211> 1233
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1233)

<400> 173
atg gcc gaa act atg aaa gat att acg atg aag aac gat gaa tca cag    48
Met Ala Glu Thr Met Lys Asp Ile Thr Met Lys Asn Asp Glu Ser Gln
 1               5                  10                  15

gaa gaa gaa atc ccc gat caa ttt ctc tgc tgc gtt tgc ctg gaa ctt    96
Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu
            20                  25                  30

ctt tac aag cca att gtg tta tct tgt ggt cat cta tca tgt ttt tgg    144
Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp
        35                  40                  45

tgc gta cat aag tcc atg aat ggc ttt cgt gag tct cat tgt ccg ata    192
Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile
    50                  55                  60

tgt aga gac ccg tat gtt cac ttt ccc tct gtg tgc cag aag ctt tat    240
Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr
65                  70                  75                  80

ttt ctg tta aag aag atg tac cca ctt gct cat aag aag aga gaa gaa    288
Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu
                85                  90                  95

caa gtt tta aag gaa gag caa gaa cga gaa tgt ttt tct cct cag att    336
Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile
            100                 105                 110
```

gat ctt gtt ttg gat ttg tct gtg tgt agt gga gat tct ctc aat gtc 384
Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val
115 120 125

tct gat aaa cag aag gtg gaa gag tgt tcg aat gca gcg aac tta tta 432
Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu
130 135 140

tct agt tca tca agt aga ggt gac att cca tgt atc ccc aaa aat caa 480
Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln
145 150 155 160

gaa ccc aca gat gca aaa gct ctt aat gtt cat gaa aat gaa tta ctt 528
Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu
165 170 175

aag gat aac aaa gtc agt aag cag att tcg aaa gat gat ttg ctc tgt 576
Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys
180 185 190

tca gca tgt aag gag ctg ctt gta cga ccc gta gtt ctc aat tgc gga 624
Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly
195 200 205

cat gtg tat tgt gaa gga tgt gta gta gat atg gct gaa gaa agc gaa 672
His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu
210 215 220

aag atc aaa tgt caa gag tgt aat gtt tgt gac cca aga gga ttt cca 720
Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro
225 230 235 240

aaa gtt tgt ttg att ctt gaa cag ctt ttg gag gaa aac ttt cct gaa 768
Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu
245 250 255

gaa tac aat tca aga agc agt aag gtt cag aaa acg ctc gcc cat aat 816
Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn
260 265 270

agc aaa gga aat att caa agc tat ctc aaa gaa ggc ccg tcc tta tca 864
Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser
275 280 285

aac gac aat aac aat gat gat ccc tgg ttg gca aac cct gga tca aat 912
Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn
290 295 300

gtt cac ttt gga gct ggt tgt gat tct tgt ggg gtg tat cca atc ata 960
Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile
305 310 315 320

ggg gat cga tac aga tgc aaa gac tgc aag gag gaa att ggg tat gac 1008
Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp
325 330 335

```
ctt tgc aaa gac tgt tac gag act cct tcg aaa gtt cca ggg aga ttc    1056
Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe
            340                 345                 350

aac cag caa cac act cct gac cac agg ctt gag ctt gca cgg tct cct    1104
Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro
        355                 360                 365

cag gtt ctg atc aat ttc aat tct atc ggt atc ctt ctc gga ccc gtt    1152
Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val
    370                 375                 380

atc tca aat gaa ggc atg gat aca gat gaa ggc gag gaa ggg cct cct    1200
Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro
385                 390                 395                 400

ggt tct tct aat gag tca tca agc aca gaa tga                        1233
Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu  *
                405                 410


<210> 174
<211> 410
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (20)...(50)
<223> Conserved domain

<400> 174
Met Ala Glu Thr Met Lys Asp Ile Thr Met Lys Asn Asp Glu Ser Gln
 1               5                  10                  15
Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu
            20                  25                  30
Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp
        35                  40                  45
Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile
    50                  55                  60
Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr
65                  70                  75                  80
Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu
                85                  90                  95
Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile
            100                 105                 110
Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val
        115                 120                 125
Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu
    130                 135                 140
Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln
145                 150                 155                 160
Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu
                165                 170                 175
Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys
            180                 185                 190
Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly
```

```
        195                     200                     205
His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu
    210                     215                     220
Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro
225                     230                     235                     240
Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu
                245                     250                     255
Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn
            260                     265                     270
Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser
        275                     280                     285
Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn
    290                     295                     300
Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile
305                     310                     315                     320
Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp
                325                     330                     335
Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe
            340                     345                     350
Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro
        355                     360                     365
Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val
    370                     375                     380
Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro
385                     390                     395                     400
Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu
                405                     410
```

<210> 175
<211> 1031
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (71)...(1003)

<400> 175

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atatgtactt gtacaccaac ccaccaaaag agataaaaga ggaaacaaaa actcgaaaag 60
agagagatat atg ggt gag gtg gct tat atg gac gaa gga gac cta gaa    109
           Met Gly Glu Val Ala Tyr Met Asp Glu Gly Asp Leu Glu
            1               5                  10

gca ata gtc aga ggc tac tcc ggc tcc gga gac gcg ttt tcc ggc gaa   157
Ala Ile Val Arg Gly Tyr Ser Gly Ser Gly Asp Ala Phe Ser Gly Glu
    15                  20                  25

agt tcc ggt acg ttt tca cct tcg ttt tgc cta ccg atg gag acg tct   205
Ser Ser Gly Thr Phe Ser Pro Ser Phe Cys Leu Pro Met Glu Thr Ser
30                  35                  40                  45

agt ttc tac gaa ccg gag atg gag aca agt ggc tta gat gag ctc ggt   253
Ser Phe Tyr Glu Pro Glu Met Glu Thr Ser Gly Leu Asp Glu Leu Gly
                50                  55                  60

gaa ctt tac aaa ccc ttt tac cct ttc tcc aca caa acg atc ctc aca   301
```

```
Glu Leu Tyr Lys Pro Phe Tyr Pro Phe Ser Thr Gln Thr Ile Leu Thr
            65                  70                  75

agc tcg gtc tct ctc cct gaa gat tca aaa cct ttc cga gat gac aag      349
Ser Ser Val Ser Leu Pro Glu Asp Ser Lys Pro Phe Arg Asp Asp Lys
        80                  85                  90

aaa caa cga tca cat ggt tgt ctt tta tcc aac gga tca aga gct gat      397
Lys Gln Arg Ser His Gly Cys Leu Leu Ser Asn Gly Ser Arg Ala Asp
    95                  100                 105

cat atc cga att tca gaa tcc aaa tca aag aaa agc aag aag aat caa      445
His Ile Arg Ile Ser Glu Ser Lys Ser Lys Lys Ser Lys Lys Asn Gln
110                 115                 120                 125

cag aag aga gtt gtt gag caa gtg aaa gaa gag aat ctg ttg tcg gac      493
Gln Lys Arg Val Val Glu Gln Val Lys Glu Glu Asn Leu Leu Ser Asp
                130                 135                 140

gca tgg gcg tgg cgt aaa tac ggg cag aaa ccc atc aaa gga tct cca      541
Ala Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro
            145                 150                 155

tac cca agg agt tat tac aga tgc agt agc tca aaa ggg tgt ttg gca      589
Tyr Pro Arg Ser Tyr Tyr Arg Cys Ser Ser Ser Lys Gly Cys Leu Ala
        160                 165                 170

aga aaa caa gtc gaa aga aat cct caa aac ccg gag aaa ttc acc ata      637
Arg Lys Gln Val Glu Arg Asn Pro Gln Asn Pro Glu Lys Phe Thr Ile
    175                 180                 185

aca tac act aat gag cac aat cat gaa cta cca acc cgg aga aac tca      685
Thr Tyr Thr Asn Glu His Asn His Glu Leu Pro Thr Arg Arg Asn Ser
190                 195                 200                 205

tta gcc ggt tcg act cga gca aaa act tcc caa ccc aaa cca acc tta      733
Leu Ala Gly Ser Thr Arg Ala Lys Thr Ser Gln Pro Lys Pro Thr Leu
                210                 215                 220

acc aaa aaa tcc gaa aaa gaa gtt gtt tct tcc cct aca agt aat cct      781
Thr Lys Lys Ser Glu Lys Glu Val Val Ser Ser Pro Thr Ser Asn Pro
            225                 230                 235

atg atc cca tcc gct gat gaa tct tct gtt gcg gtt caa gaa atg agc      829
Met Ile Pro Ser Ala Asp Glu Ser Ser Val Ala Val Gln Glu Met Ser
        240                 245                 250

gtt gcg gaa acg agt acg cac caa gcg gct gga gca atc gag ggc cgc      877
Val Ala Glu Thr Ser Thr His Gln Ala Ala Gly Ala Ile Glu Gly Arg
    255                 260                 265

cgc ttg agt aac ggt tta cca tcg gat ttg atg tcc ggg agc gga act      925
Arg Leu Ser Asn Gly Leu Pro Ser Asp Leu Met Ser Gly Ser Gly Thr
270                 275                 280                 285

ttt cca agt ttt acc ggt gac ttc gat gaa cta ttg aat agc caa gag      973
Phe Pro Ser Phe Thr Gly Asp Phe Asp Glu Leu Leu Asn Ser Gln Glu
```

```
                290                        295                         300

ttc ttc agt ggg tat tta tgg aat tac tag agagcattag gtgtatgtat      1023
Phe Phe Ser Gly Tyr Leu Trp Asn Tyr  *
            305                 310

atatatat                                                            1031

<210> 176
<211> 310
<212> PRT
<213> Arabidopsis thaliana

<400> 176
Met Gly Glu Val Ala Tyr Met Asp Glu Gly Asp Leu Glu Ala Ile Val
 1               5                  10                  15
Arg Gly Tyr Ser Gly Ser Gly Asp Ala Phe Ser Gly Glu Ser Ser Gly
            20                  25                  30
Thr Phe Ser Pro Ser Phe Cys Leu Pro Met Glu Thr Ser Ser Phe Tyr
        35                  40                  45
Glu Pro Glu Met Glu Thr Ser Gly Leu Asp Glu Leu Gly Glu Leu Tyr
    50                  55                  60
Lys Pro Phe Tyr Pro Phe Ser Thr Gln Thr Ile Leu Thr Ser Ser Val
65                  70                  75                  80
Ser Leu Pro Glu Asp Ser Lys Pro Phe Arg Asp Asp Lys Lys Gln Arg
                85                  90                  95
Ser His Gly Cys Leu Leu Ser Asn Gly Ser Arg Ala Asp His Ile Arg
            100                 105                 110
Ile Ser Glu Ser Lys Ser Lys Lys Ser Lys Lys Asn Gln Gln Lys Arg
        115                 120                 125
Val Val Glu Gln Val Lys Glu Glu Asn Leu Leu Ser Asp Ala Trp Ala
    130                 135                 140
Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro Tyr Pro Arg
145                 150                 155                 160
Ser Tyr Tyr Arg Cys Ser Ser Ser Lys Gly Cys Leu Ala Arg Lys Gln
                165                 170                 175
Val Glu Arg Asn Pro Gln Asn Pro Glu Lys Phe Thr Ile Thr Tyr Thr
            180                 185                 190
Asn Glu His Asn His Glu Leu Pro Thr Arg Arg Asn Ser Leu Ala Gly
        195                 200                 205
Ser Thr Arg Ala Lys Thr Ser Gln Pro Lys Pro Thr Leu Thr Lys Lys
    210                 215                 220
Ser Glu Lys Glu Val Val Ser Ser Pro Thr Ser Asn Pro Met Ile Pro
225                 230                 235                 240
Ser Ala Asp Glu Ser Ser Val Ala Val Gln Glu Met Ser Val Ala Glu
                245                 250                 255
Thr Ser Thr His Gln Ala Ala Gly Ala Ile Glu Gly Arg Arg Leu Ser
            260                 265                 270
Asn Gly Leu Pro Ser Asp Leu Met Ser Gly Ser Gly Thr Phe Pro Ser
        275                 280                 285
Phe Thr Gly Asp Phe Asp Glu Leu Leu Asn Ser Gln Glu Phe Phe Ser
    290                 295                 300
Gly Tyr Leu Trp Asn Tyr
305                 310


<210> 177
```

```
<211> 1320
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1320)

<400> 177
atg ttg tcc aac aag aac aca aac aca tgt tgt gtg gtt tct tct tct      48
Met Leu Ser Asn Lys Asn Thr Asn Thr Cys Cys Val Val Ser Ser Ser
 1               5                  10                  15

tct tct gat cct ttc ctc tcc tct tca gaa aat ggg gtc acc acc aca      96
Ser Ser Asp Pro Phe Leu Ser Ser Ser Glu Asn Gly Val Thr Thr Thr
            20                  25                  30

aac aca tcc act cag aag agg aaa aga aga cct gca ggt acc cca gat     144
Asn Thr Ser Thr Gln Lys Arg Lys Arg Arg Pro Ala Gly Thr Pro Asp
        35                  40                  45

cca gat gca gaa gtt gtg tct tta tca cca aga act ctt ctt gaa tca     192
Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser
    50                  55                  60

gac aga tac ata tgt gag atc tgt aac caa ggg ttt caa aga gac cag     240
Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln
65                  70                  75                  80

aat ctc cag atg cat aga aga cgt cac aaa gtt cca tgg aag ctt ctt     288
Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu
                85                  90                  95

aaa aga gac aac aac ata gag gtg aag aaa cga gtc tat gtt tgc cct     336
Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro
            100                 105                 110

gaa ccc act tgc ctt cac cat aat cct tgt cat gct ctg gga gat ctt     384
Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu
        115                 120                 125

gtc ggc atc aaa aaa cat ttc aga aga aaa cat agt aac cat aag caa     432
Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln
    130                 135                 140

tgg gtt tgt gag aga tgc tct aaa ggt tat gct gtt caa tct gat tac     480
Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr
145                 150                 155                 160

aaa gct cat ctc aaa act tgt ggt act aga gga cat tct tgt gac tgt     528
Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys
                165                 170                 175

ggt cgt gtc ttc tcc agg gtg gag agt ttt att gaa cat caa gat aat     576
Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn
            180                 185                 190
```

```
tgt tcc gca cgg aga gtt cac cgt gaa ccg cct cga cca cca caa acc    624
Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr
        195                 200                 205

gcg gta aca gtc ccg gca tgc tct tct aga acc gcc tca acc gtc agc    672
Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser
    210                 215                 220

act ccg tct agt gaa acc aat tac ggc ggt aca gtt gcg gtt acg act    720
Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr
225                 230                 235                     240

cct caa cct cta gaa ggc cgt cca att cat cag aga atc tca tct tca    768
Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser
                245                 250                 255

att ctc acc aac tca tca aac aat ctc aac ctc gaa ctc caa ctt ctt    816
Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu
            260                 265                 270

cca tta tcg tcg aat caa aac cct aat caa gaa aac caa caa caa aaa    864
Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys
        275                 280                 285

gtt aaa gaa cca tct cat cat cat aat cat aat cat gat acc aca aac    912
Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn
    290                 295                 300

tta aac ctc tcc att gca cca tca tca tca tat caa cat tac aac aac    960
Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn
305                 310                 315                     320

ttt gat cgt ata aaa gag att atg gcg agc gag caa att atg aag ata    1008
Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile
                325                 330                 335

gcg atg aag gag aaa gct tac gct gag gaa gct aaa aga gaa gcc aag    1056
Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys
            340                 345                 350

agg caa cga gag ata gcg gaa aac gag ttt gca aat gcc aaa aag att    1104
Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile
        355                 360                 365

agg caa aaa gca caa gct gaa ctc gag aga gct aag ttt tta aag gaa    1152
Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu
    370                 375                 380

caa tct atg aag aag ata agt tca acg atc atg cag gtc act tgt caa    1200
Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln
385                 390                 395                     400

aca tgt aaa gga cag ttt caa gca gtt gcg gtt ccg gcg gct acg gct    1248
Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala
                405                 410                 415

gat gag acg tct ctt gtc gtg agt tac atg tcg tca gcg aat act gac    1296
```

Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp
420 425 430

gga gag ttg gaa aat ggt ttt taa 1320
Gly Glu Leu Glu Asn Gly Phe *
435

<210> 178
<211> 439
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (69)...(89)
<223> Conserved domain

<221> DOMAIN
<222> (111)...(139)
<223> Conserved domain

<400> 178
Met Leu Ser Asn Lys Asn Thr Asn Thr Cys Cys Val Val Ser Ser Ser
1 5 10 15
Ser Ser Asp Pro Phe Leu Ser Ser Ser Glu Asn Gly Val Thr Thr Thr
20 25 30
Asn Thr Ser Thr Gln Lys Arg Lys Arg Arg Pro Ala Gly Thr Pro Asp
35 40 45
Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser
50 55 60
Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln
65 70 75 80
Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu
85 90 95
Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro
100 105 110
Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu
115 120 125
Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln
130 135 140
Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr
145 150 155 160
Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys
165 170 175
Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn
180 185 190
Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr
195 200 205
Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser
210 215 220
Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr
225 230 235 240
Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser
245 250 255
Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu
260 265 270

```
Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys
        275                 280                 285
Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn
    290                 295                 300
Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn
305                 310                 315                 320
Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile
                325                 330                 335
Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys
            340                 345                 350
Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile
        355                 360                 365
Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu
    370                 375                 380
Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln
385                 390                 395                 400
Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala
                405                 410                 415
Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp
            420                 425                 430
Gly Glu Leu Glu Asn Gly Phe
        435


&lt;210&gt; 179
&lt;211&gt; 1521
&lt;212&gt; DNA
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (1)...(1521)

&lt;400&gt; 179
atg gag tac gat gga cgg aga ccc tac tct gtt cta acg aga aat gaa      48
Met Glu Tyr Asp Gly Arg Arg Pro Tyr Ser Val Leu Thr Arg Asn Glu
 1               5                  10                  15

att acc gta aag atg aag aaa cag atc aat gaa atc tct gac atc ttc      96
Ile Thr Val Lys Met Lys Lys Gln Ile Asn Glu Ile Ser Asp Ile Phe
            20                  25                  30

ttc ata tca aac tcc gat gcg acc gta ctt ctt atg tat ctc cga tgg      144
Phe Ile Ser Asn Ser Asp Ala Thr Val Leu Leu Met Tyr Leu Arg Trp
        35                  40                  45

gac tcg ctt cgt gtt tca gag cgt tta ggt gaa aac aag gag aaa tta      192
Asp Ser Leu Arg Val Ser Glu Arg Leu Gly Glu Asn Lys Glu Lys Leu
    50                  55                  60

ttg atg gat tca ggt ttg aaa tca gtc atg atc gat ccc agt cca gat      240
Leu Met Asp Ser Gly Leu Lys Ser Val Met Ile Asp Pro Ser Pro Asp
 65                 70                  75                  80

tca tct agc gag att agc ttg gag act gat gtt tat gag ttt gat ggt      288
Ser Ser Ser Glu Ile Ser Leu Glu Thr Asp Val Tyr Glu Phe Asp Gly
                85                  90.                 95
```

```
gat aat gat tta atc tcc atg ccc ttt tgt tct cac aag ttc gac tca     336
Asp Asn Asp Leu Ile Ser Met Pro Phe Cys Ser His Lys Phe Asp Ser
            100                 105                 110

aaa tat tgg aga gag tat ctt gag aag aat ttc tac tat gtg gag aaa     384
Lys Tyr Trp Arg Glu Tyr Leu Glu Lys Asn Phe Tyr Tyr Val Glu Lys
        115                 120                 125

atc caa acc aca atc tct tgt cct gat caa gat tgt cga tct gcg gtt     432
Ile Gln Thr Thr Ile Ser Cys Pro Asp Gln Asp Cys Arg Ser Ala Val
    130                 135                 140

gga cca gac acg att gag aaa cta aca gta cgt gat caa gag atg tac     480
Gly Pro Asp Thr Ile Glu Lys Leu Thr Val Arg Asp Gln Glu Met Tyr
145                 150                 155                 160

gag agg tac att tgg aga tct tac att gaa gga aac aag gta ttg atg     528
Glu Arg Tyr Ile Trp Arg Ser Tyr Ile Glu Gly Asn Lys Val Leu Met
                165                 170                 175

atc aaa cag tgt cct gca cgg aat tgc gat tat gtt att gag ttt cat     576
Ile Lys Gln Cys Pro Ala Arg Asn Cys Asp Tyr Val Ile Glu Phe His
            180                 185                 190

caa gag aat gat gat gat gat gag tat agt tta aac gtg gtg tgt atc     624
Gln Glu Asn Asp Asp Asp Asp Glu Tyr Ser Leu Asn Val Val Cys Ile
        195                 200                 205

tgt ggt cat atc ttc tgt tgg aga tgc aga ctt gag tca cac aga cca     672
Cys Gly His Ile Phe Cys Trp Arg Cys Arg Leu Glu Ser His Arg Pro
    210                 215                 220

gtg agt tgt aac aag gcc tct gat tgg ttg tgt agt gcc aca atg aaa     720
Val Ser Cys Asn Lys Ala Ser Asp Trp Leu Cys Ser Ala Thr Met Lys
225                 230                 235                 240

ata tca gat gaa tca ttt agc ctt tat ccg acc aaa acc aag aca gtg     768
Ile Ser Asp Glu Ser Phe Ser Leu Tyr Pro Thr Lys Thr Lys Thr Val
                245                 250                 255

act tgc cct cat tgc ctc tgt tct ctg gag tct gat aca aaa atg ccc     816
Thr Cys Pro His Cys Leu Cys Ser Leu Glu Ser Asp Thr Lys Met Pro
            260                 265                 270

cag ttc ttg act tgt gtc tgc agg ctt cgt ttc tgt tcg agg tgt ttg     864
Gln Phe Leu Thr Cys Val Cys Arg Leu Arg Phe Cys Ser Arg Cys Leu
        275                 280                 285

cgg tca gag gaa gcc cac aaa att gaa gca gta gac tct gga ttc tgt     912
Arg Ser Glu Glu Ala His Lys Ile Glu Ala Val Asp Ser Gly Phe Cys
    290                 295                 300

att aaa aca gaa gtg ggg att tta tgt gag gat cgc tgg aac gtg tgt     960
Ile Lys Thr Glu Val Gly Ile Leu Cys Glu Asp Arg Trp Asn Val Cys
305                 310                 315                 320
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cag aag tta ctg gag caa gcc aaa tcc gat cta gaa gct ttc gag gaa 1008
Gln Lys Leu Leu Glu Gln Ala Lys Ser Asp Leu Glu Ala Phe Glu Glu
325 330 335

acc aac atc aag aaa ccg agt gac tta tta agg gag caa gac att atg 1056
Thr Asn Ile Lys Lys Pro Ser Asp Leu Leu Arg Glu Gln Asp Ile Met
340 345 350

att ata aga gaa ggg ttg atg ttg att gtt caa tgc aga cga gtc ctt 1104
Ile Ile Arg Glu Gly Leu Met Leu Ile Val Gln Cys Arg Arg Val Leu
355 360 365

aaa tgg tgt tgt gtg tat gac tat ttc cac aca gag tat gag aac tcg 1152
Lys Trp Cys Cys Val Tyr Asp Tyr Phe His Thr Glu Tyr Glu Asn Ser
370 375 380

aag gag tat cta cga tac ctc caa gga aat gca atc gcc acg ctc cag 1200
Lys Glu Tyr Leu Arg Tyr Leu Gln Gly Asn Ala Ile Ala Thr Leu Gln
385 390 395 400

agt tac tca aac act tta caa gag caa aaa gat atc gtc ctc gct gca 1248
Ser Tyr Ser Asn Thr Leu Gln Glu Gln Lys Asp Ile Val Leu Ala Ala
405 410 415

gct act tat gaa gag tgt act ttc ttc aga cat acg ata cct act gcg 1296
Ala Thr Tyr Glu Glu Cys Thr Phe Phe Arg His Thr Ile Pro Thr Ala
420 425 430

aca agc aac att ggt aac tac ttt tat gat ttt atg aaa act tta caa 1344
Thr Ser Asn Ile Gly Asn Tyr Phe Tyr Asp Phe Met Lys Thr Leu Gln
435 440 445

gat ggt ttg gtc gat gta aag gtg aag tca tac aac ggc ggg act ggt 1392
Asp Gly Leu Val Asp Val Lys Val Lys Ser Tyr Asn Gly Gly Thr Gly
450 455 460

cct ttc tgg tac tgt gat cgc tgc acg tat gca aac act tgg gag gat 1440
Pro Phe Trp Tyr Cys Asp Arg Cys Thr Tyr Ala Asn Thr Trp Glu Asp
465 470 475 480

aat gag tgt gag atg tgc tat gat gat agt gcc tct ctt gtg gga gag 1488
Asn Glu Cys Glu Met Cys Tyr Asp Asp Ser Ala Ser Leu Val Gly Glu
485 490 495

ata agt gat ttg ttt ctt aac aaa gtt tct taa 1521
Ile Ser Asp Leu Phe Leu Asn Lys Val Ser *
500 505

<210> 180
<211> 506
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (214)...(287)

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<223> Conserved domain

<400> 180
Met Glu Tyr Asp Gly Arg Arg Pro Tyr Ser Val Leu Thr Arg Asn Glu
 1               5                  10                  15
Ile Thr Val Lys Met Lys Lys Gln Ile Asn Glu Ile Ser Asp Ile Phe
            20                  25                  30
Phe Ile Ser Asn Ser Asp Ala Thr Val Leu Leu Met Tyr Leu Arg Trp
        35                  40                  45
Asp Ser Leu Arg Val Ser Glu Arg Leu Gly Glu Asn Lys Glu Lys Leu
    50                  55                  60
Leu Met Asp Ser Gly Leu Lys Ser Val Met Ile Asp Pro Ser Pro Asp
65                  70                  75                  80
Ser Ser Ser Glu Ile Ser Leu Glu Thr Asp Val Tyr Glu Phe Asp Gly
                85                  90                  95
Asp Asn Asp Leu Ile Ser Met Pro Phe Cys Ser His Lys Phe Asp Ser
            100                 105                 110
Lys Tyr Trp Arg Glu Tyr Leu Glu Lys Asn Phe Tyr Tyr Val Glu Lys
        115                 120                 125
Ile Gln Thr Thr Ile Ser Cys Pro Asp Gln Asp Cys Arg Ser Ala Val
    130                 135                 140
Gly Pro Asp Thr Ile Glu Lys Leu Thr Val Arg Asp Gln Glu Met Tyr
145                 150                 155                 160
Glu Arg Tyr Ile Trp Arg Ser Tyr Ile Glu Gly Asn Lys Val Leu Met
                165                 170                 175
Ile Lys Gln Cys Pro Ala Arg Asn Cys Asp Tyr Val Ile Glu Phe His
            180                 185                 190
Gln Glu Asn Asp Asp Asp Asp Glu Tyr Ser Leu Asn Val Val Cys Ile
        195                 200                 205
Cys Gly His Ile Phe Cys Trp Arg Cys Arg Leu Glu Ser His Arg Pro
    210                 215                 220
Val Ser Cys Asn Lys Ala Ser Asp Trp Leu Cys Ser Ala Thr Met Lys
225                 230                 235                 240
Ile Ser Asp Glu Ser Phe Ser Leu Tyr Pro Thr Lys Thr Lys Thr Val
                245                 250                 255
Thr Cys Pro His Cys Leu Cys Ser Leu Glu Ser Asp Thr Lys Met Pro
            260                 265                 270
Gln Phe Leu Thr Cys Val Cys Arg Leu Arg Phe Cys Ser Arg Cys Leu
        275                 280                 285
Arg Ser Glu Glu Ala His Lys Ile Glu Ala Val Asp Ser Gly Phe Cys
    290                 295                 300
Ile Lys Thr Glu Val Gly Ile Leu Cys Glu Asp Arg Trp Asn Val Cys
305                 310                 315                 320
Gln Lys Leu Leu Glu Gln Ala Lys Ser Asp Leu Glu Ala Phe Glu Glu
                325                 330                 335
Thr Asn Ile Lys Lys Pro Ser Asp Leu Leu Arg Glu Gln Asp Ile Met
            340                 345                 350
Ile Ile Arg Glu Gly Leu Met Leu Ile Val Gln Cys Arg Arg Val Leu
        355                 360                 365
Lys Trp Cys Cys Val Tyr Asp Tyr Phe His Thr Glu Tyr Glu Asn Ser
    370                 375                 380
Lys Glu Tyr Leu Arg Tyr Leu Gln Gly Asn Ala Ile Ala Thr Leu Gln
385                 390                 395                 400
Ser Tyr Ser Asn Thr Leu Gln Glu Gln Lys Asp Ile Val Leu Ala Ala
                405                 410                 415
Ala Thr Tyr Glu Glu Cys Thr Phe Phe Arg His Thr Ile Pro Thr Ala
            420                 425                 430
```

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Thr Ser Asn Ile Gly Asn Tyr Phe Tyr Asp Phe Met Lys Thr Leu Gln
        435                 440                 445
Asp Gly Leu Val Asp Val Lys Val Lys Ser Tyr Asn Gly Gly Thr Gly
    450                 455                 460
Pro Phe Trp Tyr Cys Asp Arg Cys Thr Tyr Ala Asn Thr Trp Glu Asp
465                 470                 475                 480
Asn Glu Cys Glu Met Cys Tyr Asp Asp Ser Ala Ser Leu Val Gly Glu
                485                 490                 495
Ile Ser Asp Leu Phe Leu Asn Lys Val Ser
            500                 505


<210> 181
<211> 955
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (54)...(785)

<400> 181
tcgacccacc ttgaatctga gagagagaga gaagtacgtc cccacacctt gac atg      56
                                                           Met
                                                            1

gtc atg gag ccc aag aag aac caa aat cta cca agt ttc tta aac cca     104
Val Met Glu Pro Lys Lys Asn Gln Asn Leu Pro Ser Phe Leu Asn Pro
            5                   10                  15

tca cga cag aat cag gac aac gac aag aag agg aaa caa aca gag gtt     152
Ser Arg Gln Asn Gln Asp Asn Asp Lys Lys Arg Lys Gln Thr Glu Val
        20                  25                  30

aaa ggt ttc gac att gtg gtc ggc gaa aag agg aag aag aag gag aat     200
Lys Gly Phe Asp Ile Val Val Gly Glu Lys Arg Lys Lys Lys Glu Asn
    35                  40                  45

gaa gag gaa gac caa gaa att cag att ctt tat gag aag gag aag aag     248
Glu Glu Glu Asp Gln Glu Ile Gln Ile Leu Tyr Glu Lys Glu Lys Lys
 50                  55                  60                  65

aaa cca aac aaa gat cgt cac ctt aaa gtt gaa gga aga ggt cgt aga     296
Lys Pro Asn Lys Asp Arg His Leu Lys Val Glu Gly Arg Gly Arg Arg
                70                  75                  80

gtt agg tta cct cca ctc tgt gca gca agg att tat caa ttg act aaa     344
Val Arg Leu Pro Pro Leu Cys Ala Ala Arg Ile Tyr Gln Leu Thr Lys
            85                  90                  95

gaa tta ggt cac aaa tca gat ggt gag act ctt gaa tgg ttg ctt caa     392
Glu Leu Gly His Lys Ser Asp Gly Glu Thr Leu Glu Trp Leu Leu Gln
        100                 105                 110

cat gct gag cca tcg ata ctc tct gct act gta aat ggt atc aaa ccc     440
His Ala Glu Pro Ser Ile Leu Ser Ala Thr Val Asn Gly Ile Lys Pro
    115                 120                 125
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act gag tct gtt gtt tct caa cct cct ctc acg gct gat ttg atg att    488
Thr Glu Ser Val Val Ser Gln Pro Pro Leu Thr Ala Asp Leu Met Ile
130                 135                 140                 145

tgt cat agc gtt gaa gaa gct tca agg act caa atg gag gca aat ggg    536
Cys His Ser Val Glu Glu Ala Ser Arg Thr Gln Met Glu Ala Asn Gly
                150                 155                 160

ttg tgg aga aat gaa aca gga cag acc att gga ggg ttt gat ctg aat    584
Leu Trp Arg Asn Glu Thr Gly Gln Thr Ile Gly Gly Phe Asp Leu Asn
            165                 170                 175

tac gga att ggg ttt gat ttc aat ggt gtt cca gag att ggt ttt gga    632
Tyr Gly Ile Gly Phe Asp Phe Asn Gly Val Pro Glu Ile Gly Phe Gly
        180                 185                 190

gat aat caa acg cct gga ctt gaa tta agg ctg tct caa gtt ggg gtt    680
Asp Asn Gln Thr Pro Gly Leu Glu Leu Arg Leu Ser Gln Val Gly Val
    195                 200                 205

ttg aat cca cag gtt ttt caa caa atg ggt aaa gaa cag ttc agg gtt    728
Leu Asn Pro Gln Val Phe Gln Gln Met Gly Lys Glu Gln Phe Arg Val
210                 215                 220                 225

ctt cat cat cat tca cat gaa gat cag cag cag agt gca gag gaa aat    776
Leu His His His Ser His Glu Asp Gln Gln Gln Ser Ala Glu Glu Asn
                230                 235                 240

ggt tca taa agctcaaacc tttaaatggc ttttaattag atatatttag            825
Gly Ser  *

cgagaatgtg attgctagtg aaatctcaaa cttgatagct tattcatagc ttattttact 885
tcgatcagca agagaacaat ggttcctaaa gctcaaacct tttttggcgt ttgctttaga 945
ttgtgcatac                                                        955

&lt;210&gt; 182
&lt;211&gt; 243
&lt;212&gt; PRT
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; DOMAIN
&lt;222&gt; (64)...(129)
&lt;223&gt; Conserved domain

&lt;400&gt; 182
Met Val Met Glu Pro Lys Lys Asn Gln Asn Leu Pro Ser Phe Leu Asn
 1               5                  10                  15
Pro Ser Arg Gln Asn Gln Asp Asn Asp Lys Lys Arg Lys Gln Thr Glu
            20                  25                  30
Val Lys Gly Phe Asp Ile Val Val Gly Glu Lys Arg Lys Lys Lys Glu
        35                  40                  45
Asn Glu Glu Glu Asp Gln Glu Ile Gln Ile Leu Tyr Glu Lys Glu Lys
    50                  55                  60
Lys Lys Pro Asn Lys Asp Arg His Leu Lys Val Glu Gly Arg Gly Arg
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65                  70                  75                  80
Arg Val Arg Leu Pro Pro Leu Cys Ala Ala Arg Ile Tyr Gln Leu Thr
                85                  90                  95
Lys Glu Leu Gly His Lys Ser Asp Gly Glu Thr Leu Glu Trp Leu Leu
            100                 105                 110
Gln His Ala Glu Pro Ser Ile Leu Ser Ala Thr Val Asn Gly Ile Lys
        115                 120                 125
Pro Thr Glu Ser Val Val Ser Gln Pro Pro Leu Thr Ala Asp Leu Met
    130                 135                 140
Ile Cys His Ser Val Glu Glu Ala Ser Arg Thr Gln Met Glu Ala Asn
145                 150                 155                 160
Gly Leu Trp Arg Asn Glu Thr Gly Gln Thr Ile Gly Gly Phe Asp Leu
                165                 170                 175
Asn Tyr Gly Ile Gly Phe Asp Phe Asn Gly Val Pro Glu Ile Gly Phe
            180                 185                 190
Gly Asp Asn Gln Thr Pro Gly Leu Glu Leu Arg Leu Ser Gln Val Gly
        195                 200                 205
Val Leu Asn Pro Gln Val Phe Gln Gln Met Gly Lys Glu Gln Phe Arg
    210                 215                 220
Val Leu His His His Ser His Glu Asp Gln Gln Gln Ser Ala Glu Glu
225                 230                 235                 240
Asn Gly Ser


<210> 183
<211> 883
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (42)...(764)

<400> 183
ctgaattcga actttggaag aagaagaagc tttgatcaat c atg gaa att gca acc 56
                                              Met Glu Ile Ala Thr
                                               1               5

gat aca gca aag cag atg aga gac gaa gag ttg ttc aaa gca gcg gaa    104
Asp Thr Ala Lys Gln Met Arg Asp Glu Glu Leu Phe Lys Ala Ala Glu
                10                  15                  20

tgg gga gat tca tcg ttg ttc atg tca tta tct gaa gaa cag ctc tct    152
Trp Gly Asp Ser Ser Leu Phe Met Ser Leu Ser Glu Glu Gln Leu Ser
            25                  30                  35

aaa tct ctc aat ttc aga aac gaa gat ggt cgc tct ctc ctc cat gtc    200
Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg Ser Leu Leu His Val
        40                  45                  50

gct gct tcc ttc ggc cat tct caa ata gtg aag ttg tta tca agt tca    248
Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys Leu Leu Ser Ser Ser
    55                  60                  65

gat gaa gca aag act gta atc aat agc aag gat gat gaa gga tgg gct    296
Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp Asp Glu Gly Trp Ala
```

70 75 80 85

cct ttg cat tcc gct gct agc atc ggt aat gct gag ctc gtt gag gtg 344
Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala Glu Leu Val Glu Val
90 95 100

ctt ttg acc aga ggt gct gat gtc aat gcc aaa aat aac ggt ggt cgc 392
Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys Asn Asn Gly Gly Arg
105 110 115

act gct ctt cac tat gct gct agc aaa ggc cgg ttg gag att gct cag 440
Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg Leu Glu Ile Ala Gln
120 125 130

ctt tta tta aca cac ggt gca aag att aac atc aca gac aag gtt ggt 488
Leu Leu Leu Thr His Gly Ala Lys Ile Asn Ile Thr Asp Lys Val Gly
135 140 145

tgc act ccg ctt cac agg gca gca agc gtg gga aag tta gaa gtt tgt 536
Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly Lys Leu Glu Val Cys
150 155 160 165

gaa ttt ctt att gaa gaa gga gca gag atc gat gct acg gat aaa atg 584
Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp Ala Thr Asp Lys Met
170 175 180

ggt caa act gca ctc atg cat tca gtt atc tgc gat gac aaa cag gtt 632
Gly Gln Thr Ala Leu Met His Ser Val Ile Cys Asp Asp Lys Gln Val
185 190 195

gcg ttc ctg ctt ata aga cat ggt gca gat gtg gat gta gaa gac aag 680
Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val Asp Val Glu Asp Lys
200 205 210

gaa ggc tac act gtt cta ggc cga gct acc aat gaa ttc cga cct gca 728
Glu Gly Tyr Thr Val Leu Gly Arg Ala Thr Asn Glu Phe Arg Pro Ala
215 220 225

ctt atc gat gct gct aag gcc atg ctt gaa gga taa aatgactctg 774
Leu Ile Asp Ala Ala Lys Ala Met Leu Glu Gly *
230 235 240

gattacttta aaacttacta actctgagag ttgtttagtt acttaaaagg atttttcttt 834
actgtatcat gtttgcaaaa tgtttctgcc ttatcaattc atgttctgt 883

<210> 184
<211> 240
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (65)...(228)
<223> Conserved domain

<400> 184
Met Glu Ile Ala Thr Asp Thr Ala Lys Gln Met Arg Asp Glu Glu Leu

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 1               5                   10                  15
Phe Lys Ala Ala Glu Trp Gly Asp Ser Ser Leu Phe Met Ser Leu Ser
            20                  25                  30
Glu Glu Gln Leu Ser Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg
        35                  40                  45
Ser Leu Leu His Val Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys
    50                  55                  60
Leu Leu Ser Ser Ser Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp
65                  70                  75                  80
Asp Glu Gly Trp Ala Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala
                85                  90                  95
Glu Leu Val Glu Val Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys
            100                 105                 110
Asn Asn Gly Gly Arg Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg
        115                 120                 125
Leu Glu Ile Ala Gln Leu Leu Leu Thr His Gly Ala Lys Ile Asn Ile
    130                 135                 140
Thr Asp Lys Val Gly Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly
145                 150                 155                 160
Lys Leu Glu Val Cys Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp
                165                 170                 175
Ala Thr Asp Lys Met Gly Gln Thr Ala Leu Met His Ser Val Ile Cys
            180                 185                 190
Asp Asp Lys Gln Val Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val
        195                 200                 205
Asp Val Glu Asp Lys Glu Gly Tyr Thr Val Leu Gly Arg Ala Thr Asn
    210                 215                 220
Glu Phe Arg Pro Ala Leu Ile Asp Ala Ala Lys Ala Met Leu Glu Gly
225                 230                 235                 240

<210> 185
<211> 1026
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1026)

<400> 185
atg gaa gga gga gga aga gga cca aat caa acg att ctc agt gaa ata      48
Met Glu Gly Gly Gly Arg Gly Pro Asn Gln Thr Ile Leu Ser Glu Ile
 1               5                   10                  15

gaa cat atg cct gaa gct cca cgt caa cgt atc tct cat cac cgt cga      96
Glu His Met Pro Glu Ala Pro Arg Gln Arg Ile Ser His His Arg Arg
            20                  25                  30

gct cgc tct gaa acc ttc ttc tcc ggc gaa tca atc gac gat ctc ctc     144
Ala Arg Ser Glu Thr Phe Phe Ser Gly Glu Ser Ile Asp Asp Leu Leu
        35                  40                  45

tta ttc gat cct tcc gat atc gat ttc tct tct cta gac ttc ctc aac     192
Leu Phe Asp Pro Ser Asp Ile Asp Phe Ser Ser Leu Asp Phe Leu Asn
    50                  55                  60
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gct cca cca cca cca caa caa tca caa caa caa ccg caa gct tct ccc      240
Ala Pro Pro Pro Pro Gln Gln Ser Gln Gln Gln Pro Gln Ala Ser Pro
 65                 70                  75                  80

atg tcc gtt gat tcg gaa gaa acc tca tcg aac ggt gtt gtt cct cct      288
Met Ser Val Asp Ser Glu Glu Thr Ser Ser Asn Gly Val Val Pro Pro
                85                  90                  95

aat tct ctt cct cca aaa ccc gaa gct aga ttc ggt cgc cat gtt cgt      336
Asn Ser Leu Pro Pro Lys Pro Glu Ala Arg Phe Gly Arg His Val Arg
            100                 105                 110

agc ttc tcg gtt gat tcc gat ttc ttc gat gat ttg ggt gtt act gag      384
Ser Phe Ser Val Asp Ser Asp Phe Phe Asp Asp Leu Gly Val Thr Glu
        115                 120                 125

gag aag ttt ata gct aca agt tca gga gag aag aag aaa ggg aat cat      432
Glu Lys Phe Ile Ala Thr Ser Ser Gly Glu Lys Lys Lys Gly Asn His
    130                 135                 140

cat cat agc agg agt aat tct atg gat gga gag atg agt tcg gcg tcg      480
His His Ser Arg Ser Asn Ser Met Asp Gly Glu Met Ser Ser Ala Ser
145                 150                 155                 160

ttt aat atc gaa tcg att tta gct tct gtg agt ggt aaa gat agt ggg      528
Phe Asn Ile Glu Ser Ile Leu Ala Ser Val Ser Gly Lys Asp Ser Gly
                165                 170                 175

aag aag aat atg ggt atg ggt ggt gat aga ctt gct gag ctt gct ttg      576
Lys Lys Asn Met Gly Met Gly Gly Asp Arg Leu Ala Glu Leu Ala Leu
            180                 185                 190

ctt gat cct aaa aga gct aaa agg att tta gcg aat aga caa tct gcg      624
Leu Asp Pro Lys Arg Ala Lys Arg Ile Leu Ala Asn Arg Gln Ser Ala
        195                 200                 205

gcg agg tcg aaa gag agg aag att agg tat act ggt gag tta gag agg      672
Ala Arg Ser Lys Glu Arg Lys Ile Arg Tyr Thr Gly Glu Leu Glu Arg
    210                 215                 220

aag gtt cag aca ctt cag aat gaa gct act aca ttg tct gct caa gtc      720
Lys Val Gln Thr Leu Gln Asn Glu Ala Thr Thr Leu Ser Ala Gln Val
225                 230                 235                 240

act atg tta cag aga gga aca tca gag ctg aac act gaa aat aaa cac      768
Thr Met Leu Gln Arg Gly Thr Ser Glu Leu Asn Thr Glu Asn Lys His
                245                 250                 255

ctc aaa atg cgg ctt caa gct tta gag caa caa gct gaa ctt agg gat      816
Leu Lys Met Arg Leu Gln Ala Leu Glu Gln Gln Ala Glu Leu Arg Asp
            260                 265                 270

gct ttg aat gaa gcg ctg cgg gat gaa ctg aac cga ctt aag gtg gta      864
Ala Leu Asn Glu Ala Leu Arg Asp Glu Leu Asn Arg Leu Lys Val Val
        275                 280                 285

gct gga gaa att cct cag ggg aat gga aat tct tac aac cgt gct caa      912
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```
Ala Gly Glu Ile Pro Gln Gly Asn Gly Asn Ser Tyr Asn Arg Ala Gln
    290                 295                 300

ttc tca tct cag caa tcg gca atg aat cag ttt ggg aac aaa acg aac      960
Phe Ser Ser Gln Gln Ser Ala Met Asn Gln Phe Gly Asn Lys Thr Asn
305                 310                 315                 320

caa cag atg agt aca aac ggg cag cca tcg ctc cca agc tac atg gat      1008
Gln Gln Met Ser Thr Asn Gly Gln Pro Ser Leu Pro Ser Tyr Met Asp
                325                 330                 335

ttc acc aag aga ggc tga                                              1026
Phe Thr Lys Arg Gly  *
            340


<210> 186
<211> 341
<212> PRT
<213> Arabidopsis thaliana

<400> 186
Met Glu Gly Gly Gly Arg Gly Pro Asn Gln Thr Ile Leu Ser Glu Ile
 1               5                  10                  15
Glu His Met Pro Glu Ala Pro Arg Gln Arg Ile Ser His His Arg Arg
            20                  25                  30
Ala Arg Ser Glu Thr Phe Phe Ser Gly Glu Ser Ile Asp Asp Leu Leu
        35                  40                  45
Leu Phe Asp Pro Ser Asp Ile Asp Phe Ser Ser Leu Asp Phe Leu Asn
    50                  55                  60
Ala Pro Pro Pro Pro Gln Gln Ser Gln Gln Gln Pro Gln Ala Ser Pro
65                  70                  75                  80
Met Ser Val Asp Ser Glu Glu Thr Ser Ser Asn Gly Val Val Pro Pro
                85                  90                  95
Asn Ser Leu Pro Pro Lys Pro Glu Ala Arg Phe Gly Arg His Val Arg
            100                 105                 110
Ser Phe Ser Val Asp Ser Asp Phe Phe Asp Asp Leu Gly Val Thr Glu
        115                 120                 125
Glu Lys Phe Ile Ala Thr Ser Ser Gly Glu Lys Lys Lys Gly Asn His
    130                 135                 140
His His Ser Arg Ser Asn Ser Met Asp Gly Glu Met Ser Ser Ala Ser
145                 150                 155                 160
Phe Asn Ile Glu Ser Ile Leu Ala Ser Val Ser Gly Lys Asp Ser Gly
                165                 170                 175
Lys Lys Asn Met Gly Met Gly Gly Asp Arg Leu Ala Glu Leu Ala Leu
            180                 185                 190
Leu Asp Pro Lys Arg Ala Lys Arg Ile Leu Ala Asn Arg Gln Ser Ala
        195                 200                 205
Ala Arg Ser Lys Glu Arg Lys Ile Arg Tyr Thr Gly Glu Leu Glu Arg
    210                 215                 220
Lys Val Gln Thr Leu Gln Asn Glu Ala Thr Thr Leu Ser Ala Gln Val
225                 230                 235                 240
Thr Met Leu Gln Arg Gly Thr Ser Glu Leu Asn Thr Glu Asn Lys His
                245                 250                 255
Leu Lys Met Arg Leu Gln Ala Leu Glu Gln Gln Ala Glu Leu Arg Asp
            260                 265                 270
Ala Leu Asn Glu Ala Leu Arg Asp Glu Leu Asn Arg Leu Lys Val Val
```

```
        275                      280                      285
Ala Gly Glu Ile Pro Gln Gly Asn Gly Asn Ser Tyr Asn Arg Ala Gln
    290                      295                      300
Phe Ser Ser Gln Gln Ser Ala Met Asn Gln Phe Gly Asn Lys Thr Asn
305                      310                      315                      320
Gln Gln Met Ser Thr Asn Gly Gln Pro Ser Leu Pro Ser Tyr Met Asp
                    325                      330                      335
Phe Thr Lys Arg Gly
                340


<210> 187
<211> 1107
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (16)...(930)

<400> 187
aaaagatctg tttca atg gcg gat cgt gtt aaa ggt cca tgg agt caa gaa   51
                 Met Ala Asp Arg Val Lys Gly Pro Trp Ser Gln Glu
                  1               5                  10

gaa gat gag cag cta cga agg atg gtt gag aaa tac gga ccg agg aat   99
Glu Asp Glu Gln Leu Arg Arg Met Val Glu Lys Tyr Gly Pro Arg Asn
         15                  20                  25

tgg tct gcg att agc aaa tcg att cca ggt cga tct ggt aaa tcg tgt   147
Trp Ser Ala Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys
     30                  35                  40

aga tta cgt tgg tgt aat cag tta tct ccg gag gtt gag cat cgt cct   195
Arg Leu Arg Trp Cys Asn Gln Leu Ser Pro Glu Val Glu His Arg Pro
 45                  50                  55                  60

ttc tcg ccg gag gaa gat gag act att gta acc gcc cgt gct cag ttt   243
Phe Ser Pro Glu Glu Asp Glu Thr Ile Val Thr Ala Arg Ala Gln Phe
                 65                  70                  75

ggt aac aag tgg gcg acg att gct cgt ctt ctt aac ggt cgt acg gat   291
Gly Asn Lys Trp Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp
             80                  85                  90

aac gcc gtt aaa aat cac tgg aac tct acg ctt aag agg aaa tgc agc   339
Asn Ala Val Lys Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Ser
         95                 100                 105

gga ggt gtg gcg gtt acg acg gtg acg gag acg gag gaa gat cag gat   387
Gly Gly Val Ala Val Thr Thr Val Thr Glu Thr Glu Glu Asp Gln Asp
    110                 115                 120

cgg ccg aag aag agg aga tct gtt agc ttt gat cct gct ttt gct ccg   435
Arg Pro Lys Lys Arg Arg Ser Val Ser Phe Asp Pro Ala Phe Ala Pro
125                 130                 135                 140
```

```
gtg gat act gga ttg tac atg agt cct gag agt cct aac gga atc gat     483
Val Asp Thr Gly Leu Tyr Met Ser Pro Glu Ser Pro Asn Gly Ile Asp
                145                 150                 155

gtt agt gat tct agc acg att ccg tca ccg tcg tct cct gtt gct cag     531
Val Ser Asp Ser Ser Thr Ile Pro Ser Pro Ser Ser Pro Val Ala Gln
            160                 165                 170

ctg ttt aaa cca atg ccg att tcc ggc ggt ttt acg gtg gtt ccg cag     579
Leu Phe Lys Pro Met Pro Ile Ser Gly Gly Phe Thr Val Val Pro Gln
        175                 180                 185

ccg tta ccg gtt gaa atg tct tcg tct tcg gag gat cca cct act tcg     627
Pro Leu Pro Val Glu Met Ser Ser Ser Ser Glu Asp Pro Pro Thr Ser
    190                 195                 200

ttg agt ttg tca cta cct gga gct gag aac acg agt tcg agc cat aac     675
Leu Ser Leu Ser Leu Pro Gly Ala Glu Asn Thr Ser Ser Ser His Asn
205                 210                 215                 220

aat aac aac aac gcg ttg atg ttt ccg aga ttt gag agt cag atg aag     723
Asn Asn Asn Asn Ala Leu Met Phe Pro Arg Phe Glu Ser Gln Met Lys
                225                 230                 235

att aat gta gag gag aga gga gga gga gga gaa gga cgt aga ggt gag     771
Ile Asn Val Glu Glu Arg Gly Gly Gly Gly Glu Gly Arg Arg Gly Glu
            240                 245                 250

ttt atg acg gtg gtg cag gag atg ata aaa gct gaa gtg agg agt tac     819
Phe Met Thr Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
        255                 260                 265

atg gcg gaa atg cag aaa aca agt ggt gga ttc gtc gtc gga ggt tta     867
Met Ala Glu Met Gln Lys Thr Ser Gly Gly Phe Val Val Gly Gly Leu
    270                 275                 280

tac gaa tcc ggc ggc aat ggt ggt ttt agg gat tgt gga gta ata aca     915
Tyr Glu Ser Gly Gly Asn Gly Gly Phe Arg Asp Cys Gly Val Ile Thr
285                 290                 295                 300

cct aag gtt gag tag ttttggttta gggttaaaac ttgaatcgat tggggatttt     970
Pro Lys Val Glu  *


caagagcatt catttttggg gtttatggta aaattaaaaa caaaaacaaa atgtacagag 1030
gaattaaaat ttctatggaa taatcttaaa tctcaaatat ttgttacttg ttttggtgat 1090
tcataaccaa aatcaaa                                                1107
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<210> 188
<211> 304
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (6)...(106)
<223> Conserved domain

<400> 188
Met Ala Asp Arg Val Lys Gly Pro Trp Ser Gln Glu Glu Asp Glu Gln
1 5 10 15
Leu Arg Arg Met Val Glu Lys Tyr Gly Pro Arg Asn Trp Ser Ala Ile
20 25 30
Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
35 40 45
Cys Asn Gln Leu Ser Pro Glu Val Glu His Arg Pro Phe Ser Pro Glu
50 55 60
Glu Asp Glu Thr Ile Val Thr Ala Arg Ala Gln Phe Gly Asn Lys Trp
65 70 75 80
Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys
85 90 95
Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Ser Gly Gly Val Ala
100 105 110
Val Thr Thr Val Thr Glu Thr Glu Glu Asp Gln Asp Arg Pro Lys Lys
115 120 125
Arg Arg Ser Val Ser Phe Asp Pro Ala Phe Ala Pro Val Asp Thr Gly
130 135 140
Leu Tyr Met Ser Pro Glu Ser Pro Asn Gly Ile Asp Val Ser Asp Ser
145 150 155 160
Ser Thr Ile Pro Ser Pro Ser Ser Pro Val Ala Gln Leu Phe Lys Pro
165 170 175
Met Pro Ile Ser Gly Gly Phe Thr Val Val Pro Gln Pro Leu Pro Val
180 185 190
Glu Met Ser Ser Ser Ser Glu Asp Pro Pro Thr Ser Leu Ser Leu Ser
195 200 205
Leu Pro Gly Ala Glu Asn Thr Ser Ser Ser His Asn Asn Asn Asn Asn
210 215 220
Ala Leu Met Phe Pro Arg Phe Glu Ser Gln Met Lys Ile Asn Val Glu
225 230 235 240
Glu Arg Gly Gly Gly Gly Glu Gly Arg Arg Gly Glu Phe Met Thr Val
245 250 255
Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr Met Ala Glu Met
260 265 270
Gln Lys Thr Ser Gly Gly Phe Val Val Gly Gly Leu Tyr Glu Ser Gly
275 280 285
Gly Asn Gly Gly Phe Arg Asp Cys Gly Val Ile Thr Pro Lys Val Glu
290 295 300

<210> 189
<211> 1001
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (360)...(932)

<400> 189
tggcgacgcc ttcgccgacc tcctctcctc cctctgattc aaaccctaat tctgccgcta 60
ctccgccgca tcagaaacaa ccaccctctc ctcctcaacc cacgaatcca tcctctccac 120
caccgcacac caccgtcgta gctttagccg catcaacctc cgccgtcgcc agaaaaaccc 180
aacctgttct ctggactcaa gacgagaccc tcctcttaat cgaatcatac aaagagaaat 240
ggttcgcaat tggtcgtggt cctctaaaat caactcactg ggaagagatc gccgttgctg 300

cctcatctcg ttccggcgtt gaacggacat ctacacagtg taggcataag atcgagaag 359
atg cgt aaa aga ttc cga tct gag aga cag agt atg gga cct atc tca 407
Met Arg Lys Arg Phe Arg Ser Glu Arg Gln Ser Met Gly Pro Ile Ser
1 5 10 15

att tgg cct ttc tat aat caa atg gag gaa ttg gat tct tca aat cct 455
Ile Trp Pro Phe Tyr Asn Gln Met Glu Glu Leu Asp Ser Ser Asn Pro
20 25 30

gct ccg atc tca gct cgt cct ctc act cgt ctt cct cct aat tcg aat 503
Ala Pro Ile Ser Ala Arg Pro Leu Thr Arg Leu Pro Pro Asn Ser Asn
35 40 45

aat cgc tac gta gac gac gaa gaa gaa gat gaa gaa gag gat aac aat 551
Asn Arg Tyr Val Asp Asp Glu Glu Glu Asp Glu Glu Glu Asp Asn Asn
50 55 60

aac tac gaa gaa gag gaa gaa gaa gat gag aga cag agc aaa tcg agg 599
Asn Tyr Glu Glu Glu Glu Glu Glu Asp Glu Arg Gln Ser Lys Ser Arg
65 70 75 80

agt att aat tac ata ttg aga aga cct gga act gtt aac aga ttt gct 647
Ser Ile Asn Tyr Ile Leu Arg Arg Pro Gly Thr Val Asn Arg Phe Ala
85 90 95

gga gtt ggt gga gga ttg ttg tca tgg gga caa aaa gag aga tca tcg 695
Gly Val Gly Gly Gly Leu Leu Ser Trp Gly Gln Lys Glu Arg Ser Ser
100 105 110

aag agg aag agg aac gat gga gac ggt ggt gag agg cgg agg aaa gga 743
Lys Arg Lys Arg Asn Asp Gly Asp Gly Gly Glu Arg Arg Arg Lys Gly
115 120 125

atg cga gcc gtt gca gcg gag att agg gcg ttt gct gag aga gta atg 791
Met Arg Ala Val Ala Ala Glu Ile Arg Ala Phe Ala Glu Arg Val Met
130 135 140

gta atg gag aag aag aag att gag ttt gct aaa gag act gtg aga ctt 839
Val Mét Glu Lys Lys Lys Ile Glu Phe Ala Lys Glu Thr Val Arg Leu
145 150 155 160

cgt aag gaa atg gag att cgt aga atc aat ttg att cag agt tct caa 887
Arg Lys Glu Met Glu Ile Arg Arg Ile Asn Leu Ile Gln Ser Ser Gln
165 170 175

act cag ctt ctt caa ttt atc aac aat gct ttt gat tct ttc taa 932
Thr Gln Leu Leu Gln Phe Ile Asn Asn Ala Phe Asp Ser Phe *
180 185 190

cgtagagatt tagtcattgt tgcttttaga tttgtaacat aggtaacgga tttgaagaaa 992
tgcactatg 1001

<210> 190
<211> 190
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (107)...(181)
<223> Conserved domain

<400> 190
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Met Arg Lys Arg Phe Arg Ser Glu Arg Gln Ser Met Gly Pro Ile Ser
 1               5                  10                  15
Ile Trp Pro Phe Tyr Asn Gln Met Glu Glu Leu Asp Ser Ser Asn Pro
            20                  25                  30
Ala Pro Ile Ser Ala Arg Pro Leu Thr Arg Leu Pro Pro Asn Ser Asn
        35                  40                  45
Asn Arg Tyr Val Asp Asp Glu Glu Glu Asp Glu Glu Glu Asp Asn Asn
    50                  55                  60
Asn Tyr Glu Glu Glu Glu Glu Glu Asp Glu Arg Gln Ser Lys Ser Arg
65                  70                  75                  80
Ser Ile Asn Tyr Ile Leu Arg Arg Pro Gly Thr Val Asn Arg Phe Ala
                85                  90                  95
Gly Val Gly Gly Gly Leu Leu Ser Trp Gly Gln Lys Glu Arg Ser Ser
            100                 105                 110
Lys Arg Lys Arg Asn Asp Gly Asp Gly Gly Glu Arg Arg Arg Lys Gly
        115                 120                 125
Met Arg Ala Val Ala Ala Glu Ile Arg Ala Phe Ala Glu Arg Val Met
    130                 135                 140
Val Met Glu Lys Lys Lys Ile Glu Phe Ala Lys Glu Thr Val Arg Leu
145                 150                 155                 160
Arg Lys Glu Met Glu Ile Arg Arg Ile Asn Leu Ile Gln Ser Ser Gln
                165                 170                 175
Thr Gln Leu Leu Gln Phe Ile Asn Asn Ala Phe Asp Ser Phe
            180                 185                 190
```

<210> 191
<211> 1317
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (19)...(1314)

<400> 191
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tcgacagttg gtgtttaa atg gaa ttc tca ttg atc tcc gat gaa aat ttc      51
                    Met Glu Phe Ser Leu Ile Ser Asp Glu Asn Phe
                     1               5                  10

atc tta aac gat gct cat cga tgt cct gtt aat gat gat gca tcg cat      99
Ile Leu Asn Asp Ala His Arg Cys Pro Val Asn Asp Asp Ala Ser His
            15                  20                  25

ata cca aaa aat aat ctt aac ttt ttc aat gac aat tta ggt caa tct     147
Ile Pro Lys Asn Asn Leu Asn Phe Phe Asn Asp Asn Leu Gly Gln Ser
        30                  35                  40

tct cgt act gga tgg tct ttt tca cca gat ctg act gat atc tct aat     195
Ser Arg Thr Gly Trp Ser Phe Ser Pro Asp Leu Thr Asp Ile Ser Asn
    45                  50                  55
```

cag cac cac caa aat ctt ata cct ttg atc cca aat tat gat tct caa 243
Gln His His Gln Asn Leu Ile Pro Leu Ile Pro Asn Tyr Asp Ser Gln
60 65 70 75

aat cag aat ttg gat act aat caa aac cat ttg gtt tac aac tct tcc 291
Asn Gln Asn Leu Asp Thr Asn Gln Asn His Leu Val Tyr Asn Ser Ser
80 85 90

tcc tat gaa att cca tca aac tac cca ttc atg agt atc aaa tcc tac 339
Ser Tyr Glu Ile Pro Ser Asn Tyr Pro Phe Met Ser Ile Lys Ser Tyr
95 100 105

tca aat att gat act ctt gag caa tct atg aat aac ata gtc aac aac 387
Ser Asn Ile Asp Thr Leu Glu Gln Ser Met Asn Asn Ile Val Asn Asn
110 115 120

gga aaa atc cat atg atc gat aat ccc cca att ttt gca aac cct aag 435
Gly Lys Ile His Met Ile Asp Asn Pro Pro Ile Phe Ala Asn Pro Lys
125 130 135

ggt ata ttc gaa aat ttt cat gat ttg cag gaa tac act ata ggg aat 483
Gly Ile Phe Glu Asn Phe His Asp Leu Gln Glu Tyr Thr Ile Gly Asn
140 145 150 155

gag att gta cac aat gaa gaa ctg act aat aag ggt tat gag cca act 531
Glu Ile Val His Asn Glu Glu Leu Thr Asn Lys Gly Tyr Glu Pro Thr
160 165 170

ctt gat aag gta atg ggt gaa cct caa tta ttt gat gtg cca gtg cta 579
Leu Asp Lys Val Met Gly Glu Pro Gln Leu Phe Asp Val Pro Val Leu
175 180 185

gaa ggt atc aaa aat aca acc aac gaa atc atg aat caa ctt gaa gat 627
Glu Gly Ile Lys Asn Thr Thr Asn Glu Ile Met Asn Gln Leu Glu Asp
190 195 200

gat aag atg aaa aaa act tat gag aat aaa aag gag gcg agc aca agc 675
Asp Lys Met Lys Lys Thr Tyr Glu Asn Lys Lys Glu Ala Ser Thr Ser
205 210 215

aaa tat ttg aag aaa agt gac atc acc aaa aaa aga tgg aca gaa tct 723
Lys Tyr Leu Lys Lys Ser Asp Ile Thr Lys Lys Arg Trp Thr Glu Ser
220 225 230 235

gag gac ata aaa ttg aaa gag atg gtg gca ctt gaa ccc aaa aaa tgg 771
Glu Asp Ile Lys Leu Lys Glu Met Val Ala Leu Glu Pro Lys Lys Trp
240 245 250

aca aag gtc gca aaa cat ttt gaa gga cga aca cca aaa caa tgc aga 819
Thr Lys Val Ala Lys His Phe Glu Gly Arg Thr Pro Lys Gln Cys Arg
255 260 265

gag agg tgg cat aac cat gct cgt cct aac gtt aag aaa act act tgg 867
Glu Arg Trp His Asn His Ala Arg Pro Asn Val Lys Lys Thr Thr Trp
270 275 280

```
agt gaa gaa gaa gat caa ata cta att gaa gta cac aaa gta att ggt    915
Ser Glu Glu Glu Asp Gln Ile Leu Ile Glu Val His Lys Val Ile Gly
    285                 290                 295

gcc aaa tgg atc cag atc tca gag caa ctt ccg ggg agg agc tat aac    963
Ala Lys Trp Ile Gln Ile Ser Glu Gln Leu Pro Gly Arg Ser Tyr Asn
300                 305                 310                 315

aat gtt aag aac cat tgg aat acc aca aag cgt cgg gtg caa aat aaa    1011
Asn Val Lys Asn His Trp Asn Thr Thr Lys Arg Arg Val Gln Asn Lys
                320                 325                 330

agt ggt cga act gtc aac cgt gtc ggc aat aac atc ctt gaa aac tac    1059
Ser Gly Arg Thr Val Asn Arg Val Gly Asn Asn Ile Leu Glu Asn Tyr
            335                 340                 345

ata agg agt atc aca atc aac aac gat gat gaa tct gat ggt gaa ccg    1107
Ile Arg Ser Ile Thr Ile Asn Asn Asp Asp Glu Ser Asp Gly Glu Pro
        350                 355                 360

aca aac att gag aat tat cat gat gac tct gaa gat atg tta tat ggg    1155
Thr Asn Ile Glu Asn Tyr His Asp Asp Ser Glu Asp Met Leu Tyr Gly
    365                 370                 375

gag atg aat ttg agt cca gag gct ata acg cag acc acc aaa cca ttg    1203
Glu Met Asn Leu Ser Pro Glu Ala Ile Thr Gln Thr Thr Lys Pro Leu
380                 385                 390                 395

acc gat gct tct aca ata tca cct tat att ccg atg cca aaa gaa aac    1251
Thr Asp Ala Ser Thr Ile Ser Pro Tyr Ile Pro Met Pro Lys Glu Asn
                400                 405                 410

tat act ctg gag gtt tgt gaa tca ctg gag gac tat cta gag ctg ctg    1299
Tyr Thr Leu Glu Val Cys Glu Ser Leu Glu Asp Tyr Leu Glu Leu Leu
            415                 420                 425

cgt tgg tgg gat taa tgc                                            1317
Arg Trp Trp Asp  *
        430
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<210> 192
<211> 431
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (264)...(332)
<223> Conserved domain

<400> 192

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Met Glu Phe Ser Leu Ile Ser Asp Glu Asn Phe Ile Leu Asn Asp Ala
 1               5                  10                  15
His Arg Cys Pro Val Asn Asp Asp Ala Ser His Ile Pro Lys Asn Asn
            20                  25                  30
Leu Asn Phe Phe Asn Asp Asn Leu Gly Gln Ser Ser Arg Thr Gly Trp
```

35 40 45
Ser Phe Ser Pro Asp Leu Thr Asp Ile Ser Asn Gln His His Gln Asn
50 55 60
Leu Ile Pro Leu Ile Pro Asn Tyr Asp Ser Gln Asn Gln Asn Leu Asp
65 70 75 80
Thr Asn Gln Asn His Leu Val Tyr Asn Ser Ser Ser Tyr Glu Ile Pro
85 90 95
Ser Asn Tyr Pro Phe Met Ser Ile Lys Ser Tyr Ser Asn Ile Asp Thr
100 105 110
Leu Glu Gln Ser Met Asn Asn Ile Val Asn Asn Gly Lys Ile His Met
115 120 125
Ile Asp Asn Pro Pro Ile Phe Ala Asn Pro Lys Gly Ile Phe Glu Asn
130 135 140
Phe His Asp Leu Gln Glu Tyr Thr Ile Gly Asn Glu Ile Val His Asn
145 150 155 160
Glu Glu Leu Thr Asn Lys Gly Tyr Glu Pro Thr Leu Asp Lys Val Met
165 170 175
Gly Glu Pro Gln Leu Phe Asp Val Pro Val Leu Glu Gly Ile Lys Asn
180 185 190
Thr Thr Asn Glu Ile Met Asn Gln Leu Glu Asp Asp Lys Met Lys Lys
195 200 205
Thr Tyr Glu Asn Lys Lys Glu Ala Ser Thr Ser Lys Tyr Leu Lys Lys
210 215 220
Ser Asp Ile Thr Lys Lys Arg Trp Thr Glu Ser Glu Asp Ile Lys Leu
225 230 235 240
Lys Glu Met Val Ala Leu Glu Pro Lys Lys Trp Thr Lys Val Ala Lys
245 250 255
His Phe Glu Gly Arg Thr Pro Lys Gln Cys Arg Glu Arg Trp His Asn
260 265 270
His Ala Arg Pro Asn Val Lys Lys Thr Thr Trp Ser Glu Glu Glu Asp
275 280 285
Gln Ile Leu Ile Glu Val His Lys Val Ile Gly Ala Lys Trp Ile Gln
290 295 300
Ile Ser Glu Gln Leu Pro Gly Arg Ser Tyr Asn Asn Val Lys Asn His
305 310 315 320
Trp Asn Thr Thr Lys Arg Arg Val Gln Asn Lys Ser Gly Arg Thr Val
325 330 335
Asn Arg Val Gly Asn Asn Ile Leu Glu Asn Tyr Ile Arg Ser Ile Thr
340 345 350
Ile Asn Asn Asp Asp Glu Ser Asp Gly Glu Pro Thr Asn Ile Glu Asn
355 360 365
Tyr His Asp Asp Ser Glu Asp Met Leu Tyr Gly Glu Met Asn Leu Ser
370 375 380
Pro Glu Ala Ile Thr Gln Thr Thr Lys Pro Leu Thr Asp Ala Ser Thr
385 390 395 400
Ile Ser Pro Tyr Ile Pro Met Pro Lys Glu Asn Tyr Thr Leu Glu Val
405 410 415
Cys Glu Ser Leu Glu Asp Tyr Leu Glu Leu Leu Arg Trp Trp Asp
420 425 430

<210> 193
<211> 1167
<212> DNA
<213> Arabidopsis thaliana

<220>

<221> CDS
<222> (177)...(956)

<400> 193
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ctgtttttgt atccgtgtaa attaatcaca cggtagtttt tgatgaaaag acaacaatcg 60
gagaacaatc tggtctgctg ctaaaattta ataaattgtt ttgtctaatt gtctccaccc 120
ataaaaaagc gcgaattcaa ttcaccgact aaagacattc tccggtggag accccg atg 179
                                                              Met
                                                               1

caa tcc act cat ata agc ggc gga agt agc ggt ggt ggt ggt gga gga    227
Gln Ser Thr His Ile Ser Gly Gly Ser Ser Gly Gly Gly Gly Gly Gly
            5                  10                  15

gga gga gag gtg agt cga agt gga tta tct cgg atc cgt tca gct cca    275
Gly Gly Glu Val Ser Arg Ser Gly Leu Ser Arg Ile Arg Ser Ala Pro
         20                  25                  30

gct act tgg att gaa acc cta ctc gaa gaa gat gaa gaa gaa ggt tta    323
Ala Thr Trp Ile Glu Thr Leu Leu Glu Glu Asp Glu Glu Glu Gly Leu
     35                  40                  45

aaa cct aac ctt tgt tta aca gag ctg ctt act ggt aat aat aac tct    371
Lys Pro Asn Leu Cys Leu Thr Glu Leu Leu Thr Gly Asn Asn Asn Ser
 50                  55                  60                  65

gga gga gtg ata acg agt cgt gac gac tcg ttc gag ttc ctg agt tct    419
Gly Gly Val Ile Thr Ser Arg Asp Asp Ser Phe Glu Phe Leu Ser Ser
                 70                  75                  80

gtt gag caa gga ttg tat aat cat cat caa ggt ggt ggc ttt cac cgt    467
Val Glu Gln Gly Leu Tyr Asn His His Gln Gly Gly Gly Phe His Arg
             85                  90                  95

cag aat agt tct ccg gct gat ttt ctt agt ggg tct ggt tct ggg act    515
Gln Asn Ser Ser Pro Ala Asp Phe Leu Ser Gly Ser Gly Ser Gly Thr
        100                 105                 110

gat ggg tat ttc tct aat ttt ggt att ccg gcg aat tat gac tat ttg    563
Asp Gly Tyr Phe Ser Asn Phe Gly Ile Pro Ala Asn Tyr Asp Tyr Leu
    115                 120                 125

tcg acc aac gtt gat att tct ccg act aaa cgg tct aga gat atg gaa    611
Ser Thr Asn Val Asp Ile Ser Pro Thr Lys Arg Ser Arg Asp Met Glu
130                 135                 140                 145

aca cag ttt tct tct cag ctg aaa gaa gag caa atg agt ggt ggg ata    659
Thr Gln Phe Ser Ser Gln Leu Lys Glu Glu Gln Met Ser Gly Gly Ile
                150                 155                 160

tca gga atg atg gat atg aac atg gac aag att ttt gag gat tca gtt    707
Ser Gly Met Met Asp Met Asn Met Asp Lys Ile Phe Glu Asp Ser Val
            165                 170                 175

cct tgt agg gtt cgt gct aaa cgt ggt tgt gct act cat cct cgt agc    755
Pro Cys Arg Val Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser
        180                 185                 190
```

```
att gct gaa cgg gtg aga aga acg cga ata agt gat cgg att agg agg    803
Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp Arg Ile Arg Arg
    195                 200                 205

ctg caa gag ctt gtt cct aac atg gat aag caa acc aac act gca gac    851
Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Asn Thr Ala Asp
210                 215                 220                 225

atg ttg gaa gaa gct gtg gag tat gtg aag gct ctt caa agc cag atc    899
Met Leu Glu Glu Ala Val Glu Tyr Val Lys Ala Leu Gln Ser Gln Ile
                230                 235                 240

cag gaa ttg aca gag cag cag aag aga tgc aaa tgc aaa cct aaa gaa    947
Gln Glu Leu Thr Glu Gln Gln Lys Arg Cys Lys Cys Lys Pro Lys Glu
            245                 250                 255

gaa caa taa tgtatccttt aggatttgat atatctgtat tttattttg             996
Glu Gln  *

tactatctaa aaatggtgat gatctgttcg aaaattcgaa acatgatctt atatattgaa 1056
ctagaaaaaa tagatatata tgaattttag ctgtaaaatt tttgtacaat aaggagaaaa 1116
agatttagaa gagtcaataa aaagatgatg tttacaagtc aaaaaaaaaa a          1167

&lt;210&gt; 194
&lt;211&gt; 259
&lt;212&gt; PRT
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; DOMAIN
&lt;222&gt; (175)...(245)
&lt;223&gt; Conserved domain

&lt;400&gt; 194
Met Gln Ser Thr His Ile Ser Gly Gly Ser Ser Gly Gly Gly Gly Gly
 1               5                  10                  15
Gly Gly Gly Glu Val Ser Arg Ser Gly Leu Ser Arg Ile Arg Ser Ala
            20                  25                  30
Pro Ala Thr Trp Ile Glu Thr Leu Leu Glu Glu Asp Glu Glu Glu Gly
        35                  40                  45
Leu Lys Pro Asn Leu Cys Leu Thr Glu Leu Leu Thr Gly Asn Asn Asn
    50                  55                  60
Ser Gly Gly Val Ile Thr Ser Arg Asp Asp Ser Phe Glu Phe Leu Ser
65                  70                  75                  80
Ser Val Glu Gln Gly Leu Tyr Asn His His Gln Gly Gly Gly Phe His
                85                  90                  95
Arg Gln Asn Ser Ser Pro Ala Asp Phe Leu Ser Gly Ser Gly Ser Gly
            100                 105                 110
Thr Asp Gly Tyr Phe Ser Asn Phe Gly Ile Pro Ala Asn Tyr Asp Tyr
        115                 120                 125
Leu Ser Thr Asn Val Asp Ile Ser Pro Thr Lys Arg Ser Arg Asp Met
    130                 135                 140
Glu Thr Gln Phe Ser Ser Gln Leu Lys Glu Glu Gln Met Ser Gly Gly
145                 150                 155                 160
Ile Ser Gly Met Met Asp Met Asn Met Asp Lys Ile Phe Glu Asp Ser
```

```
                165                 170                 175
Val Pro Cys Arg Val Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg
            180                 185                 190
Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp Arg Ile Arg
        195                 200                 205
Arg Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Asn Thr Ala
    210                 215                 220
Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Ala Leu Gln Ser Gln
225                 230                 235                 240
Ile Gln Glu Leu Thr Glu Gln Gln Lys Arg Cys Lys Cys Lys Pro Lys
                245                 250                 255
Glu Glu Gln


<210> 195
<211> 964
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (63)...(869)

<400> 195
gaaatctcaa caagaaccaa accaaacaac aaaaaaacat tcttaataat tatctttctg 60
tt atg tcg atg acg gcg gat tct caa tct gat tat gct ttt ctt gag    107
   Met Ser Met Thr Ala Asp Ser Gln Ser Asp Tyr Ala Phe Leu Glu
    1               5                  10                  15

tcc ata cga cga cac tta cta gga gaa tcg gag ccg ata ctc agt gag   155
Ser Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu
                20                  25                  30

tcg aca gcg agt tcg gtt act caa tct tgt gta acc ggt cag agc att   203
Ser Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile
            35                  40                  45

aaa ccg gtg tac gga cga aac cct agc ttt agc aaa ctg tat cct tgc   251
Lys Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys
        50                  55                  60

ttc acc gag agc tgg gga gat ttg ccg ttg aaa gaa aac gat tct gag   299
Phe Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu
    65                  70                  75

gat atg tta gtt tac ggt atc ctc aac gac gcc ttt cac ggc ggt tgg   347
Asp Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp
80                  85                  90                  95

gag ccg tct tct tcg tct tcc gac gaa gat cgt agc tct ttc ccg agt   395
Glu Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser
                100                 105                 110

gtt aag atc gag act ccg gag agt ttc gcg gcg gtg gat tct gtt ccg   443
Val Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro
            115                 120                 125
```

```
gtc aag aag gag aag acg agt cct gtt tcg gcg gcg gtg acg gcg gcg    491
Val Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala
        130                 135                 140

aag gga aag cat tat aga gga gtg aga caa agg ccg tgg ggg aaa ttt    539
Lys Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe
    145                 150                 155

gcg gcg gag att aga gat ccg gcg aag aac gga gct agg gtt tgg tta    587
Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu
160                 165                 170                 175

gga acg ttt gag acg gcg gag gac gcg gcg ttg gct tac gac aga gct    635
Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala
                180                 185                 190

gct ttc agg atg cgt ggt tcc cgc gct ttg ttg aat ttt ccg ttg aga    683
Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg
            195                 200                 205

gtt aat tca gga gaa ccc gac ccg gtt cga atc aag tcc aag aga tct    731
Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser
        210                 215                 220

tct ttt tct tct tct aac gag aac gga gct ccg aag aag agg aga acg    779
Ser Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr
    225                 230                 235

gtg gcc gcc ggt ggt gga atg gat aag gga ttg acg gtg aag tgc gag    827
Val Ala Ala Gly Gly Gly Met Asp Lys Gly Leu Thr Val Lys Cys Glu
240                 245                 250                 255

gtt gtt gaa gtg gca cgt ggc gat cgt tta ttg gtt tta taa            869
Val Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu  *
                260                 265

ttttgatttt tctttgttgg atgattatat gattcttcaa aaaagaagaa cgttaataaa 929
aaaattcgtt tattattaaa aaaaaaaaaa aaaaa                            964

<210> 196
<211> 268
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (145)...(213)
<223> Conserved domain

<400> 196
Met Ser Met Thr Ala Asp Ser Gln Ser Asp Tyr Ala Phe Leu Glu Ser
 1               5                  10                  15
Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu Ser
            20                  25                  30
Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile Lys
        35                  40                  45
```

```
Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys Phe
    50                  55                  60
Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu Asp
65                  70                  75                  80
Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp Glu
                85                  90                  95
Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser Val
            100                 105                 110
Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro Val
        115                 120                 125
Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala Lys
    130                 135                 140
Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
145                 150                 155                 160
Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
                165                 170                 175
Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala Ala
            180                 185                 190
Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val
        195                 200                 205
Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser Ser
    210                 215                 220
Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr Val
225                 230                 235                 240
Ala Ala Gly Gly Gly Met Asp Lys Gly Leu Thr Val Lys Cys Glu Val
                245                 250                 255
Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu
            260                 265


<210> 197
<211> 582
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(582)

<400> 197
atg gag att gag aag gat gag gac gac aca aca ttg gtt gat tct gga     48
Met Glu Ile Glu Lys Asp Glu Asp Asp Thr Thr Leu Val Asp Ser Gly
 1               5                  10                  15

gga gac ttc gac tgc aac ata tgt ttg gat cag gtt cga gac ccg gtc     96
Gly Asp Phe Asp Cys Asn Ile Cys Leu Asp Gln Val Arg Asp Pro Val
            20                  25                  30

gtg act tta tgt ggc cac ctg ttt tgt tgg ccc tgc att cac aag tgg    144
Val Thr Leu Cys Gly His Leu Phe Cys Trp Pro Cys Ile His Lys Trp
        35                  40                  45

act tat gcg tcc aac aat tca aga caa cga gtc gat caa tac gat cat    192
Thr Tyr Ala Ser Asn Asn Ser Arg Gln Arg Val Asp Gln Tyr Asp His
    50                  55                  60

aag agg gaa cca cca aaa tgt ccg gta tgc aaa tct gat gtc tcc gag    240
```

```
Lys Arg Glu Pro Pro Lys Cys Pro Val Cys Lys Ser Asp Val Ser Glu
 65                 70                  75                  80

gct acg ctt gtc ccg atc tac gga cga gga cag aaa gct ccc cag tcc      288
Ala Thr Leu Val Pro Ile Tyr Gly Arg Gly Gln Lys Ala Pro Gln Ser
                 85                  90                  95

ggt tca aat gta ccg agc aga cca act ggt ccg gtt tat gac tta aga      336
Gly Ser Asn Val Pro Ser Arg Pro Thr Gly Pro Val Tyr Asp Leu Arg
            100                 105                 110

gga gtt ggt caa cgt tta gga gaa ggg gag agt caa cgt tac atg tat      384
Gly Val Gly Gln Arg Leu Gly Glu Gly Glu Ser Gln Arg Tyr Met Tyr
        115                 120                 125

aga atg cct gat ccg gtg atg ggt gtg gta tgc gaa atg gta tac cgg      432
Arg Met Pro Asp Pro Val Met Gly Val Val Cys Glu Met Val Tyr Arg
    130                 135                 140

aga cta ttt gga gag tct tcg agc aac atg gca cct tac cgc gat atg      480
Arg Leu Phe Gly Glu Ser Ser Ser Asn Met Ala Pro Tyr Arg Asp Met
145                 150                 155                 160

aat gtc cgg tct agg cga cgg gca atg cag gct gag gag tca tta agc      528
Asn Val Arg Ser Arg Arg Arg Ala Met Gln Ala Glu Glu Ser Leu Ser
                165                 170                 175

aga gtc tac ttg ttt cta ctt tgc ttc atg ttt atg tgt cta ttt ctc      576
Arg Val Tyr Leu Phe Leu Leu Cys Phe Met Phe Met Cys Leu Phe Leu
            180                 185                 190

ttc taa                                                              582
Phe  *
```

```
<210> 198
<211> 193
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (21)...(74)
<223> Conserved domain

<400> 198
Met Glu Ile Glu Lys Asp Glu Asp Asp Thr Thr Leu Val Asp Ser Gly
 1               5                  10                  15
Gly Asp Phe Asp Cys Asn Ile Cys Leu Asp Gln Val Arg Asp Pro Val
            20                  25                  30
Val Thr Leu Cys Gly His Leu Phe Cys Trp Pro Cys Ile His Lys Trp
        35                  40                  45
Thr Tyr Ala Ser Asn Asn Ser Arg Gln Arg Val Asp Gln Tyr Asp His
    50                  55                  60
Lys Arg Glu Pro Pro Lys Cys Pro Val Cys Lys Ser Asp Val Ser Glu
65                  70                  75                  80
```

```
Ala Thr Leu Val Pro Ile Tyr Gly Arg Gly Gln Lys Ala Pro Gln Ser
                85                  90                  95
Gly Ser Asn Val Pro Ser Arg Pro Thr Gly Pro Val Tyr Asp Leu Arg
            100                 105                 110
Gly Val Gly Gln Arg Leu Gly Glu Gly Glu Ser Gln Arg Tyr Met Tyr
        115                 120                 125
Arg Met Pro Asp Pro Val Met Gly Val Val Cys Glu Met Val Tyr Arg
    130                 135                 140
Arg Leu Phe Gly Glu Ser Ser Ser Asn Met Ala Pro Tyr Arg Asp Met
145                 150                 155                 160
Asn Val Arg Ser Arg Arg Arg Ala Met Gln Ala Glu Glu Ser Leu Ser
                165                 170                 175
Arg Val Tyr Leu Phe Leu Leu Cys Phe Met Phe Met Cys Leu Phe Leu
            180                 185                 190
Phe
```

```
<210> 199
<211> 952
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (65)...(883)

<400> 199
tcgaaatcat caagaatctt gtctttaatt tccaattggg tttttcaaaa cccgttacct 60
cagg atg atg aac ccg ttt ctc ccg gaa ggc tgc gat cca cca cca cca   109
     Met Met Asn Pro Phe Leu Pro Glu Gly Cys Asp Pro Pro Pro Pro
      1               5                  10                  15

cca caa cca atg gag ggt tta cac gaa aat gct cca cct cca ttt ctg   157
Pro Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu
                20                  25                  30

acc aag aca ttt gag atg gtg gat gat cca aac act gac cac atc gta   205
Thr Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val
            35                  40                  45

tct tgg aac aga gga gga aca agt ttt gtc gtc tgg gat ttg cat tct   253
Ser Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser
        50                  55                  60

ttc tcc acg att ctc ctt cct cgt cat ttc aaa cac agc aat ttc tca   301
Phe Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser
    65                  70                  75

agt ttc atc aga caa ctc aat act tat ggt ttc aga aag ata gaa gca   349
Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala
80                  85                  90                  95

gag aga tgg gaa ttt gca aac gaa gag ttt ttg tta gga caa aga cag   397
Glu Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln
                100                 105                 110
```

```
ttg ttg aag aac atc aag agg aga aac cct ttt act cca tca tct tca    445
Leu Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser
            115                 120                 125

cca agc cat gac gct tgc aac gag ctt cgc aga gag aag caa gtg cta    493
Pro Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu
        130                 135                 140

atg atg gag ata gtg agt cta aga cag cag caa caa aca acg aaa agc    541
Met Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser
    145                 150                 155

tac atc aaa gct atg gaa cag agg ata gaa gga aca gag agg aaa cag    589
Tyr Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln
160                 165                 170                 175

aga caa atg atg tcg ttt ctg gct aga gca atg cag agt cct tcg ttt    637
Arg Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe
                180                 185                 190

ttg cat cag ttg ttg aaa caa aga gat aaa aaa att aag gag ctt gag    685
Leu His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu
            195                 200                 205

gat aat gag tca gca aag agg aaa aga ggt tct tct tcg atg tcg gaa    733
Asp Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu
        210                 215                 220

ttg gaa gtt ttg gct ttg gag atg caa ggg cat gga aaa cag agg aat    781
Leu Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn
    225                 230                 235

atg ttg gaa gaa gag gat cat caa ctg gtg gta gag aga gag ttg gat    829
Met Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp
240                 245                 250                 255

gat ggt ttc tgg gaa gag ttg ctt agt gat gag agt ttg gct tcc acc    877
Asp Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr
                260                 265                 270

tcc taa ctagatggat ttctttttgg ttttgttttt agtttcttct actttcaagc    933
Ser  *

tcattttctt ctgtcacaa                                                 952
```

<210> 200
<211> 272
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (31)...(120)
<223> Conserved domain

<400> 200

```
Met Met Asn Pro Phe Leu Pro Glu Gly Cys Asp Pro Pro Pro Pro Pro
 1               5                  10                  15
Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu Thr
            20                  25                  30
Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val Ser
        35                  40                  45
Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser Phe
    50                  55                  60
Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser Ser
65                  70                  75                  80
Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu
                85                  90                  95
Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln Leu
            100                 105                 110
Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser Pro
        115                 120                 125
Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu Met
    130                 135                 140
Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser Tyr
145                 150                 155                 160
Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln Arg
                165                 170                 175
Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe Leu
            180                 185                 190
His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu Asp
        195                 200                 205
Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu Leu
    210                 215                 220
Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn Met
225                 230                 235                 240
Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp Asp
                245                 250                 255
Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr Ser
            260                 265                 270


<210> 201
<211> 1126
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (282)...(920)

<400> 201
atccccactt gttgttcatc accaagccaa gctccatgtc ctagtcactc cacagattcc 60
ctatcatcat caattcgttt caaacttagt tcctttcaaa gtcttgtaca tatatacaca 120
cacacctatt attctcttgg tgtgtttgtg tgttacatat acgtgtgagt acatactttg 180
ttgtaaaagt ggatcggagg tatggaaagg gaccggttcc accggaaaca tcggcggcgg 240
cggatgataa ttcgtcttgg aacgagactg atgtcaccgc c atg gtc tcc gct ctc 296
                                              Met Val Ser Ala Leu
                                               1               5

agc cgt gtc ata gag aat ccg aca gac ccg ccg gtc aaa caa gag ctt   344
Ser Arg Val Ile Glu Asn Pro Thr Asp Pro Pro Val Lys Gln Glu Leu
                10                  15                  20
```

```
gat aaa tcg gat caa cat caa cca gac caa gat caa cca aga aga aga     392
Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp Gln Pro Arg Arg Arg
            25                  30                  35

cac tat aga ggc gta agg cag aga cca tgg ggt aaa tgg gcg gca gaa     440
His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
        40                  45                  50

atc cgc gat cca aag aaa gca gcc cgt gtc tgg ctc ggg act ttc gag     488
Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu
    55                  60                  65

acg gca gag gaa gct gct tta gcc tat gac cga gct gcc ctc aaa ttc     536
Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg Ala Ala Leu Lys Phe
70                  75                  80                  85

aaa ggc acc aag gct aaa ctg aac ttc cct gaa cgg gtc caa ggc cct     584
Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu Arg Val Gln Gly Pro
                90                  95                  100

act acc acc aca acc att tct cat gca cca aga gga gtt agt gaa tcc     632
Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg Gly Val Ser Glu Ser
            105                 110                 115

atg aac tca cct cct cct cga cct ggt cca cct tca act act act act     680
Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro Ser Thr Thr Thr Thr
        120                 125                 130

tcg tgg cca atg act tat aac cag gac ata ctt caa tac gct cag ttg     728
Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu Gln Tyr Ala Gln Leu
    135                 140                 145

ctt acg agt aac aat gag gtt gat tta tca tac tac acg tcg act ctc     776
Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr Tyr Thr Ser Thr Leu
150                 155                 160                 165

ttc agt caa cct ttt tca acg cct tct tca tct tct tct tcc tcc caa     824
Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser Ser Ser Ser Ser Gln
                170                 175                 180

cag acg cag caa cag cag cta caa caa caa caa cag cag cgt gaa gaa     872
Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln Gln Arg Glu Glu
            185                 190                 195

gaa gag aag aat tat ggt tac aat tat tat aac tac cca aga gaa taa     920
Glu Glu Lys Asn Tyr Gly Tyr Asn Tyr Tyr Asn Tyr Pro Arg Glu  *
        200                 205                 210

tctaattatt attgttggtc gaatcagttt tataaatagc tatcatagtt tcatttttgg 980
tttccgtaac ctttgttgca tggaaaatat gaatgaacga gggacatgtg taacaatttg 1040
tttgtgtttc gtaaatgtta gttgtatttg gatttgctga agtttgattt tctgagcata 1100
aatcatttga cggtcaaaaa aaaaaa                                      1126
```

<210> 202
<211> 212
<212> PRT

<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (36)...(103)
<223> Conserved domain

<400> 202
Met Val Ser Ala Leu Ser Arg Val Ile Glu Asn Pro Thr Asp Pro Pro
1   5   10   15
Val Lys Gln Glu Leu Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp
            20   25   30
Gln Pro Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly
        35   40   45
Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp
    50   55   60
Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg
65   70   75   80
Ala Ala Leu Lys Phe Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu
                85   90   95
Arg Val Gln Gly Pro Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg
            100   105   110
Gly Val Ser Glu Ser Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro
        115   120   125
Ser Thr Thr Thr Thr Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu
    130   135   140
Gln Tyr Ala Gln Leu Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr
145   150   155   160
Tyr Thr Ser Thr Leu Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser
                165   170   175
Ser Ser Ser Ser Gln Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln
            180   185   190
Gln Gln Arg Glu Glu Glu Glu Lys Asn Tyr Gly Tyr Asn Tyr Tyr Asn
        195   200   205
Tyr Pro Arg Glu
    210

<210> 203
<211> 2057
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (102)...(1805)

<400> 203
ttcccctgag aacgacagga gaaagaataa aaaccctaaa tttctttaat ttcggcgctt 60
cagattatcg ttgttaaagg tttttgattg attttgttta a atg ggc gat ctt gct 116
                                              Met Gly Asp Leu Ala
                                              1   5

atg tcc gta gca gac atc agg atg gag aat gag cct gat gat tta gct 164
Met Ser Val Ala Asp Ile Arg Met Glu Asn Glu Pro Asp Asp Leu Ala
                10   15   20

```
agt gat aat gtt gct gag att gat gtg agt gat gaa gag att gat gct    212
Ser Asp Asn Val Ala Glu Ile Asp Val Ser Asp Glu Glu Ile Asp Ala
            25                  30                  35

gac gac ctt gag aga cgg atg tgg aaa gat cgt gtc agg ctt aaa aga    260
Asp Asp Leu Glu Arg Arg Met Trp Lys Asp Arg Val Arg Leu Lys Arg
        40                  45                  50

atc aaa gag cga caa aaa gct ggc tct caa gga gct caa acg aag gag    308
Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly Ala Gln Thr Lys Glu
    55                  60                  65

aca cct aag aaa atc tct gat caa gct cag agg aag aaa atg tct aga    356
Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg Lys Lys Met Ser Arg
70                  75                  80                  85

gct caa gat ggt atc ctt aag tac atg ttg aag ctt atg gaa gtc tgc    404
Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Leu Met Glu Val Cys
                90                  95                  100

aaa gtt cgc ggg ttt gtc tat ggt ata ata ccg gaa aag ggc aag cct    452
Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro
            105                 110                 115

gtg agt ggt tcc tct gac aat ata aga gct tgg tgg aaa gag aaa gtg    500
Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp Trp Lys Glu Lys Val
        120                 125                 130

aag ttt gat aag aac ggt cct gct gct att gct aaa tac gaa gag gag    548
Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala Lys Tyr Glu Glu Glu
    135                 140                 145

tgt tta gcg ttt ggg aaa tct gat ggg aat agg aat tca cag ttt gtt    596
Cys Leu Ala Phe Gly Lys Ser Asp Gly Asn Arg Asn Ser Gln Phe Val
150                 155                 160                 165

ctc cag gat ttg caa gat gct act tta ggg tct ttg tta tct tct ttg    644
Leu Gln Asp Leu Gln Asp Ala Thr Leu Gly Ser Leu Leu Ser Ser Leu
                170                 175                 180

atg caa cat tgt gat cct cct caa agg aag tat ccg ttg gag aaa ggg    692
Met Gln His Cys Asp Pro Pro Gln Arg Lys Tyr Pro Leu Glu Lys Gly
            185                 190                 195

acg cct ccg cct tgg tgg cca acg ggg aat gaa gaa tgg tgg gtg aaa    740
Thr Pro Pro Pro Trp Trp Pro Thr Gly Asn Glu Glu Trp Trp Val Lys
        200                 205                 210

ctc ggt ctg cct aaa agc cag agt cct cct tac cga aaa cct cat gat    788
Leu Gly Leu Pro Lys Ser Gln Ser Pro Pro Tyr Arg Lys Pro His Asp
    215                 220                 225

ctc aag aag atg tgg aag gtt gga gtt tta acg gca gtg atc aat cat    836
Leu Lys Lys Met Trp Lys Val Gly Val Leu Thr Ala Val Ile Asn His
230                 235                 240                 245

atg tta cct gat att gca aag att aag agg cat gtt cgt cag tcg aaa    884
```

```
Met Leu Pro Asp Ile Ala Lys Ile Lys Arg His Val Arg Gln Ser Lys
                250                 255                 260

tgt tta cag gac aag atg aca gct aaa gag agt gcg att tgg ttg gcg      932
Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Ile Trp Leu Ala
            265                 270                 275

gtt ttg aac caa gag gaa tct ttg att cag cag cct agc agt gac aat      980
Val Leu Asn Gln Glu Glu Ser Leu Ile Gln Gln Pro Ser Ser Asp Asn
        280                 285                 290

gga aac tcc aat gtg act gag aca cat cgt agg ggt aat aac gct gac     1028
Gly Asn Ser Asn Val Thr Glu Thr His Arg Arg Gly Asn Asn Ala Asp
    295                 300                 305

agg agg aaa cct gtg gtc aac agt gac agt gac tat gat gtt gat ggg     1076
Arg Arg Lys Pro Val Val Asn Ser Asp Ser Asp Tyr Asp Val Asp Gly
310                 315                 320                 325

aca gag gaa gct tca ggt tca gtt tca tct aaa gac agt aga aga aat     1124
Thr Glu Glu Ala Ser Gly Ser Val Ser Ser Lys Asp Ser Arg Arg Asn
                330                 335                 340

cag att caa aaa gaa caa cca aca gcc atc tca cat tca gta aga gat     1172
Gln Ile Gln Lys Glu Gln Pro Thr Ala Ile Ser His Ser Val Arg Asp
            345                 350                 355

caa gat aaa gca gag aaa cat cgc aga agg aaa aga cct cga att aga     1220
Gln Asp Lys Ala Glu Lys His Arg Arg Arg Lys Arg Pro Arg Ile Arg
        360                 365                 370

tcc gga act gtc aat cga caa gag gaa gaa caa cct gaa gct caa caa     1268
Ser Gly Thr Val Asn Arg Gln Glu Glu Glu Gln Pro Glu Ala Gln Gln
    375                 380                 385

aga aac atc tta cct gat atg aat cat gtt gat gcc cct ctg cta gaa     1316
Arg Asn Ile Leu Pro Asp Met Asn His Val Asp Ala Pro Leu Leu Glu
390                 395                 400                 405

tat aac atc aac ggt act cat caa gag gac gat gtt gtc gac cca aat     1364
Tyr Asn Ile Asn Gly Thr His Gln Glu Asp Asp Val Val Asp Pro Asn
                410                 415                 420

att gcc tta gga cca gag gat aat ggt ctg gaa cta gtg gtt cct gag     1412
Ile Ala Leu Gly Pro Glu Asp Asn Gly Leu Glu Leu Val Val Pro Glu
            425                 430                 435

ttc aat aac aac tat act tat ctt cca ctt gtt aat gaa caa act atg     1460
Phe Asn Asn Asn Tyr Thr Tyr Leu Pro Leu Val Asn Glu Gln Thr Met
        440                 445                 450

atg cct gta gac gaa agg cca atg ctt tat gga cca aac cct aac caa     1508
Met Pro Val Asp Glu Arg Pro Met Leu Tyr Gly Pro Asn Pro Asn Gln
    455                 460                 465

gag ctt caa ttt ggg tca ggg tac aac ttc tac aat ccc tct gca gtg     1556
Glu Leu Gln Phe Gly Ser Gly Tyr Asn Phe Tyr Asn Pro Ser Ala Val
```

```
470               475               480               485

ttt gta cat aac cag gaa gac gac att ctc cat aca cag ata gaa atg    1604
Phe Val His Asn Gln Glu Asp Asp Ile Leu His Thr Gln Ile Glu Met
                490                 495                 500

aat aca caa gca cca cct cac aac agt ggg ttc gag gag gcc cca gga    1652
Asn Thr Gln Ala Pro Pro His Asn Ser Gly Phe Glu Glu Ala Pro Gly
            505                 510                 515

gga gta ctt caa ccc ctt ggt tta ctc gga aat gaa gac ggt gta aca    1700
Gly Val Leu Gln Pro Leu Gly Leu Leu Gly Asn Glu Asp Gly Val Thr
        520                 525                 530

ggg agt gag ttg cct cag tat cag agt ggc att ctg tct cca ttg act    1748
Gly Ser Glu Leu Pro Gln Tyr Gln Ser Gly Ile Leu Ser Pro Leu Thr
    535                 540                 545

gac ttg gac ttt gac tat ggt ggt ttt ggt gat gat ttc tca tgg ttt    1796
Asp Leu Asp Phe Asp Tyr Gly Gly Phe Gly Asp Asp Phe Ser Trp Phe
550                 555                 560                 565

gga gct tag tgtcttgcca tttttttgg gagattacat agttcaaaag             1845
Gly Ala  *


gacatggcaa tagtctggct agtacagtta ctttctcttc ttcatttctt ctgatcttat 1905
attcttcctc ttttttctt ataatatttt cttagatttg ttaagagaaa caattttcct 1965
tttgaataag ttgccagaag aactgctttg cccgttgtaa tggtctctag ggaaagcagt 2025
tagcgtatca tcatttgtaa atttactgtg ag                                2057
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<210> 204
<211> 567
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (86)...(96)
<223> Conserved domain

<400> 204

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Met Gly Asp Leu Ala Met Ser Val Ala Asp Ile Arg Met Glu Asn Glu
 1               5                  10                  15
Pro Asp Asp Leu Ala Ser Asp Asn Val Ala Glu Ile Asp Val Ser Asp
            20                  25                  30
Glu Glu Ile Asp Ala Asp Asp Leu Glu Arg Arg Met Trp Lys Asp Arg
        35                  40                  45
Val Arg Leu Lys Arg Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly
    50                  55                  60
Ala Gln Thr Lys Glu Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg
65                  70                  75                  80
Lys Lys Met Ser Arg Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys
                85                  90                  95
Leu Met Glu Val Cys Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro
            100                 105                 110
Glu Lys Gly Lys Pro Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp
```

```
        115                     120                     125
Trp Lys Glu Lys Val Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala
    130                     135                     140
Lys Tyr Glu Glu Glu Cys Leu Ala Phe Gly Lys Ser Asp Gly Asn Arg
145                     150                     155                     160
Asn Ser Gln Phe Val Leu Gln Asp Leu Gln Asp Ala Thr Leu Gly Ser
                165                     170                     175
Leu Leu Ser Ser Leu Met Gln His Cys Asp Pro Pro Gln Arg Lys Tyr
            180                     185                     190
Pro Leu Glu Lys Gly Thr Pro Pro Pro Trp Trp Pro Thr Gly Asn Glu
        195                     200                     205
Glu Trp Trp Val Lys Leu Gly Leu Pro Lys Ser Gln Ser Pro Pro Tyr
    210                     215                     220
Arg Lys Pro His Asp Leu Lys Lys Met Trp Lys Val Gly Val Leu Thr
225                     230                     235                     240
Ala Val Ile Asn His Met Leu Pro Asp Ile Ala Lys Ile Lys Arg His
                245                     250                     255
Val Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser
            260                     265                     270
Ala Ile Trp Leu Ala Val Leu Asn Gln Glu Glu Ser Leu Ile Gln Gln
        275                     280                     285
Pro Ser Ser Asp Asn Gly Asn Ser Asn Val Thr Glu Thr His Arg Arg
    290                     295                     300
Gly Asn Asn Ala Asp Arg Arg Lys Pro Val Val Asn Ser Asp Ser Asp
305                     310                     315                     320
Tyr Asp Val Asp Gly Thr Glu Glu Ala Ser Gly Ser Val Ser Ser Lys
                325                     330                     335
Asp Ser Arg Arg Asn Gln Ile Gln Lys Glu Gln Pro Thr Ala Ile Ser
            340                     345                     350
His Ser Val Arg Asp Gln Asp Lys Ala Glu Lys His Arg Arg Arg Lys
        355                     360                     365
Arg Pro Arg Ile Arg Ser Gly Thr Val Asn Arg Gln Glu Glu Glu Gln
    370                     375                     380
Pro Glu Ala Gln Gln Arg Asn Ile Leu Pro Asp Met Asn His Val Asp
385                     390                     395                     400
Ala Pro Leu Leu Glu Tyr Asn Ile Asn Gly Thr His Gln Glu Asp Asp
                405                     410                     415
Val Val Asp Pro Asn Ile Ala Leu Gly Pro Glu Asp Asn Gly Leu Glu
            420                     425                     430
Leu Val Val Pro Glu Phe Asn Asn Asn Tyr Thr Tyr Leu Pro Leu Val
        435                     440                     445
Asn Glu Gln Thr Met Met Pro Val Asp Glu Arg Pro Met Leu Tyr Gly
    450                     455                     460
Pro Asn Pro Asn Gln Glu Leu Gln Phe Gly Ser Gly Tyr Asn Phe Tyr
465                     470                     475                     480
Asn Pro Ser Ala Val Phe Val His Asn Gln Glu Asp Asp Ile Leu His
                485                     490                     495
Thr Gln Ile Glu Met Asn Thr Gln Ala Pro Pro His Asn Ser Gly Phe
            500                     505                     510
Glu Glu Ala Pro Gly Gly Val Leu Gln Pro Leu Gly Leu Leu Gly Asn
        515                     520                     525
Glu Asp Gly Val Thr Gly Ser Glu Leu Pro Gln Tyr Gln Ser Gly Ile
    530                     535                     540
Leu Ser Pro Leu Thr Asp Leu Asp Phe Asp Tyr Gly Gly Phe Gly Asp
545                     550                     555                     560
Asp Phe Ser Trp Phe Gly Ala
                565
```

<210> 205
<211> 1638
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (267)...(1259)

<400> 205
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ggaatttcgg atcgtgtctc tctctgtttc tttgtttcaa tccgatttcg aatcaagccc 60
tttacttgtg caccttcaag atttcgtttt ttccagcgcc cagaatgctc cgggtgacca 120
acatttgttc ctgattcatt tcctattggt tcgtattgtc tgtgcacaca agagaaattt 180
caagaagttg ttactaaaag agaggccaca agtggatatt gtctttgtta tcaagtgtta 240
gtacagaaaa gtggtgagaa agtaat atg gct gat acc agt ccg aga act gat  293
                             Met Ala Asp Thr Ser Pro Arg Thr Asp
                              1               5

gtc tca aca gat gac gac aca gat cat cct gat ctt ggg tcg gag gga   341
Val Ser Thr Asp Asp Asp Thr Asp His Pro Asp Leu Gly Ser Glu Gly
 10                  15                  20                  25

gca cta gtg aat act gct gct tct gat tcg agt gac cga tcg aag gga   389
Ala Leu Val Asn Thr Ala Ala Ser Asp Ser Ser Asp Arg Ser Lys Gly
                 30                  35                  40

aag atg gat caa aag act ctt cgt agg ctt gct caa aac cgt gag gca   437
Lys Met Asp Gln Lys Thr Leu Arg Arg Leu Ala Gln Asn Arg Glu Ala
             45                  50                  55

gca agg aaa agc aga ttg agg aag aag gct tat gtt cag cag cta gag   485
Ala Arg Lys Ser Arg Leu Arg Lys Lys Ala Tyr Val Gln Gln Leu Glu
         60                  65                  70

aac agc cgc ttg aaa cta acc cag ctt gag cag gag ctg caa aga gca   533
Asn Ser Arg Leu Lys Leu Thr Gln Leu Glu Gln Glu Leu Gln Arg Ala
     75                  80                  85

aga cag cag ggc gtc ttc att tca ggc aca gga gac cag gcc cat tct   581
Arg Gln Gln Gly Val Phe Ile Ser Gly Thr Gly Asp Gln Ala His Ser
 90                  95                 100                 105

act ggt gga aat ggt gct ttg gcg ttt gat gct gaa cat tca cgg tgg   629
Thr Gly Gly Asn Gly Ala Leu Ala Phe Asp Ala Glu His Ser Arg Trp
                110                 115                 120

ttg gaa gaa aag aac aag caa atg aac gag ctg agg tct gct ctg aat   677
Leu Glu Glu Lys Asn Lys Gln Met Asn Glu Leu Arg Ser Ala Leu Asn
            125                 130                 135

gcg cat gca ggt gat tct gag ctt cga ata ata gtc gat ggt gtg atg   725
Ala His Ala Gly Asp Ser Glu Leu Arg Ile Ile Val Asp Gly Val Met
        140                 145                 150

gct cac tat gag gag ctt ttc agg ata aag agc aat gca gct aag aat   773
```

```
Ala His Tyr Glu Glu Leu Phe Arg Ile Lys Ser Asn Ala Ala Lys Asn
    155                 160                 165

gat gtc ttt cac ttg cta tct ggc atg tgg aaa aca cca gct gag aga     821
Asp Val Phe His Leu Leu Ser Gly Met Trp Lys Thr Pro Ala Glu Arg
170                 175                 180                 185

tgt ttc ttg tgg ctc ggt gga ttt cgt tca tcc gaa ctt cta aag ctt     869
Cys Phe Leu Trp Leu Gly Gly Phe Arg Ser Ser Glu Leu Leu Lys Leu
                190                 195                 200

ctg gcg aat cag ttg gag cca atg aca gag aga cag ttg atg ggc ata     917
Leu Ala Asn Gln Leu Glu Pro Met Thr Glu Arg Gln Leu Met Gly Ile
            205                 210                 215

aat aac ctg caa cag aca tcg cag cag gct gaa gat gct ttg tct caa     965
Asn Asn Leu Gln Gln Thr Ser Gln Gln Ala Glu Asp Ala Leu Ser Gln
        220                 225                 230

ggg atg gag agc tta caa cag tca cta gct gat act tta tcg agc ggg     1013
Gly Met Glu Ser Leu Gln Gln Ser Leu Ala Asp Thr Leu Ser Ser Gly
    235                 240                 245

act ctt ggt tca agt tca tca ggg aat gtc gca agc tac atg ggt cag     1061
Thr Leu Gly Ser Ser Ser Ser Gly Asn Val Ala Ser Tyr Met Gly Gln
250                 255                 260                 265

atg gcc atg gca atg gga aag tta ggt aca ctc gaa gga ttt atc cgc     1109
Met Ala Met Ala Met Gly Lys Leu Gly Thr Leu Glu Gly Phe Ile Arg
                270                 275                 280

cag gct gat aat ttg aga cta caa aca ttg caa cag atg ata aga gta     1157
Gln Ala Asp Asn Leu Arg Leu Gln Thr Leu Gln Gln Met Ile Arg Val
            285                 290                 295

tta aca acg aga cag tca gca cgt gct cta ctt gca ata cac gat tac     1205
Leu Thr Thr Arg Gln Ser Ala Arg Ala Leu Leu Ala Ile His Asp Tyr
        300                 305                 310

ttc tca cgg cta cga gct cta agc tcc tta tgg ctt gct cga ccc aga     1253
Phe Ser Arg Leu Arg Ala Leu Ser Ser Leu Trp Leu Ala Arg Pro Arg
    315                 320                 325

gag tga aactgtattt tggtcacatg tcagctgtac aaaatccata tggacacaaa     1309
Glu  *
330

accaggagag actattaatc aacacttgtc agattcttct taccaaatcc atcaacaaat 1369
aagcaaattt ctgggaaaca aaagactctt tgtatgtagg tttcttctac atggttgtgg 1429
taattcatgt tgttttagtt gtagtcatca gtttttaatt tagcatttga aaagttcaat 1489
gttgtttata tagcatcttc gattatctta gaaaggttat tgaattttgt tttttttttgt 1549
tacttttgtg tgtggtaaag gtgttttaac cttgcaactt ctgtactgta atcatttaac 1609
aatattaaga tgttctattt gagttttgt                                  1638

&lt;210&gt; 206
&lt;211&gt; 330
&lt;212&gt; PRT
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<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (45)...(105)
<223> Conserved domain

<400> 206
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Met Ala Asp Thr Ser Pro Arg Thr Asp Val Ser Thr Asp Asp Asp Thr
 1               5                  10                  15
Asp His Pro Asp Leu Gly Ser Glu Gly Ala Leu Val Asn Thr Ala Ala
            20                  25                  30
Ser Asp Ser Ser Asp Arg Ser Lys Gly Lys Met Asp Gln Lys Thr Leu
        35                  40                  45
Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg
    50                  55                  60
Lys Lys Ala Tyr Val Gln Gln Leu Glu Asn Ser Arg Leu Lys Leu Thr
65                  70                  75                  80
Gln Leu Glu Gln Glu Leu Gln Arg Ala Arg Gln Gln Gly Val Phe Ile
                85                  90                  95
Ser Gly Thr Gly Asp Gln Ala His Ser Thr Gly Gly Asn Gly Ala Leu
            100                 105                 110
Ala Phe Asp Ala Glu His Ser Arg Trp Leu Glu Glu Lys Asn Lys Gln
        115                 120                 125
Met Asn Glu Leu Arg Ser Ala Leu Asn Ala His Ala Gly Asp Ser Glu
    130                 135                 140
Leu Arg Ile Ile Val Asp Gly Val Met Ala His Tyr Glu Glu Leu Phe
145                 150                 155                 160
Arg Ile Lys Ser Asn Ala Ala Lys Asn Asp Val Phe His Leu Leu Ser
                165                 170                 175
Gly Met Trp Lys Thr Pro Ala Glu Arg Cys Phe Leu Trp Leu Gly Gly
            180                 185                 190
Phe Arg Ser Ser Glu Leu Leu Lys Leu Leu Ala Asn Gln Leu Glu Pro
        195                 200                 205
Met Thr Glu Arg Gln Leu Met Gly Ile Asn Asn Leu Gln Gln Thr Ser
    210                 215                 220
Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly Met Glu Ser Leu Gln Gln
225                 230                 235                 240
Ser Leu Ala Asp Thr Leu Ser Ser Gly Thr Leu Gly Ser Ser Ser Ser
                245                 250                 255
Gly Asn Val Ala Ser Tyr Met Gly Gln Met Ala Met Ala Met Gly Lys
            260                 265                 270
Leu Gly Thr Leu Glu Gly Phe Ile Arg Gln Ala Asp Asn Leu Arg Leu
        275                 280                 285
Gln Thr Leu Gln Gln Met Ile Arg Val Leu Thr Thr Arg Gln Ser Ala
    290                 295                 300
Arg Ala Leu Leu Ala Ile His Asp Tyr Phe Ser Arg Leu Arg Ala Leu
305                 310                 315                 320
Ser Ser Leu Trp Leu Ala Arg Pro Arg Glu
                325                 330
```

<210> 207
<211> 1370
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (184)...(969)

<400> 207
gtcgacccac gcgtccgggt ttttctttta tcctcttatc gctaatctgg agctctatat 60
agactataaa gggtttttga ttgattcggg agctcgagat ttgacttctt ttagctgatt 120
cggcaagttt gtatctagaa aggatcgatt ggtgaggtca atagtggttg gtgggtttta 180
gta atg gaa gac ggt gag ctt gat ttc tcc aat cag gaa gtg ttt tcg   228
    Met Glu Asp Gly Glu Leu Asp Phe Ser Asn Gln Glu Val Phe Ser
     1               5                  10                  15

agt tcg gag atg ggt gaa tta cca cct agc aat tgt tcg atg gat agt   276
Ser Ser Glu Met Gly Glu Leu Pro Pro Ser Asn Cys Ser Met Asp Ser
                20                  25                  30

ttc ttt gat ggg ctt tta atg gat act aat gct gct tgt acc cac act   324
Phe Phe Asp Gly Leu Leu Met Asp Thr Asn Ala Ala Cys Thr His Thr
            35                  40                  45

cac acc tgt aac ccc act gga cca gag aac act cat act cac acg tgc   372
His Thr Cys Asn Pro Thr Gly Pro Glu Asn Thr His Thr His Thr Cys
        50                  55                  60

ttc cat gtc cac acc aag att ctc ccg gat gag agc gat gaa aaa gtt   420
Phe His Val His Thr Lys Ile Leu Pro Asp Glu Ser Asp Glu Lys Val
    65                  70                  75

tct act gat gat aca gct gag tct tgt ggg aag aag ggt gaa aag aga   468
Ser Thr Asp Asp Thr Ala Glu Ser Cys Gly Lys Lys Gly Glu Lys Arg
 80                  85                  90                  95

cct ttg gga aac cgg gaa gcg gtt aga aag tat aga gag aag aag aag   516
Pro Leu Gly Asn Arg Glu Ala Val Arg Lys Tyr Arg Glu Lys Lys Lys
                100                 105                 110

gct aaa gct gct tct ttg gag gat gag gtt gca agg ctt agg gcg gtg   564
Ala Lys Ala Ala Ser Leu Glu Asp Glu Val Ala Arg Leu Arg Ala Val
            115                 120                 125

aat cag cag ctg gtg aag agg ttg caa aat cag gct acc ttg gaa gct   612
Asn Gln Gln Leu Val Lys Arg Leu Gln Asn Gln Ala Thr Leu Glu Ala
        130                 135                 140

gag gtt tcg agg ctt aag tgt ttg ctt gtg gat ttg aga gga aga ata   660
Glu Val Ser Arg Leu Lys Cys Leu Leu Val Asp Leu Arg Gly Arg Ile
    145                 150                 155

gat gga gag att gga tct ttt cct tat cag aaa cct atg gct gca aat   708
Asp Gly Glu Ile Gly Ser Phe Pro Tyr Gln Lys Pro Met Ala Ala Asn
160                 165                 170                 175

att cct tct ttc tcg cac atg atg aat cct tgt aat gta caa tgt gat   756
Ile Pro Ser Phe Ser His Met Met Asn Pro Cys Asn Val Gln Cys Asp
                180                 185                 190

gat gaa gtt tat tgc cct cag aat gtg ttt gga gtg aat agc caa gaa   804
```

```
Asp Glu Val Tyr Cys Pro Gln Asn Val Phe Gly Val Asn Ser Gln Glu
            195                 200                 205

ggt gcc tcg atc aat gac caa ggg tta agt ggt tgt gat ttt gat cag      852
Gly Ala Ser Ile Asn Asp Gln Gly Leu Ser Gly Cys Asp Phe Asp Gln
        210                 215                 220

cta caa tgc atg gct aat cag aac tta aat gga aat gga aac gga tca      900
Leu Gln Cys Met Ala Asn Gln Asn Leu Asn Gly Asn Gly Asn Gly Ser
    225                 230                 235

ttc agc aac gtc aat aca tct gtc tcg aat aag aga aaa ggt ggg cat      948
Phe Ser Asn Val Asn Thr Ser Val Ser Asn Lys Arg Lys Gly Gly His
240                 245                 250                 255

cgt gca tca aga gca gtt tga agcatcatca agcttgtact atctatttcc        999
Arg Ala Ser Arg Ala Val  *
                260

accagcatag atattgtatt ccaaataagt tgtagagttc agctgcagga tcagcttcgc 1059
tcagctttga ggggttggtg gtgtggtctt tctttgtggc acgagtgaga tctatggaca 1119
gaacccagat ttagtagtag tagaggcagg atttcgactt ccactaacca tcatgttgct 1179
tggtgaagaa caaggtatgc ccatgaagca cactgttttg tacattgagc ttgaggggct 1239
gtctctgatc tagccttact gtaacattgc aacgttctca caattgtgat cccaagttgc 1299
tttgttgact taaatgtgat aatatagctt aacttttact tgaaaaaaaa aaaaaaaaaa 1359
aaaaaaaaaa a                                                      1370

<210> 208
<211> 261
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (90)...(153)
<223> Conserved domain

<400> 208
Met Glu Asp Gly Glu Leu Asp Phe Ser Asn Gln Glu Val Phe Ser Ser
 1               5                  10                  15
Ser Glu Met Gly Glu Leu Pro Pro Ser Asn Cys Ser Met Asp Ser Phe
            20                  25                  30
Phe Asp Gly Leu Leu Met Asp Thr Asn Ala Ala Cys Thr His Thr His
        35                  40                  45
Thr Cys Asn Pro Thr Gly Pro Glu Asn Thr His Thr His Thr Cys Phe
    50                  55                  60
His Val His Thr Lys Ile Leu Pro Asp Glu Ser Asp Glu Lys Val Ser
65                  70                  75                  80
Thr Asp Asp Thr Ala Glu Ser Cys Gly Lys Lys Gly Glu Lys Arg Pro
                85                  90                  95
Leu Gly Asn Arg Glu Ala Val Arg Lys Tyr Arg Glu Lys Lys Lys Ala
            100                 105                 110
Lys Ala Ala Ser Leu Glu Asp Glu Val Ala Arg Leu Arg Ala Val Asn
        115                 120                 125
Gln Gln Leu Val Lys Arg Leu Gln Asn Gln Ala Thr Leu Glu Ala Glu
    130                 135                 140
Val Ser Arg Leu Lys Cys Leu Leu Val Asp Leu Arg Gly Arg Ile Asp
```

```
145                 150                 155                 160
Gly Glu Ile Gly Ser Phe Pro Tyr Gln Lys Pro Met Ala Ala Asn Ile
                165                 170                 175
Pro Ser Phe Ser His Met Met Asn Pro Cys Asn Val Gln Cys Asp Asp
            180                 185                 190
Glu Val Tyr Cys Pro Gln Asn Val Phe Gly Val Asn Ser Gln Glu Gly
        195                 200                 205
Ala Ser Ile Asn Asp Gln Gly Leu Ser Gly Cys Asp Phe Asp Gln Leu
    210                 215                 220
Gln Cys Met Ala Asn Gln Asn Leu Asn Gly Asn Gly Asn Gly Ser Phe
225                 230                 235                 240
Ser Asn Val Asn Thr Ser Val Ser Asn Lys Arg Lys Gly Gly His Arg
                245                 250                 255
Ala Ser Arg Ala Val
            260


<210> 209
<211> 859
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (62)...(718)

<400> 209
caatccacta acgatcccta accgaaaaca gagtagtcaa gaaacagagt atttttttcta 60
c atg gat cca ttt tta att cag tcc cca ttc tcc ggc ttc tca ccg gaa 109
  Met Asp Pro Phe Leu Ile Gln Ser Pro Phe Ser Gly Phe Ser Pro Glu
   1               5                  10                  15

tat tct atc gga tct tct cca gat tct ttc tca tcc tct tct tct aac   157
Tyr Ser Ile Gly Ser Ser Pro Asp Ser Phe Ser Ser Ser Ser Ser Asn
            20                  25                  30

aat tac tct ctt ccc ttc aac gag aac gac tca gag gaa atg ttt ctc   205
Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu
        35                  40                  45

tac ggt cta atc gag cag tcc acg caa caa acc tat att gac tcg gat   253
Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp
    50                  55                  60

agt caa gac ctt ccg atc aaa tcc gta agc tca aga aag tca gag aag   301
Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys
 65                  70                  75                  80

tct tac aga ggc gta aga cga cgg cca tgg ggg aaa ttc gcg gcg gag   349
Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
                85                  90                  95

ata aga gat tcg act aga aac ggt att agg gtt tgg ctc ggg acg ttc   397
Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe
            100                 105                 110

gaa agc gcg gaa gag gcg gct tta gcc tac gat caa gct gct ttc tcg   445
```

```
Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser
        115                 120                 125

atg aga ggg tcc tcg gcg att ctc aat ttt tcg gcg gag aga gtt caa     493
Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln
    130                 135                 140

gag tcg ctt tcg gag att aaa tat acc tac gag gat ggt tgt tct ccg     541
Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro
145                 150                 155                 160

gtt gtg gcg ttg aag agg aaa cac tcg atg aga cgg aga atg acc aat     589
Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn
                165                 170                 175

aag aag acg aaa gat agt gac ttt gat cac cgc tcc gtg aag tta gat     637
Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp
            180                 185                 190

aat gta gtt gtc ttt gag gat ttg gga gaa cag tac ctt gag gag ctt     685
Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu
        195                 200                 205

ttg ggg tct tct gaa aat agt ggg act tgg tga aagattagga tttgtattag 738
Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp  *
    210                 215

ggaccttaag tttgaagtgg ttgattaatt ttaaccctaa tatgtttttt gtttgcttaa 798
atatttgatt ctattgagaa acatcgaaaa cagtttgtat gtacttttgt gatacttggc 858
g                                                                  859

<210> 210
<211> 218
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (79)...(147)
<223> Conserved domain

<400> 210
Met Asp Pro Phe Leu Ile Gln Ser Pro Phe Ser Gly Phe Ser Pro Glu
 1               5                  10                  15
Tyr Ser Ile Gly Ser Ser Pro Asp Ser Phe Ser Ser Ser Ser Ser Asn
            20                  25                  30
Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu
        35                  40                  45
Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp
    50                  55                  60
Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys
65                  70                  75                  80
Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
                85                  90                  95
Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe
            100                 105                 110
Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser
```

```
        115                 120                 125
Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln
    130                 135                 140
Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro
145                 150                 155                 160
Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn
                165                 170                 175
Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp
            180                 185                 190
Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu
        195                 200                 205
Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp
    210                 215


<210> 211
<211> 1055
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (70)...(816)

<400> 211
ataaaggcat ttcagctcca ccgtaggaaa ctttctcttg aaagaaaccc acagcaacaa 60
acagagaaa atg tgt ggc ggt gct att att tcc gat tat gcc cct ctc gtc 111
          Met Cys Gly Gly Ala Ile Ile Ser Asp Tyr Ala Pro Leu Val
           1               5                  10

acc aag gcc aag ggc cgt aaa ctc acg gct gag gaa ctc tgg tca gag   159
Thr Lys Ala Lys Gly Arg Lys Leu Thr Ala Glu Glu Leu Trp Ser Glu
 15                 20                  25                  30

ctc gat gct tcc gcc gcc gac gac ttc tgg ggt ttc tat tcc acc tcc   207
Leu Asp Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser
                35                  40                  45

aaa ctc cat ccc acc aac caa gtt aac gtg aaa gag gag gca gtg aag   255
Lys Leu His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys
            50                  55                  60

aag gag cag gca aca gag ccg ggg aaa cgg agg aag agg aag aat gtt   303
Lys Glu Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val
        65                  70                  75

tat aga ggg ata cgt aag cgt cca tgg gga aaa tgg gcg gct gag att   351
Tyr Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile
    80                  85                  90

cga gat cca cga aaa ggt gtt aga gtt tgg ctt ggt acg ttc aac acg   399
Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr
 95                 100                 105                 110

gcg gag gaa gct gcc atg gct tat gat gtt gcg gcc aag cag atc cgt   447
Ala Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg
                115                 120                 125
```

```
ggt gat aaa gcc aag ctc aac ttc cca gat ctg cac cat cct cct cct    495
Gly Asp Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro
            130                 135                 140

cct aat tat act cct ccg ccg tca tcg cca cga tca acc gat cag cct    543
Pro Asn Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro
        145                 150                 155

ccg gcg aag aag gtc tgc gtt gtc tct cag agt gag agc gag tta agt    591
Pro Ala Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser
    160                 165                 170

cag ccg agt ttc ccg gtg gag tgt ata gga ttt gga aat ggg gac gag    639
Gln Pro Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu
175                 180                 185                 190

ttt cag aac ctg agt tac gga ttt gag ccg gat tat gat ctg aaa cag    687
Phe Gln Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln
                195                 200                 205

cag ata tcg agc ttg gaa tcg ttc ctt gag ctg gac ggt aac acg gcg    735
Gln Ile Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala
            210                 215                 220

gag caa ccg agt cag ctt gat gag tcc gtt tcc gag gtg gat atg tgg    783
Glu Gln Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp
        225                 230                 235

atg ctt gat gat gtc att gcg tcg tat gag taa aagaaaaaaa ataagtttaa 836
Met Leu Asp Asp Val Ile Ala Ser Tyr Glu  *
    240                 245

aaaaagttaa ataaagtctg taatatatat gtaaccgccg ttacttttaa aaggttttta 896
ccgtcgcatt ggactgctga tgatgtctgt tgtgtaatgt gtagaatgtg accaaatgga 956
cgttatatta cggtttgtgg tattattagt ttcttagatg gaaaaactta catgtgtaaa 1016
taagatttgt aatgtaagac gaagtactta taacttctt                        1055

<210> 212
<211> 248
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (76)...(145)
<223> Conserved domain

<400> 212
Met Cys Gly Gly Ala Ile Ile Ser Asp Tyr Ala Pro Leu Val Thr Lys
 1               5                  10                  15
Ala Lys Gly Arg Lys Leu Thr Ala Glu Glu Leu Trp Ser Glu Leu Asp
            20                  25                  30
Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser Lys Leu
        35                  40                  45
His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys Lys Glu
    50                  55                  60
```

```
Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr Arg
65                  70                  75                  80
Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
                85                  90                  95
Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu
            100                 105                 110
Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly Asp
        115                 120                 125
Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro Pro Asn
    130                 135                 140
Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro Pro Ala
145                 150                 155                 160
Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser Gln Pro
                165                 170                 175
Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu Phe Gln
            180                 185                 190
Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile
        195                 200                 205
Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala Glu Gln
    210                 215                 220
Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp Met Leu
225                 230                 235                 240
Asp Asp Val Ile Ala Ser Tyr Glu
                245


<210> 213
<211> 920
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(852)

<400> 213
atg gcg aag acg aaa tat gga gag aga cat agg aaa ggg tta tgg tca      48
Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser
 1               5                  10                  15

cct gaa gaa gac gag aag cta agg agc ttc atc ctc tct tat ggc cat      96
Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His
            20                  25                  30

tct tgc tgg acc act gtt ccc atc aaa gct ggg tta caa agg aat ggg     144
Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly
        35                  40                  45

aag agc tgc aga tta aga tgg att aat tac cta aga cca ggg tta aag     192
Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
    50                  55                  60

agg gat atg att agt gca gaa gaa gaa gag act atc ttg acg ttt cat     240
Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His
 65                  70                  75                  80

tct ccc ttg ggt aac aag tgg tcg caa ata gct aaa ttc tta ccg gga     288
```

```
Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly
                85                  90                  95

aga aca gac aat gag ata aag aac tat tgg cac tct cat ttg aaa aag     336
Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys
            100                 105                 110

aaa tgg ctc aag tct cag agc tta caa gat gca aaa tct att tcc cct     384
Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro
        115                 120                 125

cct tcg tct tca tca tca tca ctt gtt gct tgt gga gaa aga aat ccg     432
Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro
    130                 135                 140

gaa acc ttg atc tcg aat cac gtg ttc tcc ctc cag aga ctt cta gag     480
Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu
145                 150                 155                 160

aac aaa tct tca tct ccc tca caa gaa agc aac gga aat aac agc cat     528
Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
                165                 170                 175

caa tgt tct tct gct cct gag att cca agg ctt ttc ttc tct gaa tgg     576
Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
            180                 185                 190

ctt tct tct tca tat ccc cac acc gat tat tcc tct gag ttt acc gac     624
Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
        195                 200                 205

tct aag cac agt caa gct cca aat gtc gaa gag act ctc tca gct tat     672
Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
    210                 215                 220

gaa gaa atg ggt gat gtt gat cag ttc cat tac aac gaa atg atg atc     720
Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
225                 230                 235                 240

aac aac agc aac tgg act ctt aac gac att gtg ttt ggt tcc aaa tgt     768
Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
                245                 250                 255

aag aag cag gag cat cat att tat aga gag gct tca gat tgt aat tct     816
Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
            260                 265                 270

tct gct gaa ttc ttt tct cca cca aca acg acg taa attgcgttta          862
Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr  *
        275                 280

ttgtaatgta aatcaaattt ctaaggcaaa accggaaaaa aaaaaaaaaa aaaaaaa      920
```

<210> 214
<211> 283
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (11)...(113)
<223> Conserved domain

<400> 214
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Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser
 1               5                  10                  15
Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His
            20                  25                  30
Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly
        35                  40                  45
Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
    50                  55                  60
Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His
65                  70                  75                  80
Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly
                85                  90                  95
Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys
            100                 105                 110
Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro
        115                 120                 125
Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro
    130                 135                 140
Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu
145                 150                 155                 160
Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
                165                 170                 175
Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
            180                 185                 190
Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
        195                 200                 205
Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
    210                 215                 220
Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
225                 230                 235                 240
Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
                245                 250                 255
Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
            260                 265                 270
Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr
        275                 280
```

<210> 215
<211> 726
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(726)

<400> 215
```
atg gcc tcg tca tca tca tca tct tat aga ttc caa tct ggg tct tac     48
Met Ala Ser Ser Ser Ser Ser Ser Tyr Arg Phe Gln Ser Gly Ser Tyr
```

```
1               5                   10                  15

cct ctt tcg tca agt cct tct ctt ggg aat ttc gtc gaa cgc att aaa    96
Pro Leu Ser Ser Ser Pro Ser Leu Gly Asn Phe Val Glu Arg Ile Lys
            20                  25                  30

gac gct tgt cat ttc ctt gtc tct gct gtt ttg ggt acc att atc tcc    144
Asp Ala Cys His Phe Leu Val Ser Ala Val Leu Gly Thr Ile Ile Ser
        35                  40                  45

gcg atc ttg acc ttc ttc ttc gca cta gtg ggc aca ttg cta ggg gca    192
Ala Ile Leu Thr Phe Phe Phe Ala Leu Val Gly Thr Leu Leu Gly Ala
    50                  55                  60

ctt aca gga gct ttg ata ggt caa gaa act gag agt ggt ttc att aga    240
Leu Thr Gly Ala Leu Ile Gly Gln Glu Thr Glu Ser Gly Phe Ile Arg
65                  70                  75                      80

gga gca gca att gga gcc att tcg gga gct gtt ttc tct atc gag gtc    288
Gly Ala Ala Ile Gly Ala Ile Ser Gly Ala Val Phe Ser Ile Glu Val
                85                  90                  95

ttt gaa tca tct ctg gat ctc tgg aaa tcc gat gag tcg ggt ttc gga    336
Phe Glu Ser Ser Leu Asp Leu Trp Lys Ser Asp Glu Ser Gly Phe Gly
            100                 105                 110

tgt ttt ctc tac ttg att gat gtc att gtt agt ctt cta agc ggg aga    384
Cys Phe Leu Tyr Leu Ile Asp Val Ile Val Ser Leu Leu Ser Gly Arg
        115                 120                 125

ctt gta cga gag cgc att ggt cct gca atg cta agt gca gtg caa agt    432
Leu Val Arg Glu Arg Ile Gly Pro Ala Met Leu Ser Ala Val Gln Ser
    130                 135                 140

caa atg gga gct gtg gat aca gct ttt gat gat cac aca agc ctt ttt    480
Gln Met Gly Ala Val Asp Thr Ala Phe Asp Asp His Thr Ser Leu Phe
145                 150                 155                 160

gat aca gga ggc tca aaa gga ttg aca gga gac ctt gtt gag aaa atc    528
Asp Thr Gly Gly Ser Lys Gly Leu Thr Gly Asp Leu Val Glu Lys Ile
                165                 170                 175

cca aag atg aca atc act ggc aac aat aac act gat gct tct gag aac    576
Pro Lys Met Thr Ile Thr Gly Asn Asn Asn Thr Asp Ala Ser Glu Asn
            180                 185                 190

aca gac tca tgt tct gtt tgt ctt cag gat ttc cag ctc ggt gaa aca    624
Thr Asp Ser Cys Ser Val Cys Leu Gln Asp Phe Gln Leu Gly Glu Thr
        195                 200                 205

gtt aga agc ttg cct cat tgt cat cac atg ttt cac tta cct tgc ata    672
Val Arg Ser Leu Pro His Cys His His Met Phe His Leu Pro Cys Ile
    210                 215                 220

gac aat tgg ctc ctt aga cac ggt tct tgc ccg atg tgt aga cgt gat    720
Asp Asn Trp Leu Leu Arg His Gly Ser Cys Pro Met Cys Arg Arg Asp
225                 230                 235                 240
```

```
att taa                                                            726
Ile  *


<210> 216
<211> 241
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (196)...(237)
<223> Conserved domain

<400> 216
Met Ala Ser Ser Ser Ser Ser Ser Tyr Arg Phe Gln Ser Gly Ser Tyr
 1               5                  10                  15
Pro Leu Ser Ser Ser Pro Ser Leu Gly Asn Phe Val Glu Arg Ile Lys
            20                  25                  30
Asp Ala Cys His Phe Leu Val Ser Ala Val Leu Gly Thr Ile Ile Ser
        35                  40                  45
Ala Ile Leu Thr Phe Phe Phe Ala Leu Val Gly Thr Leu Leu Gly Ala
    50                  55                  60
Leu Thr Gly Ala Leu Ile Gly Gln Glu Thr Glu Ser Gly Phe Ile Arg
65                  70                  75                  80
Gly Ala Ala Ile Gly Ala Ile Ser Gly Ala Val Phe Ser Ile Glu Val
                85                  90                  95
Phe Glu Ser Ser Leu Asp Leu Trp Lys Ser Asp Glu Ser Gly Phe Gly
            100                 105                 110
Cys Phe Leu Tyr Leu Ile Asp Val Ile Val Ser Leu Leu Ser Gly Arg
        115                 120                 125
Leu Val Arg Glu Arg Ile Gly Pro Ala Met Leu Ser Ala Val Gln Ser
    130                 135                 140
Gln Met Gly Ala Val Asp Thr Ala Phe Asp Asp His Thr Ser Leu Phe
145                 150                 155                 160
Asp Thr Gly Gly Ser Lys Gly Leu Thr Gly Asp Leu Val Glu Lys Ile
                165                 170                 175
Pro Lys Met Thr Ile Thr Gly Asn Asn Asn Thr Asp Ala Ser Glu Asn
            180                 185                 190
Thr Asp Ser Cys Ser Val Cys Leu Gln Asp Phe Gln Leu Gly Glu Thr
        195                 200                 205
Val Arg Ser Leu Pro His Cys His His Met Phe His Leu Pro Cys Ile
    210                 215                 220
Asp Asn Trp Leu Leu Arg His Gly Ser Cys Pro Met Cys Arg Arg Asp
225                 230                 235                 240
Ile


<210> 217
<211> 1302
<212> DNA
<213> Arabidopsis thaliana

<220>
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<221> CDS
<222> (331)...(1149)

<400> 217
tgtctctctc tctggctctc tttctcttaa cgtgatcata acgtgattcg aaaattggat 60
atagataggt ttcttgttgg atcttgatcc ctctggaaaa ggaggggaga atagcagttc 120
atgatgggat tttgtatctg cccgttggag tcacctgcga gattactatg gagtacaagc 180
ttcttccgcc ataagatcat gatcttctaa tccttcctac ttcttcccat ctttttaatc 240
atcttctcgc tatctctgct tcctctttct ctctgtttcc tctttctcag aactcagaag 300
tagttgttgt tttatttctg ttgatcaaaa atg gaa tcc aat tcg ttt ttc ttc 354
Met Glu Ser Asn Ser Phe Phe Phe
1 5

gat cca tct gct tca cac ggc aac agc atg ttc ttc ctt ggg aat ctc 402
Asp Pro Ser Ala Ser His Gly Asn Ser Met Phe Phe Leu Gly Asn Leu
10 15 20

aat ccc gtc gtc caa gga gga gga gca aga tcg atg atg aac atg gag 450
Asn Pro Val Val Gln Gly Gly Gly Ala Arg Ser Met Met Asn Met Glu
25 30 35 40

gaa act tcg aag cga agg ccc ttc ttt agc tcc cct gag gat ctc tac 498
Glu Thr Ser Lys Arg Arg Pro Phe Phe Ser Ser Pro Glu Asp Leu Tyr
45 50 55

gac gat gac ttt tac gac gac cag ttg cct gaa aag aag cgt cgc ctc 546
Asp Asp Asp Phe Tyr Asp Asp Gln Leu Pro Glu Lys Lys Arg Arg Leu
60 65 70

act acc gaa caa gtg cat ctg ctg gag aaa agc ttc gag aca gag aac 594
Thr Thr Glu Gln Val His Leu Leu Glu Lys Ser Phe Glu Thr Glu Asn
75 80 85

aag cta gag cct gaa cgc aag act cag ctt gcc aag aag ctt ggt cta 642
Lys Leu Glu Pro Glu Arg Lys Thr Gln Leu Ala Lys Lys Leu Gly Leu
90 95 100

cag cca agg caa gtg gct gtc tgg ttt cag aat cgc cga gct cgt tgg 690
Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp
105 110 115 120

aaa aca aaa cag ctt gag aga gac tac gat ctt ctc aag tcc act tac 738
Lys Thr Lys Gln Leu Glu Arg Asp Tyr Asp Leu Leu Lys Ser Thr Tyr
125 130 135

gac caa ctt ctt tct aac tac gac tcc atc gtc atg gac aac gat aag 786
Asp Gln Leu Leu Ser Asn Tyr Asp Ser Ile Val Met Asp Asn Asp Lys
140 145 150

ctc aga tcc gag gtt act tcc ctg acc gaa aag ctt cag ggc aaa caa 834
Leu Arg Ser Glu Val Thr Ser Leu Thr Glu Lys Leu Gln Gly Lys Gln
155 160 165

gag aca gct aat gaa cca cct ggt caa gtg ccc gaa cca aac caa ctt 882
Glu Thr Ala Asn Glu Pro Pro Gly Gln Val Pro Glu Pro Asn Gln Leu
170 175 180

```
gat ccg gtt tac att aat gcg gca gca atc aaa acc gag gac cgg tta    930
Asp Pro Val Tyr Ile Asn Ala Ala Ala Ile Lys Thr Glu Asp Arg Leu
185                 190                 195                 200

agt tca ggg agc gtt ggg agc gcg gta cta gac gac gac gca cct caa    978
Ser Ser Gly Ser Val Gly Ser Ala Val Leu Asp Asp Asp Ala Pro Gln
                205                 210                 215

cta cta gac agc tgt gac tct tac ttc cca agc atc gta ccc atc caa    1026
Leu Leu Asp Ser Cys Asp Ser Tyr Phe Pro Ser Ile Val Pro Ile Gln
            220                 225                 230

gac aac agc aac gcc agt gat cat gac aat gac cgg agc tgt ttc gcc    1074
Asp Asn Ser Asn Ala Ser Asp His Asp Asn Asp Arg Ser Cys Phe Ala
        235                 240                 245

gac gtc ttt gtg ccc acc act tca ccg tcg cac gat cat cac ggt gaa    1122
Asp Val Phe Val Pro Thr Thr Ser Pro Ser His Asp His His Gly Glu
    250                 255                 260

tca ttg gct ttc tgg gga tgg cct tag aaaaccactc tgataataaa          1169
Ser Leu Ala Phe Trp Gly Trp Pro  *
265                 270

tgtgtgttta tttaagttca agagtcatct tcttgttgtt tccatgttga cgataattgt 1229
tgactcgtgg aataattccg ctgttcaacg gtatttttat cagttgcatt atatgctttt 1289
atgaaaaaaa aaa                                                    1302

<210> 218
<211> 272
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (64)...(124)
<223> Conserved domain

<400> 218
Met Glu Ser Asn Ser Phe Phe Phe Asp Pro Ser Ala Ser His Gly Asn
 1               5                  10                  15
Ser Met Phe Phe Leu Gly Asn Leu Asn Pro Val Val Gln Gly Gly Gly
            20                  25                  30
Ala Arg Ser Met Met Asn Met Glu Glu Thr Ser Lys Arg Arg Pro Phe
        35                  40                  45
Phe Ser Ser Pro Glu Asp Leu Tyr Asp Asp Asp Phe Tyr Asp Asp Gln
    50                  55                  60
Leu Pro Glu Lys Lys Arg Arg Leu Thr Thr Glu Gln Val His Leu Leu
65                  70                  75                  80
Glu Lys Ser Phe Glu Thr Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr
                85                  90                  95
Gln Leu Ala Lys Lys Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp
            100                 105                 110
Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Arg Asp
        115                 120                 125
Tyr Asp Leu Leu Lys Ser Thr Tyr Asp Gln Leu Leu Ser Asn Tyr Asp
    130                 135                 140
```

```
Ser Ile Val Met Asp Asn Asp Lys Leu Arg Ser Glu Val Thr Ser Leu
145                 150                 155                 160
Thr Glu Lys Leu Gln Gly Lys Gln Glu Thr Ala Asn Glu Pro Pro Gly
                165                 170                 175
Gln Val Pro Glu Pro Asn Gln Leu Asp Pro Val Tyr Ile Asn Ala Ala
            180                 185                 190
Ala Ile Lys Thr Glu Asp Arg Leu Ser Ser Gly Ser Val Gly Ser Ala
        195                 200                 205
Val Leu Asp Asp Asp Ala Pro Gln Leu Leu Asp Ser Cys Asp Ser Tyr
    210                 215                 220
Phe Pro Ser Ile Val Pro Ile Gln Asp Asn Ser Asn Ala Ser Asp His
225                 230                 235                 240
Asp Asn Asp Arg Ser Cys Phe Ala Asp Val Phe Val Pro Thr Thr Ser
                245                 250                 255
Pro Ser His Asp His His Gly Glu Ser Leu Ala Phe Trp Gly Trp Pro
            260                 265                 270


<210> 219
<211> 1240
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (88)...(1020)

<400> 219
gtaaatctct ctttgaaggt tcctaactcg ttaatcgtaa ctcacagtga ctcgttcgag 60
tcaaagtctc tgtctttagc tcaaacc atg gct agt aac aac cct cac gac aac 114
                              Met Ala Ser Asn Asn Pro His Asp Asn
                               1               5

ctt tct gac caa act cct tct gat gat ttc ttc gag caa atc ctc ggc    162
Leu Ser Asp Gln Thr Pro Ser Asp Asp Phe Phe Glu Gln Ile Leu Gly
 10                  15                  20                  25

ctt cct aac ttc tca gcc tct tct gcc gcc ggt tta tct gga gtt gac    210
Leu Pro Asn Phe Ser Ala Ser Ser Ala Ala Gly Leu Ser Gly Val Asp
                 30                  35                  40

gga gga tta ggt ggt gga gca ccg cct atg atg ctg cag ttg ggt tcc    258
Gly Gly Leu Gly Gly Gly Ala Pro Pro Met Met Leu Gln Leu Gly Ser
             45                  50                  55

gga gaa gaa gga agt cac atg ggt ggc tta gga gga agt gga cca act    306
Gly Glu Glu Gly Ser His Met Gly Gly Leu Gly Gly Ser Gly Pro Thr
         60                  65                  70

ggg ttt cac aat cag atg ttt cct ttg ggg tta agt ctt gat caa ggg    354
Gly Phe His Asn Gln Met Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly
     75                  80                  85

aaa gga cct ggg ttt ctt aga cct gaa gga gga cat gga agt ggg aaa    402
Lys Gly Pro Gly Phe Leu Arg Pro Glu Gly Gly His Gly Ser Gly Lys
 90                  95                 100                 105
```

```
aga ttc tca gat gat gtt gtt gat aat cga tgt tct tct atg aaa cct    450
Arg Phe Ser Asp Asp Val Val Asp Asn Arg Cys Ser Ser Met Lys Pro
                110                 115                 120

gtt ttc cac ggg cag cct atg caa cag cca cct cca tcg gcc cca cat    498
Val Phe His Gly Gln Pro Met Gln Gln Pro Pro Pro Ser Ala Pro His
            125                 130                 135

cag cct act tca atc cgt ccc agg gtt cga gct agg cgt ggt cag gct    546
Gln Pro Thr Ser Ile Arg Pro Arg Val Arg Ala Arg Arg Gly Gln Ala
        140                 145                 150

act gat cca cat agc atc gct gag cgg cta cgt aga gaa aga ata gca    594
Thr Asp Pro His Ser Ile Ala Glu Arg Leu Arg Arg Glu Arg Ile Ala
    155                 160                 165

gaa cgg atc agg gcg ctg cag gaa ctt gta cct act gtg aac aag acc    642
Glu Arg Ile Arg Ala Leu Gln Glu Leu Val Pro Thr Val Asn Lys Thr
170                 175                 180                 185

gat aga gct gct atg atc gat gag att gtc gat tat gta aag ttt ctc    690
Asp Arg Ala Ala Met Ile Asp Glu Ile Val Asp Tyr Val Lys Phe Leu
                190                 195                 200

agg ctc caa gtc aag gtt ttg agc atg aac cga ctt ggt gga gcc ggt    738
Arg Leu Gln Val Lys Val Leu Ser Met Asn Arg Leu Gly Gly Ala Gly
            205                 210                 215

gcg gtt gct cca ctt gtt act gat atg cct ctt tca tca tca gtt gag    786
Ala Val Ala Pro Leu Val Thr Asp Met Pro Leu Ser Ser Ser Val Glu
        220                 225                 230

gat gaa acg ggt gag ggt gga agg act ccg caa cca gcg tgg gag aaa    834
Asp Glu Thr Gly Glu Gly Gly Arg Thr Pro Gln Pro Ala Trp Glu Lys
    235                 240                 245

tgg tct aac gat ggg act gaa cgt caa gtg gct aaa ctg atg gaa gag    882
Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala Lys Leu Met Glu Glu
250                 255                 260                 265

aac gtt gga gcc gcg atg cag ctt ctt caa tca aag gct ctt tgt atg    930
Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser Lys Ala Leu Cys Met
                270                 275                 280

atg cca atc tca ttg gca atg gca att tac cat tct caa cct ccg gat    978
Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His Ser Gln Pro Pro Asp
            285                 290                 295

aca tct tca gtg gtc aag cct gag aac aat cct cca cag tag            1020
Thr Ser Ser Val Val Lys Pro Glu Asn Asn Pro Pro Gln  *
        300                 305                 310

gatttctgca ataaagagtt tgtacagcta atccaactgt ccaacatggg tttttcttct 1080
gctctaatga ctctggtttc ttctctcctc tctcaccgac ttgaaaggta aaaaagtgaa 1140
aaaggctttg tagatggaat caatgtagga tttgcagtag agggcaaaaa aatgtcatat 1200
agctcaattg atcaagtctt aaaaaaaaaa aaaaaaaaaa                       1240
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<210> 220
<211> 310
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (143)...(240)
<223> Conserved domain

<400> 220
Met Ala Ser Asn Asn Pro His Asp Asn Leu Ser Asp Gln Thr Pro Ser
1 5 10 15
Asp Asp Phe Phe Glu Gln Ile Leu Gly Leu Pro Asn Phe Ser Ala Ser
20 25 30
Ser Ala Ala Gly Leu Ser Gly Val Asp Gly Gly Leu Gly Gly Gly Ala
35 40 45
Pro Pro Met Met Leu Gln Leu Gly Ser Gly Glu Glu Gly Ser His Met
50 55 60
Gly Gly Leu Gly Gly Ser Gly Pro Thr Gly Phe His Asn Gln Met Phe
65 70 75 80
Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly Pro Gly Phe Leu Arg
85 90 95
Pro Glu Gly Gly His Gly Ser Gly Lys Arg Phe Ser Asp Asp Val Val
100 105 110
Asp Asn Arg Cys Ser Ser Met Lys Pro Val Phe His Gly Gln Pro Met
115 120 125
Gln Gln Pro Pro Pro Ser Ala Pro His Gln Pro Thr Ser Ile Arg Pro
130 135 140
Arg Val Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His Ser Ile Ala
145 150 155 160
Glu Arg Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ala Leu Gln
165 170 175
Glu Leu Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp
180 185 190
Glu Ile Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu
195 200 205
Ser Met Asn Arg Leu Gly Gly Ala Gly Ala Val Ala Pro Leu Val Thr
210 215 220
Asp Met Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gly Glu Gly Gly
225 230 235 240
Arg Thr Pro Gln Pro Ala Trp Glu Lys Trp Ser Asn Asp Gly Thr Glu
245 250 255
Arg Gln Val Ala Lys Leu Met Glu Glu Asn Val Gly Ala Ala Met Gln
260 265 270
Leu Leu Gln Ser Lys Ala Leu Cys Met Met Pro Ile Ser Leu Ala Met
275 280 285
Ala Ile Tyr His Ser Gln Pro Pro Asp Thr Ser Ser Val Val Lys Pro
290 295 300
Glu Asn Asn Pro Pro Gln
305 310

<210> 221
<211> 1431
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (129)...(1211)

<400> 221
ctttaaatcc caaaccaacc ctaaagtttt gatttttaat tttgggggta accaaaaaaa 60
aaacaaaacc ctaatttttt ttctttagtg atgagattat tggtgatgat gaaatgattg 120
gagatcta atg aag aat aac aac aat ggc gac gtt gtg gat aac gaa gtg  170
         Met Lys Asn Asn Asn Asn Gly Asp Val Val Asp Asn Glu Val
          1               5                  10

aac aac cgg tta agc cgg tgg cat cac aat tct tcc cgg ata att agg   218
Asn Asn Arg Leu Ser Arg Trp His His Asn Ser Ser Arg Ile Ile Arg
 15                  20                  25                  30

gtt tca cga gct tcc ggt ggt aaa gat cga cac agc aaa gtc ttg act   266
Val Ser Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys Val Leu Thr
                 35                  40                  45

tct aaa gga cca cgt gac cgt cgt gtc cgg tta tca gtc tcc acc gct   314
Ser Lys Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val Ser Thr Ala
             50                  55                  60

ctt caa ttc tat gat ctt caa gat cgg tta ggt tat gat caa cct agc   362
Leu Gln Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp Gln Pro Ser
         65                  70                  75

aaa gct gtt gaa tgg tta atc aaa gct gct gaa gat tca atc tct gag   410
Lys Ala Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser Ile Ser Glu
     80                  85                  90

ctt cct tca ctc aac aac act cat ttt ccg acc gat gac gag aat cac   458
Leu Pro Ser Leu Asn Asn Thr His Phe Pro Thr Asp Asp Glu Asn His
 95                 100                 105                 110

cag aat cag aca tta aca aca gtt gct gct aat tcc ttg tct aaa tct   506
Gln Asn Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu Ser Lys Ser
                115                 120                 125

gct tgt agt agc aat tca gac acg agc aag aac tct tct ggt ttg tct   554
Ala Cys Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Ser Gly Leu Ser
            130                 135                 140

tta tca aga tcg gag ctt aga gat aaa gct aga gag agg gct aga gag   602
Leu Ser Arg Ser Glu Leu Arg Asp Lys Ala Arg Glu Arg Ala Arg Glu
        145                 150                 155

aga aca gct aaa gag acc aag gaa aga gat cat aac cac act tcg ttt   650
Arg Thr Ala Lys Glu Thr Lys Glu Arg Asp His Asn His Thr Ser Phe
    160                 165                 170

acg gat ttg tta aat tcc ggt tca gat ccg gtt aac tca aac cgg caa   698
Thr Asp Leu Leu Asn Ser Gly Ser Asp Pro Val Asn Ser Asn Arg Gln
175                 180                 185                 190

tgg atg gct tca gct cct tct tca tct cca atg gag tat ttc agt tcg   746
```

```
Trp Met Ala Ser Ala Pro Ser Ser Ser Pro Met Glu Tyr Phe Ser Se
                195                 200                 205

ggt tta att ctc ggg tcg ggt caa caa acc cat ttc cct att tca aca     794
Gly Leu Ile Leu Gly Ser Gly Gln Gln Thr His Phe Pro Ile Ser Thr
            210                 215                 220

aat tct cat cct ttc tca tca atc tcc gat cat cat cat cat cat cct     842
Asn Ser His Pro Phe Ser Ser Ile Ser Asp His His His His His Pro
        225                 230                 235

cat cat cag cat caa gag ttt tca ttc gtt ccc gac cat ttg ata tca     890
His His Gln His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser
    240                 245                 250

ccg gca gaa tcc aac ggc gga gca ttc aat ctt gat ttt aat atg tca     938
Pro Ala Glu Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser
255                 260                 265                 270

aca ccc tcc ggc gcc gga gct gcc gtc tcc gcc gca tca ggt ggt ggc     986
Thr Pro Ser Gly Ala Gly Ala Ala Val Ser Ala Ala Ser Gly Gly Gly
                275                 280                 285

ttc agt ggt ttc aac agg ggg acc ctt cag tcc aat tca aca aat cag     1034
Phe Ser Gly Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln
            290                 295                 300

cat cag tca ttc ctc gct aat cta cag agg ttt cca aca tca gaa agt     1082
His Gln Ser Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser
        305                 310                 315

gga gga ggt cca cag ttc tta ttc ggt gca ctg cct gca gag aat cac     1130
Gly Gly Gly Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His
    320                 325                 330

cac cac aat cac cag ttt cag ctt tac tat gaa aat gga tgc aga aac     1178
His His Asn His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn
335                 340                 345                 350

tca tca gaa cat aag ggt aaa ggc aag aac tga tgatattaat tattgcatct 1231
Ser Ser Glu His Lys Gly Lys Gly Lys Asn  *
                355                 360

ttggttttgt tcaaatgctc attttgtatg tttatctttg gtttatttca aacaaatgt 1291
taatctcttt cgttgtctga tgtgtgttag ggttttgttt tatgtattga gggtctttgg 1351
aaatcttttt gcattgtgct tgtaatgttg tatttgtgat aatagcattt tgtttgtgag 1411
ttaaaaaaaa aaaaaaaaaa                                              1431

<210> 222
<211> 360
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (39)...(95)
<223> Conserved domain
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<400> 222

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Met Lys Asn Asn Asn Asn Gly Asp Val Val Asp Asn Glu Val Asn Asn
1               5                   10                  15
Arg Leu Ser Arg Trp His His Asn Ser Ser Arg Ile Ile Arg Val Ser
            20                  25                  30
Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys Val Leu Thr Ser Lys
        35                  40                  45
Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val Ser Thr Ala Leu Gln
    50                  55                  60
Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp Gln Pro Ser Lys Ala
65                  70                  75                  80
Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser Ile Ser Glu Leu Pro
                85                  90                  95
Ser Leu Asn Asn Thr His Phe Pro Thr Asp Asp Glu Asn His Gln Asn
            100                 105                 110
Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu Ser Lys Ser Ala Cys
        115                 120                 125
Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Ser Gly Leu Ser Leu Ser
    130                 135                 140
Arg Ser Glu Leu Arg Asp Lys Ala Arg Glu Arg Ala Arg Glu Arg Thr
145                 150                 155                 160
Ala Lys Glu Thr Lys Glu Arg Asp His Asn His Thr Ser Phe Thr Asp
                165                 170                 175
Leu Leu Asn Ser Gly Ser Asp Pro Val Asn Ser Asn Arg Gln Trp Met
            180                 185                 190
Ala Ser Ala Pro Ser Ser Ser Pro Met Glu Tyr Phe Ser Ser Gly Leu
        195                 200                 205
Ile Leu Gly Ser Gly Gln Gln Thr His Phe Pro Ile Ser Thr Asn Ser
    210                 215                 220
His Pro Phe Ser Ser Ile Ser Asp His His His His His Pro His His
225                 230                 235                 240
Gln His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser Pro Ala
                245                 250                 255
Glu Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser Thr Pro
            260                 265                 270
Ser Gly Ala Gly Ala Ala Val Ser Ala Ala Ser Gly Gly Gly Phe Ser
        275                 280                 285
Gly Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln His Gln
    290                 295                 300
Ser Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser Gly Gly
305                 310                 315                 320
Gly Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His His His
                325                 330                 335
Asn His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn Ser Ser
            340                 345                 350
Glu His Lys Gly Lys Gly Lys Asn
        355                 360
```

<210> 223
<211> 1571
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS

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<222> (428)...(1402)

<400> 223
aggaacagtg aaaggttcgg ttttttgggt ttcgatctga taatcaacaa gaaaaaaggg 60
tttgatttat gtcggctggg tttgaatcga ctgtgatttt gtctttgatt catatctctt 120
ctccgatttc atcatcatct tccccatcat cgtcgtcttt gaaatcttgt cttctcaacg 180
ctcttcactt ctgctgtaat aagcagaggc ttgttctgga gactccttct ctttccatgc 240
gcttaagacc caaaaggact tgttctagtg ttgaagtctt tggggtttt cacataaagc 300
agcaaaagtt ttctttttc atagttcgct gagagttttg agttttgata ccaaaaaagt 360
tttgaccttt tagagtgatt ttttgttctt tctgttttct gggtattttt gaggagtggg 420
tttaaca atg gtt gcg att aga aag gaa cag tct ttg agt ggt gtt agt   469
        Met Val Ala Ile Arg Lys Glu Gln Ser Leu Ser Gly Val Ser
         1               5                  10

agc gag att aag aag aga gct aag aga aac act cta tcg tcc ctt cct   517
Ser Glu Ile Lys Lys Arg Ala Lys Arg Asn Thr Leu Ser Ser Leu Pro
 15                  20                  25                  30

caa gaa acc caa cct ttg agg aaa gtc cgt att att gtg aat gat cct   565
Gln Glu Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro
                 35                  40                  45

tat gct act gat gat tcc tct agt gat gag gaa gag ctt aag gtt cct   613
Tyr Ala Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro
             50                  55                  60

aag cca agg aaa atg aaa cgt atc gtt cgt gag att aac ttt cct tct   661
Lys Pro Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser
         65                  70                  75

atg gaa gtt tct gaa cag cct tct gag agt tct tct cag gac agt act   709
Met Glu Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr
     80                  85                  90

aaa act gat ggc aag ata gct gtg tca gct tct cct gct gtt cct agg   757
Lys Thr Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg
 95                 100                 105                 110

aag aag cct gtt ggt gtt agg caa agg aaa tgg ggg aaa tgg gct gct   805
Lys Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala
                115                 120                 125

gag att aga gat cct att aag aaa act agg act tgg ttg ggt act ttt   853
Glu Ile Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe
            130                 135                 140

gat act ctt gaa gaa gct gct aaa gct tat gat gct aag aag ctt gag   901
Asp Thr Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu
        145                 150                 155

ttt gat gct att gtt gct gga aat gtg tcc act act aaa cgt gat gtt   949
Phe Asp Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val
    160                 165                 170

tct tca tct gag act agc caa tgc tct cgt tct tca cct gtt gtt cct   997
Ser Ser Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro
175                 180                 185                 190
```

```
gtt gag caa gat gac act tct gca tca gct ctc act tgt gtc aac aac    1045
Val Glu Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn
                195                     200                     205

cct gat gac gtc tcg acc gtt gct cca act gct cca act cca aat gtt    1093
Pro Asp Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val
            210                     215                     220

cct gct ggt gga aac aag gaa acg ttg ttc gat ttc gac ttt act aat    1141
Pro Ala Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn
        225                     230                     235

cta cag atc cct gat ttt ggt ttc ttg gca gag gag caa caa gac cta    1189
Leu Gln Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu
    240                     245                     250

gac ttc gat tgt ttc ctc gcg gat gat cag ttt gat gat ttc ggc ttg    1237
Asp Phe Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu
255                     260                     265                     270

ctt gat gac att caa gga ttc gaa gat aac ggt cca agt gcg tta cca    1285
Leu Asp Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro
                275                     280                     285

gat ttc gac ttt gcg gat gtt gaa gat ctt cag cta gct gac tct agt    1333
Asp Phe Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser
            290                     295                     300

ttc ggt ttc ctt gat caa ctt gct cct atc aac atc tct tgc cca tta    1381
Phe Gly Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu
        305                     310                     315

aaa agt ttt gca gct tca tag gatcttgctt agtaatgtta agtgagaaga       1432
Lys Ser Phe Ala Ala Ser  *
    320

gtgttttgtt ttttcgttta tgctttagta atttaagaca tacaaaagtg tgtgttccgg 1492
attgtagtaa gatcttaaga cataaagccg ggttttgcaa ttaggaatcg agttttaatg 1552
aagttttagt ttatgtttg                                              1571

<210> 224
<211> 324
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (109)...(177)
<223> Conserved domain

<400> 224
Met Val Ala Ile Arg Lys Glu Gln Ser Leu Ser Gly Val Ser Ser Glu
 1               5                  10                  15
Ile Lys Lys Arg Ala Lys Arg Asn Thr Leu Ser Ser Leu Pro Gln Glu
            20                  25                  30
Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro Tyr Ala
```

```
        35                      40                      45
Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro Lys Pro
    50                      55                      60
Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser Met Glu
65                      70                      75                      80
Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr Lys Thr
                85                      90                      95
Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg Lys Lys
            100                     105                     110
Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala Glu Ile
        115                     120                     125
Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe Asp Thr
    130                     135                     140
Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu Phe Asp
145                     150                     155                     160
Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val Ser Ser
                165                     170                     175
Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro Val Glu
            180                     185                     190
Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn Pro Asp
        195                     200                     205
Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val Pro Ala
    210                     215                     220
Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn Leu Gln
225                     230                     235                     240
Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu Asp Phe
                245                     250                     255
Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu Leu Asp
            260                     265                     270
Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro Asp Phe
        275                     280                     285
Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser Phe Gly
    290                     295                     300
Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu Lys Ser
305                     310                     315                     320
Phe Ala Ala Ser
```

```
<210> 225
<211> 1152
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (76)...(1008)

<400> 225
gtgaccgaag aaagcaaatt gagactacgc accaactagt cctttggttt gtatcttaag 60
ataaaggttt ctttt atg gac ggt tct tcg ttt ctc gac atc tct ctc gat  111
                 Met Asp Gly Ser Ser Phe Leu Asp Ile Ser Leu Asp
                  1               5                  10

ctc aac acc aat cct ttc tcc gca aaa ctt ccg aag aag gag gtc tca   159
Leu Asn Thr Asn Pro Phe Ser Ala Lys Leu Pro Lys Lys Glu Val Ser
        15                  20                  25
```

```
gtt ttg gct tct act cac tta aag agg aaa tgg ttg gag caa gac gag    207
Val Leu Ala Ser Thr His Leu Lys Arg Lys Trp Leu Glu Gln Asp Glu
     30                  35                  40

agc gca agt gag tta cga gag gag cta aac aga gtt aat tca gag aac    255
Ser Ala Ser Glu Leu Arg Glu Glu Leu Asn Arg Val Asn Ser Glu Asn
 45                  50                  55                  60

aag aag cta aca gag atg tta gct aga gtc tgt gag agc tac aac gaa    303
Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Ser Tyr Asn Glu
                 65                  70                  75

cta cat aat cat ttg gag aag ctt cag agt cgc cag agc cct gaa atc    351
Leu His Asn His Leu Glu Lys Leu Gln Ser Arg Gln Ser Pro Glu Ile
             80                  85                  90

gag cag acc gat ata ccg ata aag aaa aga aaa caa gac ccg gat gag    399
Glu Gln Thr Asp Ile Pro Ile Lys Lys Arg Lys Gln Asp Pro Asp Glu
         95                 100                 105

ttc tta ggc ttt cct att gga ctc agt agt gga aaa act gag aac agc    447
Phe Leu Gly Phe Pro Ile Gly Leu Ser Ser Gly Lys Thr Glu Asn Ser
    110                 115                 120

tcc agc aac gaa gat cat cat cat cat cat cag caa cat gag cag aaa    495
Ser Ser Asn Glu Asp His His His His His Gln Gln His Glu Gln Lys
125                 130                 135                 140

aat cag ctt ctt tca tgt aaa aga cca gtc act gat agc ttc aac aaa    543
Asn Gln Leu Leu Ser Cys Lys Arg Pro Val Thr Asp Ser Phe Asn Lys
                145                 150                 155

gca aaa gtt tcg act gtc tac gtg cct act gaa aca tcg gac aca agc    591
Ala Lys Val Ser Thr Val Tyr Val Pro Thr Glu Thr Ser Asp Thr Ser
            160                 165                 170

ttg aca gtt aaa gat gga ttt caa tgg agg aaa tac gga caa aag gtt    639
Leu Thr Val Lys Asp Gly Phe Gln Trp Arg Lys Tyr Gly Gln Lys Val
        175                 180                 185

aca aga gac aac ccg tca cct aga gct tac ttt aga tgc tcg ttt gca    687
Thr Arg Asp Asn Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ala
    190                 195                 200

ccg tct tgt cca gta aaa aag aag gta caa cgc agc gca gag gat cca    735
Pro Ser Cys Pro Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro
205                 210                 215                 220

tct tta ctt gta gcg aca tac gaa ggg acg cat aac cac ttg ggt cca    783
Ser Leu Leu Val Ala Thr Tyr Glu Gly Thr His Asn His Leu Gly Pro
                225                 230                 235

aat gct tct gaa ggg gat gct aca agc cag ggt ggg tca agc aca gtg    831
Asn Ala Ser Glu Gly Asp Ala Thr Ser Gln Gly Gly Ser Ser Thr Val
            240                 245                 250
```

```
act ttg gat ctg gtt aat ggc tgt cat aga cta gcg ttg gag aaa aa
Thr Leu Asp Leu Val Asn Gly Cys His Arg Leu Ala Leu Glu Lys Asn
        255                 260                 265

gaa agg gat aat acg atg caa gag gtt ctg att caa caa atg gcg tca    927
Glu Arg Asp Asn Thr Met Gln Glu Val Leu Ile Gln Gln Met Ala Ser
    270                 275                 280

tcg tta aca aaa gat tcg aaa ttt aca gct gct ctt gct gct gct ata    975
Ser Leu Thr Lys Asp Ser Lys Phe Thr Ala Ala Leu Ala Ala Ala Ile
285                 290                 295                 300

tct ggg agg tta atg gag caa tct aga aca tga acgtttttag tgaatgtatt 1028
Ser Gly Arg Leu Met Glu Gln Ser Arg Thr  *
                305                 310

gtttttgttt gtttagaatg attcttcgtt ttcgaattgt gtctttcgat taggagataa 1088
aagatgtata taaatattat aagtagatga agaaatcgta taagtaaaaa aaaaaaaaaa 1148
aaaa                                                              1152

<210> 226
<211> 310
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (176)...(233)
<223> Conserved domain

<400> 226
Met Asp Gly Ser Ser Phe Leu Asp Ile Ser Leu Asp Leu Asn Thr Asn
 1               5                  10                  15
Pro Phe Ser Ala Lys Leu Pro Lys Lys Glu Val Ser Val Leu Ala Ser
            20                  25                  30
Thr His Leu Lys Arg Lys Trp Leu Glu Gln Asp Glu Ser Ala Ser Glu
        35                  40                  45
Leu Arg Glu Glu Leu Asn Arg Val Asn Ser Glu Asn Lys Lys Leu Thr
    50                  55                  60
Glu Met Leu Ala Arg Val Cys Glu Ser Tyr Asn Glu Leu His Asn His
65                  70                  75                  80
Leu Glu Lys Leu Gln Ser Arg Gln Ser Pro Glu Ile Glu Gln Thr Asp
                85                  90                  95
Ile Pro Ile Lys Lys Arg Lys Gln Asp Pro Asp Glu Phe Leu Gly Phe
            100                 105                 110
Pro Ile Gly Leu Ser Ser Gly Lys Thr Glu Asn Ser Ser Ser Asn Glu
        115                 120                 125
Asp His His His His His Gln Gln His Glu Gln Lys Asn Gln Leu Leu
    130                 135                 140
Ser Cys Lys Arg Pro Val Thr Asp Ser Phe Asn Lys Ala Lys Val Ser
145                 150                 155                 160
Thr Val Tyr Val Pro Thr Glu Thr Ser Asp Thr Ser Leu Thr Val Lys
                165                 170                 175
Asp Gly Phe Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp Asn
            180                 185                 190
Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ala Pro Ser Cys Pro
        195                 200                 205
```

```
Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro Ser Leu Leu Va
    210                 215                 220
Ala Thr Tyr Glu Gly Thr His Asn His Leu Gly Pro Asn Ala Ser Glu
225                 230                 235                 240
Gly Asp Ala Thr Ser Gln Gly Gly Ser Ser Thr Val Thr Leu Asp Leu
                245                 250                 255
Val Asn Gly Cys His Arg Leu Ala Leu Glu Lys Asn Glu Arg Asp Asn
            260                 265                 270
Thr Met Gln Glu Val Leu Ile Gln Gln Met Ala Ser Ser Leu Thr Lys
        275                 280                 285
Asp Ser Lys Phe Thr Ala Ala Leu Ala Ala Ala Ile Ser Gly Arg Leu
    290                 295                 300
Met Glu Gln Ser Arg Thr
305                 310


<210> 227
<211> 715
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (20)...(703)

<400> 227
caattttaaa ccggtcatt atg atg tct act gta ccg gcc ttt acc ttt act   52
                     Met Met Ser Thr Val Pro Ala Phe Thr Phe Thr
                      1               5                  10

gaa ccg ggt ttg gtt aac caa tta tcg gat ttc cag acc gga ttc act   100
Glu Pro Gly Leu Val Asn Gln Leu Ser Asp Phe Gln Thr Gly Phe Thr
            15                  20                  25

cct tgg gaa ttg aac tgc tcc gat ctc ttc tct aca atc cat ctc gaa   148
Pro Trp Glu Leu Asn Cys Ser Asp Leu Phe Ser Thr Ile His Leu Glu
        30                  35                  40

ccg gtc gta ccg agt cct tgt tct ggt gaa tcc gat gcc ggt tct gtc   196
Pro Val Val Pro Ser Pro Cys Ser Gly Glu Ser Asp Ala Gly Ser Val
    45                  50                  55

aaa att aac acc gat ttt aac ggt ttt gac gaa tcg tgt atc ggt tcc   244
Lys Ile Asn Thr Asp Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser
 60                  65                  70                  75

atc aaa act aac tcc ggt tct gat gat tcc aac ctt ttc cac ggc gta   292
Ile Lys Thr Asn Ser Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val
                80                  85                  90

ccg agt cct caa tcc gac gaa ttg gac tca aaa aac acg aaa atc cga   340
Pro Ser Pro Gln Ser Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg
            95                 100                 105

agt aac gcc acg aat cat aac cgg aac aaa ttg aac cgg tcg gtt ttg   388
Ser Asn Ala Thr Asn His Asn Arg Asn Lys Leu Asn Arg Ser Val Leu
        110                 115                 120
```

```
cag gtg act gac gac cgt aaa cgc aaa cgg atg gaa tca aac cga gaa      436
Gln Val Thr Asp Asp Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu
    125                 130                 135

tca gcg aag cgg tcg agg atg cgt aaa caa aga cac att gat aat tta      484
Ser Ala Lys Arg Ser Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu
140                 145                 150                 155

aaa gac gaa gca aat cgt ctc ggt tta gaa aac cgg gaa ctc gca aac      532
Lys Asp Glu Ala Asn Arg Leu Gly Leu Glu Asn Arg Glu Leu Ala Asn
                160                 165                 170

cgg ctt cga att gtt ttg tac aac atc gca tta atg tgt acg gac aac      580
Arg Leu Arg Ile Val Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn
            175                 180                 185

aat cag ctt ttg tcg gaa caa gag att ctc aga cgg aga ttc ttg gag      628
Asn Gln Leu Leu Ser Glu Gln Glu Ile Leu Arg Arg Arg Phe Leu Glu
        190                 195                 200

atg agg cag att ttg att ttc aga cag ctt cag ctg aat cca tca ttg      676
Met Arg Gln Ile Leu Ile Phe Arg Gln Leu Gln Leu Asn Pro Ser Leu
    205                 210                 215

atc atc aat cat cat cat atg att tga aagaaaaaaa aa                    715
Ile Ile Asn His His His Met Ile  *
220                 225


<210> 228
<211> 227
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (129)...(180)
<223> Conserved domain

<400> 228
Met Met Ser Thr Val Pro Ala Phe Thr Phe Thr Glu Pro Gly Leu Val
 1               5                  10                  15
Asn Gln Leu Ser Asp Phe Gln Thr Gly Phe Thr Pro Trp Glu Leu Asn
            20                  25                  30
Cys Ser Asp Leu Phe Ser Thr Ile His Leu Glu Pro Val Val Pro Ser
        35                  40                  45
Pro Cys Ser Gly Glu Ser Asp Ala Gly Ser Val Lys Ile Asn Thr Asp
    50                  55                  60
Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser Ile Lys Thr Asn Ser
65                  70                  75                  80
Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val Pro Ser Pro Gln Ser
                85                  90                  95
Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg Ser Asn Ala Thr Asn
            100                 105                 110
His Asn Arg Asn Lys Leu Asn Arg Ser Val Leu Gln Val Thr Asp Asp
        115                 120                 125
```

```
Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Se
    130                 135                 140
Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu Lys Asp Glu Ala Asn
145                 150                 155                 160
Arg Leu Gly Leu Glu Asn Arg Glu Leu Ala Asn Arg Leu Arg Ile Val
                165                 170                 175
Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn Asn Gln Leu Leu Ser
            180                 185                 190
Glu Gln Glu Ile Leu Arg Arg Arg Phe Leu Glu Met Arg Gln Ile Leu
        195                 200                 205
Ile Phe Arg Gln Leu Gln Leu Asn Pro Ser Leu Ile Ile Asn His His
    210                 215                 220
His Met Ile
225


<210> 229
<211> 1011
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (57)...(983)

<400> 229
cgtctaccta ctatggtctg gagattagtt cgtttattga actaatgttt tagaca atg 59
                                                              Met
                                                               1

caa gag ttc cat agt agc aaa gat tca ttg cct tgt cct gca act tct    107
Gln Glu Phe His Ser Ser Lys Asp Ser Leu Pro Cys Pro Ala Thr Ser
            5                  10                  15

tgg gat aac tct gtc ttc acc aac tca aat gtc caa gga tca tca tcc    155
Trp Asp Asn Ser Val Phe Thr Asn Ser Asn Val Gln Gly Ser Ser Ser
        20                  25                  30

ttg acc gat aac aac act tta agc ttg aca atg gag atg aaa caa act    203
Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln Thr
    35                  40                  45

ggt ttt caa atg cag cac tat gat tcc tcc tct act caa tcc act gga    251
Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr Gly
50                  55                  60                  65

gga gaa tca tat agt gaa gtt gct agc tta agt gaa cct act aat cgt    299
Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn Arg
                70                  75                  80

tat ggc cac aac att gtt gtc act cat ctc tca ggt tac aaa gaa aac    347
Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu Asn
            85                  90                  95

ccg gaa aat cct att gga agt cat tcg ata tca aag gtg tct caa gat    395
Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln Asp
        100                 105                 110
```

```
tca gtg gtt ctt cct att gag gcg gct tct tgg cct tta cac ggc aat    443
Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly Asn
    115                 120                 125

gta acg cca cat ttc aat ggt ttc ttg tct ttt cct tat gca tca caa    491
Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser Gln
130                 135                 140                 145

cac acg gtg cag cat cct caa atc aga ggg ttg gtt ccg tct aga atg    539
His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg Met
                150                 155                 160

cct ttg cct cac aac att cca gag aac gaa cca att ttc gtc aat gca    587
Pro Leu Pro His Asn Ile Pro Glu Asn Glu Pro Ile Phe Val Asn Ala
            165                 170                 175

aaa cag tac caa gcc att ctc cgc cgc aga gag cgc cgt gca aag ctt    635
Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys Leu
        180                 185                 190

gaa gct cag aac aag ctc atc aaa gtc cgc aaa cca tat ctt cac gag    683
Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His Glu
    195                 200                 205

tcg cgg cac ctc cat gca cta aag aga gtt aga ggc tct ggt gga cgt    731
Ser Arg His Leu His Ala Leu Lys Arg Val Arg Gly Ser Gly Gly Arg
210                 215                 220                 225

ttc ctc aac aca aag aag cat caa gaa tca aat tcc tca cta tct cct    779
Phe Leu Asn Thr Lys Lys His Gln Glu Ser Asn Ser Ser Leu Ser Pro
                230                 235                 240

cca ttc ttg att cca cct cat gtc ttc aag aac tct cca gga aag ttc    827
Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys Phe
            245                 250                 255

cgg caa atg gac att tca agg ggt ggg gtt gtg tct agt gtc tcg aca    875
Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser Thr
        260                 265                 270

aca tct tgc tcg gac ata acc ggg aac aac aac gac atg ttc cag caa    923
Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln Gln
    275                 280                 285

aac cca caa ttc agg ttc tca ggt tat cca tca aac cac cat gtc tca    971
Asn Pro Gln Phe Arg Phe Ser Gly Tyr Pro Ser Asn His His Val Ser
290                 295                 300                 305

gtc ctc atg tga gagagctccc gcaagtggtg gatgaggc                     1011
Val Leu Met  *


<210> 230
<211> 308
<212> PRT
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<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (174)...(226)
<223> Conserved domain

<400> 230
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Met Gln Glu Phe His Ser Ser Lys Asp Ser Leu Pro Cys Pro Ala Thr
 1               5                  10                  15
Ser Trp Asp Asn Ser Val Phe Thr Asn Ser Asn Val Gln Gly Ser Ser
            20                  25                  30
Ser Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln
        35                  40                  45
Thr Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr
    50                  55                  60
Gly Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn
65                  70                  75                  80
Arg Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu
                85                  90                  95
Asn Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln
            100                 105                 110
Asp Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly
        115                 120                 125
Asn Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser
    130                 135                 140
Gln His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg
145                 150                 155                 160
Met Pro Leu Pro His Asn Ile Pro Glu Asn Glu Pro Ile Phe Val Asn
                165                 170                 175
Ala Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys
            180                 185                 190
Leu Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His
        195                 200                 205
Glu Ser Arg His Leu His Ala Leu Lys Arg Val Arg Gly Ser Gly Gly
    210                 215                 220
Arg Phe Leu Asn Thr Lys Lys His Gln Glu Ser Asn Ser Ser Leu Ser
225                 230                 235                 240
Pro Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys
                245                 250                 255
Phe Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser
            260                 265                 270
Thr Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln
        275                 280                 285
Gln Asn Pro Gln Phe Arg Phe Ser Gly Tyr Pro Ser Asn His His Val
    290                 295                 300
Ser Val Leu Met
305
```

<210> 231
<211> 914
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS

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<222> (37)...(672)

<400> 231
aaatcatcag atagaaggaa atattctgat tgagag atg gct cgt gga aag att    54
                                        Met Ala Arg Gly Lys Ile
                                         1               5

cag ctt aag agg att gag aac ccg gtt cac aga caa gtg act ttt tgc   102
Gln Leu Lys Arg Ile Glu Asn Pro Val His Arg Gln Val Thr Phe Cys
            10                  15                  20

aag agg aga act ggt ctt ctc aag aag gct aag gag ctc tct gtg ctc   150
Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala Lys Glu Leu Ser Val Leu
        25                  30                  35

tgt gat gcc gag atc ggt gtt gtg atc ttc tct cct cag ggc aag ctc   198
Cys Asp Ala Glu Ile Gly Val Val Ile Phe Ser Pro Gln Gly Lys Leu
    40                  45                  50

ttt gag ctc gct act aaa gga aca atg gag gga atg att gat aag tac   246
Phe Glu Leu Ala Thr Lys Gly Thr Met Glu Gly Met Ile Asp Lys Tyr
 55                  60                  65                  70

atg aag tgt act ggt ggt ggt cgt ggt tct tct tct gct act ttt act   294
Met Lys Cys Thr Gly Gly Gly Arg Gly Ser Ser Ser Ala Thr Phe Thr
                 75                  80                  85

gct caa gaa caa ctt caa cca cca aat ctt gat ccg aaa gat gag atc   342
Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu Asp Pro Lys Asp Glu Ile
            90                  95                  100

aac gtg ctt aag caa gag att gag atg ctt cag aaa ggg ata agc tat   390
Asn Val Leu Lys Gln Glu Ile Glu Met Leu Gln Lys Gly Ile Ser Tyr
        105                 110                 115

atg ttt gga gga gga gat ggg gct atg aat ctt gaa gaa ctt ctt ttg   438
Met Phe Gly Gly Gly Asp Gly Ala Met Asn Leu Glu Glu Leu Leu Leu
    120                 125                 130

ctt gag aag cat ctt gag tat tgg att tct cag att cgc tct gct aag   486
Leu Glu Lys His Leu Glu Tyr Trp Ile Ser Gln Ile Arg Ser Ala Lys
135                 140                 145                 150

atg gat gtt atg ctt caa gaa att cag tca ttg agg aac aag gaa gga   534
Met Asp Val Met Leu Gln Glu Ile Gln Ser Leu Arg Asn Lys Glu Gly
                155                 160                 165

gtc ctc aaa aac acc aac aag tat ctc ctc gac aag ata gag gaa aac   582
Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu Asp Lys Ile Glu Glu Asn
            170                 175                 180

aac aat agc ata tta gat gct aac ttc gca gtc atg gag aca aac tat   630
Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala Val Met Glu Thr Asn Tyr
        185                 190                 195

tcc tat ccg cta aca atg cca agt gaa ata ttt cag ttc tag           672
Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile Phe Gln Phe  *
```

200 205 210

accatagggt atttgaagac tatgtctcac gaatttaaat aaccttggta agtataatat 732
agtgttgtta aatcacacat aattaaaata aagcctgtgg aacttcgcta ggcagttgaa 792
aatctatccg tatgttttat cctcttgttt tacatttgtt ggtgtgaaga tgaaatgact 852
gcaagtgtgg tgtgtactta taactctttc tactttctat ctatgttttg aatttatgga 912
tt 914

<210> 232
<211> 211
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (2)...(57)
<223> Conserved domain

<400> 232
Met Ala Arg Gly Lys Ile Gln Leu Lys Arg Ile Glu Asn Pro Val His
1 5 10 15
Arg Gln Val Thr Phe Cys Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala
20 25 30
Lys Glu Leu Ser Val Leu Cys Asp Ala Glu Ile Gly Val Val Ile Phe
35 40 45
Ser Pro Gln Gly Lys Leu Phe Glu Leu Ala Thr Lys Gly Thr Met Glu
50 55 60
Gly Met Ile Asp Lys Tyr Met Lys Cys Thr Gly Gly Gly Arg Gly Ser
65 70 75 80
Ser Ser Ala Thr Phe Thr Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu
85 90 95
Asp Pro Lys Asp Glu Ile Asn Val Leu Lys Gln Glu Ile Glu Met Leu
100 105 110
Gln Lys Gly Ile Ser Tyr Met Phe Gly Gly Gly Asp Gly Ala Met Asn
115 120 125
Leu Glu Glu Leu Leu Leu Leu Glu Lys His Leu Glu Tyr Trp Ile Ser
130 135 140
Gln Ile Arg Ser Ala Lys Met Asp Val Met Leu Gln Glu Ile Gln Ser
145 150 155 160
Leu Arg Asn Lys Glu Gly Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu
165 170 175
Asp Lys Ile Glu Glu Asn Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala
180 185 190
Val Met Glu Thr Asn Tyr Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile
195 200 205
Phe Gln Phe
210

<210> 233
<211> 1276
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (47)...(1150)

<400> 233

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taatccgatt cgtcttcatc tgattccctc ccttccgaga ataata atg tac ccg      55
                                                    Met Tyr Pro
                                                    1

cca cct ccc tca agc atc tac gct cct ccg atg ctg gtg aat tgc tcc     103
Pro Pro Pro Ser Ser Ile Tyr Ala Pro Pro Met Leu Val Asn Cys Ser
    5                   10                  15

ggt tgc cgg acg cct ctc cag ctc cca tcc ggc gcc cga tct att cgc     151
Gly Cys Arg Thr Pro Leu Gln Leu Pro Ser Gly Ala Arg Ser Ile Arg
20                  25                  30                  35

tgc gct ctc tgc cag gct gtt act cat atc gcc gac cct cgc acc gcc     199
Cys Ala Leu Cys Gln Ala Val Thr His Ile Ala Asp Pro Arg Thr Ala
                40                  45                  50

cct cct ccg caa cct tcc tcc gcc cct tct ccg cct ccc caa atc cac     247
Pro Pro Pro Gln Pro Ser Ser Ala Pro Ser Pro Pro Pro Gln Ile His
            55                  60                  65

gcg cct ccc ggt cag ctg cct cac ccc cat ggc agg aag agg gcc gtg     295
Ala Pro Pro Gly Gln Leu Pro His Pro His Gly Arg Lys Arg Ala Val
        70                  75                  80

atc tgt ggc atc tcg tat cgt ttc tct cgc cac gag ctc aaa ggc tgc     343
Ile Cys Gly Ile Ser Tyr Arg Phe Ser Arg His Glu Leu Lys Gly Cys
    85                  90                  95

atc aac gac gcc aag tgc atg cgt cac ctt ctc atc aac aaa ttc aaa     391
Ile Asn Asp Ala Lys Cys Met Arg His Leu Leu Ile Asn Lys Phe Lys
100                 105                 110                 115

ttc tcc cca gat tca att ctc atg ctt acc gag gaa gaa act gat cca     439
Phe Ser Pro Asp Ser Ile Leu Met Leu Thr Glu Glu Glu Thr Asp Pro
                120                 125                 130

tat cgt atc ccg acc aag caa aac atg agg atg gca ttg tat tgg ctc     487
Tyr Arg Ile Pro Thr Lys Gln Asn Met Arg Met Ala Leu Tyr Trp Leu
            135                 140                 145

gta cag gga tgc aca gca ggc gac tca ctt gtc ttc cac tac tct ggt     535
Val Gln Gly Cys Thr Ala Gly Asp Ser Leu Val Phe His Tyr Ser Gly
        150                 155                 160

cat ggt tcg cgt caa aga aac tac aac ggt gat gaa gtt gat ggc tat     583
His Gly Ser Arg Gln Arg Asn Tyr Asn Gly Asp Glu Val Asp Gly Tyr
    165                 170                 175

gat gaa aca ctc tgt cct ctg gat ttt gaa act cag ggg atg att gta     631
Asp Glu Thr Leu Cys Pro Leu Asp Phe Glu Thr Gln Gly Met Ile Val
180                 185                 190                 195

gac gat gag atc aac gca acc att gta cgc cct ctt cca cat ggt gtc     679
Asp Asp Glu Ile Asn Ala Thr Ile Val Arg Pro Leu Pro His Gly Val
                200                 205                 210
```

```
aag ctc cat tca att atc gat gct tgc cat agt ggt acc gtt ctg gat     727
Lys Leu His Ser Ile Ile Asp Ala Cys His Ser Gly Thr Val Leu Asp
            215                 220                 225

tta ccc ttc cta tgc aga atg aac aga gct ggg cag tat gtg tgg gag     775
Leu Pro Phe Leu Cys Arg Met Asn Arg Ala Gly Gln Tyr Val Trp Glu
        230                 235                 240

gat cat cgg cct agg tca ggt ttg tgg aaa gga act gct ggt gga gaa     823
Asp His Arg Pro Arg Ser Gly Leu Trp Lys Gly Thr Ala Gly Gly Glu
    245                 250                 255

gcc att tca att agt gga tgt gat gat gat cag act tcg gcc gac aca     871
Ala Ile Ser Ile Ser Gly Cys Asp Asp Asp Gln Thr Ser Ala Asp Thr
260                 265                 270                 275

tca gcg ctg tcg aag atc acg tct acg ggt gct atg act ttc tgt ttt     919
Ser Ala Leu Ser Lys Ile Thr Ser Thr Gly Ala Met Thr Phe Cys Phe
                280                 285                 290

att caa gca att gaa cgc agc gca caa ggc aca acc tat gga agc ctt     967
Ile Gln Ala Ile Glu Arg Ser Ala Gln Gly Thr Thr Tyr Gly Ser Leu
            295                 300                 305

ctg aat tct atg cgc acc aca ata agg aat aca ggg aat gat ggt ggt     1015
Leu Asn Ser Met Arg Thr Thr Ile Arg Asn Thr Gly Asn Asp Gly Gly
        310                 315                 320

ggt agt ggt gga gtt gtg acg act gtg ctg agc atg ctt ctg aca ggg     1063
Gly Ser Gly Gly Val Val Thr Thr Val Leu Ser Met Leu Leu Thr Gly
    325                 330                 335

gga agt gcg att ggg gga tta aga cag gag cct caa ctg act gct tgc     1111
Gly Ser Ala Ile Gly Gly Leu Arg Gln Glu Pro Gln Leu Thr Ala Cys
340                 345                 350                 355

caa aca ttc gat gtc tat gca aag cct ttc act ctc tag taaaggacaa      1160
Gln Thr Phe Asp Val Tyr Ala Lys Pro Phe Thr Leu  *
                360                 365

gtcactttttt atgtatagcg agtgtgattt gagaatccgt ccatataacc accttttgtt 1220
tcttattttt atttttcttt caaaagaata aaggaaaaca ttgatttggt gattcg      1276
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<210> 234
<211> 367
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (18)...(39)
<223> Conserved domain

<400> 234

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Met Tyr Pro Pro Pro Pro Ser Ser Ile Tyr Ala Pro Pro Met Leu Val
 1               5                  10                  15
```

```
Asn Cys Ser Gly Cys Arg Thr Pro Leu Gln Leu Pro Ser Gly Ala Ar
            20                  25                  30
Ser Ile Arg Cys Ala Leu Cys Gln Ala Val Thr His Ile Ala Asp Pro
        35                  40                  45
Arg Thr Ala Pro Pro Pro Gln Pro Ser Ser Ala Pro Ser Pro Pro Pro
    50                  55                  60
Gln Ile His Ala Pro Pro Gly Gln Leu Pro His Pro His Gly Arg Lys
65                  70                  75                  80
Arg Ala Val Ile Cys Gly Ile Ser Tyr Arg Phe Ser Arg His Glu Leu
                85                  90                  95
Lys Gly Cys Ile Asn Asp Ala Lys Cys Met Arg His Leu Leu Ile Asn
            100                 105                 110
Lys Phe Lys Phe Ser Pro Asp Ser Ile Leu Met Leu Thr Glu Glu Glu
        115                 120                 125
Thr Asp Pro Tyr Arg Ile Pro Thr Lys Gln Asn Met Arg Met Ala Leu
    130                 135                 140
Tyr Trp Leu Val Gln Gly Cys Thr Ala Gly Asp Ser Leu Val Phe His
145                 150                 155                 160
Tyr Ser Gly His Gly Ser Arg Gln Arg Asn Tyr Asn Gly Asp Glu Val
                165                 170                 175
Asp Gly Tyr Asp Glu Thr Leu Cys Pro Leu Asp Phe Glu Thr Gln Gly
            180                 185                 190
Met Ile Val Asp Asp Glu Ile Asn Ala Thr Ile Val Arg Pro Leu Pro
        195                 200                 205
His Gly Val Lys Leu His Ser Ile Ile Asp Ala Cys His Ser Gly Thr
    210                 215                 220
Val Leu Asp Leu Pro Phe Leu Cys Arg Met Asn Arg Ala Gly Gln Tyr
225                 230                 235                 240
Val Trp Glu Asp His Arg Pro Arg Ser Gly Leu Trp Lys Gly Thr Ala
                245                 250                 255
Gly Gly Glu Ala Ile Ser Ile Ser Gly Cys Asp Asp Asp Gln Thr Ser
            260                 265                 270
Ala Asp Thr Ser Ala Leu Ser Lys Ile Thr Ser Thr Gly Ala Met Thr
        275                 280                 285
Phe Cys Phe Ile Gln Ala Ile Glu Arg Ser Ala Gln Gly Thr Thr Tyr
    290                 295                 300
Gly Ser Leu Leu Asn Ser Met Arg Thr Thr Ile Arg Asn Thr Gly Asn
305                 310                 315                 320
Asp Gly Gly Gly Ser Gly Gly Val Val Thr Thr Val Leu Ser Met Leu
                325                 330                 335
Leu Thr Gly Gly Ser Ala Ile Gly Gly Leu Arg Gln Glu Pro Gln Leu
            340                 345                 350
Thr Ala Cys Gln Thr Phe Asp Val Tyr Ala Lys Pro Phe Thr Leu
        355                 360                 365
```

<210> 235
<211> 2545
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (103)...(2322)

<400> 235
acatatgttt taaattcttt gtctgaatct tacaggatcc gagagagaga gctctggaac 60

```
gatattaaca tatatcatga agaaaaagat tgaagtattg at atg gga ata act
                                                Met Gly Ile Thr
                                                1

aaa act tct cct aat act aca att ctc ttg aag act ttt cac aat aat      162
Lys Thr Ser Pro Asn Thr Thr Ile Leu Leu Lys Thr Phe His Asn Asn
 5                  10                  15                  20

tct atg tcc caa gat tat cat cat cat cat cat cat aat caa cac caa      210
Ser Met Ser Gln Asp Tyr His His His His His His Asn Gln His Gln
                25                  30                  35

gga ggt atc ttc aac ttc tct aat gga ttc gac cga tca gat tct ccc      258
Gly Gly Ile Phe Asn Phe Ser Asn Gly Phe Asp Arg Ser Asp Ser Pro
            40                  45                  50

aat tta aca act cag cag aag caa gag cat caa agg gta gag atg gac      306
Asn Leu Thr Thr Gln Gln Lys Gln Glu His Gln Arg Val Glu Met Asp
        55                  60                  65

gag gaa tct tca gtc gcc gga ggt agg att ccg gtc tac gaa tca gcc      354
Glu Glu Ser Ser Val Ala Gly Gly Arg Ile Pro Val Tyr Glu Ser Ala
    70                  75                  80

ggt atg tta tcc gaa atg ttt aat ttc ccc gga agc agc ggt gga gga      402
Gly Met Leu Ser Glu Met Phe Asn Phe Pro Gly Ser Ser Gly Gly Gly
85                  90                  95                  100

aga gat ctc gac ctc ggc caa tct ttc cgg tca aat agg cag ttg ctt      450
Arg Asp Leu Asp Leu Gly Gln Ser Phe Arg Ser Asn Arg Gln Leu Leu
                105                 110                 115

gag gag caa cat cag aat att ccg gct atg aat gct acg gat tca gcc      498
Glu Glu Gln His Gln Asn Ile Pro Ala Met Asn Ala Thr Asp Ser Ala
            120                 125                 130

acc gcc acc gca gcc gcc atg cag tta ttc ttg atg aat cca ccg cca      546
Thr Ala Thr Ala Ala Ala Met Gln Leu Phe Leu Met Asn Pro Pro Pro
        135                 140                 145

ccg caa caa cca ccg tct ccg tca tcc aca act tcc cca agg agc cac      594
Pro Gln Gln Pro Pro Ser Pro Ser Ser Thr Thr Ser Pro Arg Ser His
    150                 155                 160

cac aat tct tca act ctt cac atg tta ctt cca agt cca tcc acc aac      642
His Asn Ser Ser Thr Leu His Met Leu Leu Pro Ser Pro Ser Thr Asn
165                 170                 175                 180

aca act cac cat cag aac tac act aat cat atg tct atg cat cag ctt      690
Thr Thr His His Gln Asn Tyr Thr Asn His Met Ser Met His Gln Leu
                185                 190                 195

cca cat cag cat cac caa cag ata tcg acg tgg cag tct tct ccc gat      738
Pro His Gln His His Gln Gln Ile Ser Thr Trp Gln Ser Ser Pro Asp
            200                 205                 210

cat cat cat cat cat cac aac agc caa acg gag att ggg acc gtc cac      786
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His His His His His His Asn Ser Gln Thr Glu Ile Gly Thr Val Hi
215 220 225

gtg gaa aac agc gga gga cac gga gga caa ggc ttg tcc tta tct ctc 834
Val Glu Asn Ser Gly Gly His Gly Gly Gln Gly Leu Ser Leu Ser Leu
230 235 240

tca tcg tct tta gag gct gca gca aaa gcg gaa gag tat aga aac att 882
Ser Ser Ser Leu Glu Ala Ala Ala Lys Ala Glu Glu Tyr Arg Asn Ile
245 250 255 260

tac tac gga gcc aat tct tct aac gca tca cct cat cat caa tac aat 930
Tyr Tyr Gly Ala Asn Ser Ser Asn Ala Ser Pro His His Gln Tyr Asn
265 270 275

caa ttc aag act ctt ctt gct aat tct tct caa cat cac cat caa gta 978
Gln Phe Lys Thr Leu Leu Ala Asn Ser Ser Gln His His His Gln Val
280 285 290

tta aac caa ttc cga tca tct ccg gct gct tct tcc tct tcc atg gca 1026
Leu Asn Gln Phe Arg Ser Ser Pro Ala Ala Ser Ser Ser Ser Met Ala
295 300 305

gcg gtc aat atc tta aga aac tcg agg tac aca acg gcc gcg caa gag 1074
Ala Val Asn Ile Leu Arg Asn Ser Arg Tyr Thr Thr Ala Ala Gln Glu
310 315 320

ttg ttg gaa gag ttt tgt agt gtt gga aga gga ttt ttg aag aag aac 1122
Leu Leu Glu Glu Phe Cys Ser Val Gly Arg Gly Phe Leu Lys Lys Asn
325 330 335 340

aaa ctt ggg aac agc tca aac cct aat act tgc ggt ggt gat ggt ggt 1170
Lys Leu Gly Asn Ser Ser Asn Pro Asn Thr Cys Gly Gly Asp Gly Gly
345 350 355

ggc agc tct cct tcg tcg gcc gga gca aac aag gag cat cct cct tta 1218
Gly Ser Ser Pro Ser Ser Ala Gly Ala Asn Lys Glu His Pro Pro Leu
360 365 370

tcg gcg tct gat cgg att gag cat caa aga agg aaa gtg aaa cta ctc 1266
Ser Ala Ser Asp Arg Ile Glu His Gln Arg Arg Lys Val Lys Leu Leu
375 380 385

acc atg ctt gaa gag gtg gac cga cgg tac aac cat tac tgc gag caa 1314
Thr Met Leu Glu Glu Val Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln
390 395 400

atg cag atg gtt gtg aac tct ttc gac ata gta atg ggc cac ggt gcg 1362
Met Gln Met Val Val Asn Ser Phe Asp Ile Val Met Gly His Gly Ala
405 410 415 420

gca tta ccg tac acc gca ttg gct caa aaa gct atg tca aga cat ttt 1410
Ala Leu Pro Tyr Thr Ala Leu Ala Gln Lys Ala Met Ser Arg His Phe
425 430 435

aga tgc ctt aaa gat gca gtt gcg gct cag ctt aag cag agt tgc gaa 1458
Arg Cys Leu Lys Asp Ala Val Ala Ala Gln Leu Lys Gln Ser Cys Glu

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            440                   445                   450

ctt ctt ggg gac aaa gat gca gcg gga atc tct tct tcc ggg tta aca      1506
Leu Leu Gly Asp Lys Asp Ala Ala Gly Ile Ser Ser Ser Gly Leu Thr
        455                 460                 465

aaa ggt gaa act ccg cgt ttg cgt ttg cta gag caa agt ttg cgt cag      1554
Lys Gly Glu Thr Pro Arg Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln
    470                 475                 480

caa cgt gcg ttt cat caa atg ggt atg atg gaa caa gaa gct tgg cgg      1602
Gln Arg Ala Phe His Gln Met Gly Met Met Glu Gln Glu Ala Trp Arg
485                 490                 495                 500

cca caa cgc ggt ttg cct gaa cgc tcc gtc aat ata ctt aga gct tgg      1650
Pro Gln Arg Gly Leu Pro Glu Arg Ser Val Asn Ile Leu Arg Ala Trp
                505                 510                 515

ctc ttc gaa cat ttc ctt cac ccg tat cca agt gat gca gat aaa cac      1698
Leu Phe Glu His Phe Leu His Pro Tyr Pro Ser Asp Ala Asp Lys His
            520                 525                 530

cta ttg gct cga cag act ggt tta tcc aga aat cag gta tca aat tgg      1746
Leu Leu Ala Arg Gln Thr Gly Leu Ser Arg Asn Gln Val Ser Asn Trp
        535                 540                 545

ttc ata aat gct agg gtt cgt tta tgg aaa cca atg gtg gaa gaa atg      1794
Phe Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met
    550                 555                 560

tac caa caa gaa tca aaa gaa aga gaa aga gaa gag gaa tta gaa gag      1842
Tyr Gln Gln Glu Ser Lys Glu Arg Glu Arg Glu Glu Glu Leu Glu Glu
565                 570                 575                 580

aac gaa gaa gat caa gaa aca aaa aac agc aac gac gac aag agc aca      1890
Asn Glu Glu Asp Gln Glu Thr Lys Asn Ser Asn Asp Asp Lys Ser Thr
                585                 590                 595

aaa tcc aac aac aat gaa agc aac ttc act gcc gtt cgg acc act tca      1938
Lys Ser Asn Asn Asn Glu Ser Asn Phe Thr Ala Val Arg Thr Thr Ser
            600                 605                 610

caa act cca acg aca acc gca cca gac gca tca gac gca gac gca gca      1986
Gln Thr Pro Thr Thr Thr Ala Pro Asp Ala Ser Asp Ala Asp Ala Ala
        615                 620                 625

gta gcg aca ggc cac cgt cta aga tcc aac att aat gct tac gaa aac      2034
Val Ala Thr Gly His Arg Leu Arg Ser Asn Ile Asn Ala Tyr Glu Asn
    630                 635                 640

gac gct tca tca ctt cta ctc cct tcc tct tat tcc aac gcc gcc gct      2082
Asp Ala Ser Ser Leu Leu Leu Pro Ser Ser Tyr Ser Asn Ala Ala Ala
645                 650                 655                 660

cct gcc gct gtt tct gac gac ttg aat tct cgt tac ggt ggc tca gac      2130
Pro Ala Ala Val Ser Asp Asp Leu Asn Ser Arg Tyr Gly Gly Ser Asp
                665                 670                 675
```

gcg ttt tcc gcc gtt gcc acg tgt caa caa agt gta ggt ggg ttc gat 2178
Ala Phe Ser Ala Val Ala Thr Cys Gln Gln Ser Val Gly Gly Phe Asp
680 685 690

gat gct gac atg gat ggt gtt aac gtt ata agg ttt ggg aca aac cct 2226
Asp Ala Asp Met Asp Gly Val Asn Val Ile Arg Phe Gly Thr Asn Pro
695 700 705

act ggt gac gtg tct ctc acg ctt ggt tta cgc cac gct gga aac atg 2274
Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His Ala Gly Asn Met
710 715 720

cct gac aaa gac gct tct ttc tgc gtt aga gag ttt ggg ggt ttt tag 2322
Pro Asp Lys Asp Ala Ser Phe Cys Val Arg Glu Phe Gly Gly Phe *
725 730 735

tttgcttttg tcactccatt taattaatta attatagttt tccattctta cttattttaa 2382
ttgaaaatct atttttgtct cttaaaagtc caaacaatac attagtctag ccctcctctg 2442
cttttttttt tctatctcgt gaagagaaga aaacgatacg taaatccctt cgaaaactaa 2502
tgtacgttgt acgacttatt gttttcataa aaaaaaaaaa aaa 2545

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<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (500)...(560)
<223> Conserved domain

<400> 236
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1 5 10 15
Phe His Asn Asn Ser Met Ser Gln Asp Tyr His His His His His His
20 25 30
Asn Gln His Gln Gly Gly Ile Phe Asn Phe Ser Asn Gly Phe Asp Arg
35 40 45
Ser Asp Ser Pro Asn Leu Thr Thr Gln Gln Lys Gln Glu His Gln Arg
50 55 60
Val Glu Met Asp Glu Glu Ser Ser Val Ala Gly Gly Arg Ile Pro Val
65 70 75 80
Tyr Glu Ser Ala Gly Met Leu Ser Glu Met Phe Asn Phe Pro Gly Ser
85 90 95
Ser Gly Gly Gly Arg Asp Leu Asp Leu Gly Gln Ser Phe Arg Ser Asn
100 105 110
Arg Gln Leu Leu Glu Glu Gln His Gln Asn Ile Pro Ala Met Asn Ala
115 120 125
Thr Asp Ser Ala Thr Ala Thr Ala Ala Ala Met Gln Leu Phe Leu Met
130 135 140
Asn Pro Pro Pro Pro Gln Gln Pro Pro Ser Pro Ser Ser Thr Thr Ser
145 150 155 160
Pro Arg Ser His His Asn Ser Ser Thr Leu His Met Leu Leu Pro Ser
165 170 175
Pro Ser Thr Asn Thr Thr His His Gln Asn Tyr Thr Asn His Met Ser
180 185 190

Met His Gln Leu Pro His Gln His His Gln Gln Ile Ser Thr Trp Gl
195 200 205
Ser Ser Pro Asp His His His His His His Asn Ser Gln Thr Glu Ile
210 215 220
Gly Thr Val His Val Glu Asn Ser Gly Gly His Gly Gly Gln Gly Leu
225 230 235 240
Ser Leu Ser Leu Ser Ser Ser Leu Glu Ala Ala Ala Lys Ala Glu Glu
245 250 255
Tyr Arg Asn Ile Tyr Tyr Gly Ala Asn Ser Ser Asn Ala Ser Pro His
260 265 270
His Gln Tyr Asn Gln Phe Lys Thr Leu Leu Ala Asn Ser Ser Gln His
275 280 285
His His Gln Val Leu Asn Gln Phe Arg Ser Ser Pro Ala Ala Ser Ser
290 295 300
Ser Ser Met Ala Ala Val Asn Ile Leu Arg Asn Ser Arg Tyr Thr Thr
305 310 315 320
Ala Ala Gln Glu Leu Leu Glu Glu Phe Cys Ser Val Gly Arg Gly Phe
325 330 335
Leu Lys Lys Asn Lys Leu Gly Asn Ser Ser Asn Pro Asn Thr Cys Gly
340 345 350
Gly Asp Gly Gly Gly Ser Ser Pro Ser Ser Ala Gly Ala Asn Lys Glu
355 360 365
His Pro Pro Leu Ser Ala Ser Asp Arg Ile Glu His Gln Arg Arg Lys
370 375 380
Val Lys Leu Leu Thr Met Leu Glu Glu Val Asp Arg Arg Tyr Asn His
385 390 395 400
Tyr Cys Glu Gln Met Gln Met Val Val Asn Ser Phe Asp Ile Val Met
405 410 415
Gly His Gly Ala Ala Leu Pro Tyr Thr Ala Leu Ala Gln Lys Ala Met
420 425 430
Ser Arg His Phe Arg Cys Leu Lys Asp Ala Val Ala Ala Gln Leu Lys
435 440 445
Gln Ser Cys Glu Leu Leu Gly Asp Lys Asp Ala Ala Gly Ile Ser Ser
450 455 460
Ser Gly Leu Thr Lys Gly Glu Thr Pro Arg Leu Arg Leu Leu Glu Gln
465 470 475 480
Ser Leu Arg Gln Gln Arg Ala Phe His Gln Met Gly Met Met Glu Gln
485 490 495
Glu Ala Trp Arg Pro Gln Arg Gly Leu Pro Glu Arg Ser Val Asn Ile
500 505 510
Leu Arg Ala Trp Leu Phe Glu His Phe Leu His Pro Tyr Pro Ser Asp
515 520 525
Ala Asp Lys His Leu Leu Ala Arg Gln Thr Gly Leu Ser Arg Asn Gln
530 535 540
Val Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met
545 550 555 560
Val Glu Glu Met Tyr Gln Gln Glu Ser Lys Glu Arg Glu Arg Glu Glu
565 570 575
Glu Leu Glu Glu Asn Glu Glu Asp Gln Glu Thr Lys Asn Ser Asn Asp
580 585 590
Asp Lys Ser Thr Lys Ser Asn Asn Asn Glu Ser Asn Phe Thr Ala Val
595 600 605
Arg Thr Thr Ser Gln Thr Pro Thr Thr Thr Ala Pro Asp Ala Ser Asp
610 615 620
Ala Asp Ala Ala Val Ala Thr Gly His Arg Leu Arg Ser Asn Ile Asn
625 630 635 640
Ala Tyr Glu Asn Asp Ala Ser Ser Leu Leu Leu Pro Ser Ser Tyr Ser

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                645                 650                 655
Asn Ala Ala Ala Pro Ala Ala Val Ser Asp Asp Leu Asn Ser Arg Tyr
            660                 665                 670
Gly Gly Ser Asp Ala Phe Ser Ala Val Ala Thr Cys Gln Gln Ser Val
        675                 680                 685
Gly Gly Phe Asp Asp Ala Asp Met Asp Gly Val Asn Val Ile Arg Phe
    690                 695                 700
Gly Thr Asn Pro Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His
705                 710                 715                 720
Ala Gly Asn Met Pro Asp Lys Asp Ala Ser Phe Cys Val Arg Glu Phe
                725                 730                 735
Gly Gly Phe
```

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<210> 237
<211> 1179
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (109)...(966)

<400> 237
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acaaaaatct tacaagaaga tcatttttag aaaccctatt aggataaa atg gat tac  117
                                                     Met Asp Tyr
                                                      1

gag gca tca aga atc gtc gaa atg gta gaa gat gaa gaa cat ata gat   165
Glu Ala Ser Arg Ile Val Glu Met Val Glu Asp Glu Glu His Ile Asp
  5                  10                  15

cta cca cca gga ttc aga ttt cac cct act gat gaa gaa ctc ata act   213
Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile Thr
 20                  25                  30                  35

cac tac ctc aaa cca aag gtt ttc aac act ttc ttc tct gct act gcc   261
His Tyr Leu Lys Pro Lys Val Phe Asn Thr Phe Phe Ser Ala Thr Ala
                 40                  45                  50

att ggt gaa gtt gat ctc aac aag att gag cct tgg gac tta cca tgg   309
Ile Gly Glu Val Asp Leu Asn Lys Ile Glu Pro Trp Asp Leu Pro Trp
             55                  60                  65

aag gct aag atg gga gaa aaa gaa tgg tat ttc ttc tgt gtg aga gac   357
Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp
         70                  75                  80

cgg aaa tac ccg acc ggt tta agg aca aac cgg gcg aca gaa gcc ggt   405
Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly
     85                  90                  95

tat tgg aaa gcc aca gga aaa gac aaa gag ata ttc aag gga aaa tca   453
Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys Gly Lys Ser
100                 105                 110                 115
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ctt gtg ggt atg aag aaa act ttg gtt ttc tat aaa gga aga gct cct    501
Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Lys Gly Arg Ala Pro
                120                 125                 130

aaa gga gtt aaa acc aat tgg gtt atg cat gaa tat cgt tta gaa ggc    549
Lys Gly Val Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly
            135                 140                 145

aaa tat tgt att gaa aat ctt ccc caa aca gct aag aac gaa tgg gtt    597
Lys Tyr Cys Ile Glu Asn Leu Pro Gln Thr Ala Lys Asn Glu Trp Val
        150                 155                 160

ata tgt cgt gtt ttc caa aaa cgt gcc gat ggt aca aag gtt cca atg    645
Ile Cys Arg Val Phe Gln Lys Arg Ala Asp Gly Thr Lys Val Pro Met
    165                 170                 175

tca atg ctt gat cca cac att aac cga atg gaa cca gcc ggt tta cct    693
Ser Met Leu Asp Pro His Ile Asn Arg Met Glu Pro Ala Gly Leu Pro
180                 185                 190                 195

tcg tta atg gat tgt tct caa cga gac tcc ttc acc ggt tcg tcg tct    741
Ser Leu Met Asp Cys Ser Gln Arg Asp Ser Phe Thr Gly Ser Ser Ser
                200                 205                 210

cac gtg acc tgc ttc tcc gac caa gaa acc gaa gac aaa aga ctt gtc    789
His Val Thr Cys Phe Ser Asp Gln Glu Thr Glu Asp Lys Arg Leu Val
            215                 220                 225

cac gag tcc aaa gac ggt ttt ggt tct ctg ttt tac tcg gat cct ctg    837
His Glu Ser Lys Asp Gly Phe Gly Ser Leu Phe Tyr Ser Asp Pro Leu
        230                 235                 240

ttt tta caa gac aat tat tcg cta atg aag ctg ttg ctt gac ggt caa    885
Phe Leu Gln Asp Asn Tyr Ser Leu Met Lys Leu Leu Leu Asp Gly Gln
    245                 250                 255

gaa act caa ttc tcc ggc aaa cct ttc gac ggt cgt gat tcg tcc ggt    933
Glu Thr Gln Phe Ser Gly Lys Pro Phe Asp Gly Arg Asp Ser Ser Gly
260                 265                 270                 275

aca gaa gaa ttg gat tgc gtt tgg aat ttc tga gttgtataag ttatgttgta 986
Thr Glu Glu Leu Asp Cys Val Trp Asn Phe  *
                280                 285

gacttgtagt agtcatgtgt tcgtgtgtgt gaatgaatat tcttgttaca ttttttttgta 1046
aaaaaggaga aaaaaatatg ctagaaagtc aattgctttt gttatgtagc attagtgttt 1106
tttatgtact caatagactt cctaattaaa taaaaatctt aatttatttg ccaaaaaaaa 1166
aaaaaaaaaa aaa                                                      1179
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<210> 238
<211> 285
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN

<222> (23)...(167)
<223> Conserved domain

<400> 238
Met Asp Tyr Glu Ala Ser Arg Ile Val Glu Met Val Glu Asp Glu Glu
1 5 10 15
His Ile Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu
20 25 30
Leu Ile Thr His Tyr Leu Lys Pro Lys Val Phe Asn Thr Phe Phe Ser
35 40 45
Ala Thr Ala Ile Gly Glu Val Asp Leu Asn Lys Ile Glu Pro Trp Asp
50 55 60
Leu Pro Trp Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys
65 70 75 80
Val Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr
85 90 95
Glu Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys
100 105 110
Gly Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Lys Gly
115 120 125
Arg Ala Pro Lys Gly Val Lys Thr Asn Trp Val Met His Glu Tyr Arg
130 135 140
Leu Glu Gly Lys Tyr Cys Ile Glu Asn Leu Pro Gln Thr Ala Lys Asn
145 150 155 160
Glu Trp Val Ile Cys Arg Val Phe Gln Lys Arg Ala Asp Gly Thr Lys
165 170 175
Val Pro Met Ser Met Leu Asp Pro His Ile Asn Arg Met Glu Pro Ala
180 185 190
Gly Leu Pro Ser Leu Met Asp Cys Ser Gln Arg Asp Ser Phe Thr Gly
195 200 205
Ser Ser Ser His Val Thr Cys Phe Ser Asp Gln Glu Thr Glu Asp Lys
210 215 220
Arg Leu Val His Glu Ser Lys Asp Gly Phe Gly Ser Leu Phe Tyr Ser
225 230 235 240
Asp Pro Leu Phe Leu Gln Asp Asn Tyr Ser Leu Met Lys Leu Leu Leu
245 250 255
Asp Gly Gln Glu Thr Gln Phe Ser Gly Lys Pro Phe Asp Gly Arg Asp
260 265 270
Ser Ser Gly Thr Glu Glu Leu Asp Cys Val Trp Asn Phe
275 280 285

<210> 239
<211> 1695
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)...(1695)

<400> 239
atg gtt gat tct tct cgt gat tcg tgt ttc aaa gct ggt aag ttt agt 48
Met Val Asp Ser Ser Arg Asp Ser Cys Phe Lys Ala Gly Lys Phe Ser
1 5 10 15

gct cca ggt ttt cga ttt cac cct act gat gaa gag ctt gtg gtt tat 96

```
Ala Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Val Ty
            20                  25                  30

tat ctt aag agg aag atc tgt tgt aaa aaa ctt cga gtc aat gcc att     144
Tyr Leu Lys Arg Lys Ile Cys Cys Lys Lys Leu Arg Val Asn Ala Ile
        35                  40                  45

ggt gtc gtt gat gtt tac aaa gtc gat cct tct gaa ttg cct ggt cta     192
Gly Val Val Asp Val Tyr Lys Val Asp Pro Ser Glu Leu Pro Gly Leu
    50                  55                  60

tcg atg ttg aag acg gga gat aga cag tgg ttc ttt ttc act cca agg     240
Ser Met Leu Lys Thr Gly Asp Arg Gln Trp Phe Phe Phe Thr Pro Arg
65                  70                  75                  80

aat agg aag tat cct aac gca gct agg tca agt aga ggt act gca act     288
Asn Arg Lys Tyr Pro Asn Ala Ala Arg Ser Ser Arg Gly Thr Ala Thr
                85                  90                  95

ggt tat tgg aag gcg aca gga aag gat cga gtc att gag tac aat tca     336
Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Val Ile Glu Tyr Asn Ser
            100                 105                 110

aga tct gtt gga ctc aag aag act ctt gtt ttc tat aga ggt cgt gct     384
Arg Ser Val Gly Leu Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala
        115                 120                 125

cct aat ggt gag aga act gac tgg gtg atg cat gag tac act atg gat     432
Pro Asn Gly Glu Arg Thr Asp Trp Val Met His Glu Tyr Thr Met Asp
    130                 135                 140

gaa gaa gag cta ggg aga tgt aag aac gct aag gag tat tat gct ctt     480
Glu Glu Glu Leu Gly Arg Cys Lys Asn Ala Lys Glu Tyr Tyr Ala Leu
145                 150                 155                 160

tat aag ctt tat aag aag agt ggg gct ggt cct aag aat ggt gaa cag     528
Tyr Lys Leu Tyr Lys Lys Ser Gly Ala Gly Pro Lys Asn Gly Glu Gln
                165                 170                 175

tat ggt gct ccg ttc caa gaa gaa gaa tgg gtt gat agt gat agt gaa     576
Tyr Gly Ala Pro Phe Gln Glu Glu Glu Trp Val Asp Ser Asp Ser Glu
            180                 185                 190

gat gca gat agt gtc gct gta ccg gat tat ccc gtg gtc cgt tat gag     624
Asp Ala Asp Ser Val Ala Val Pro Asp Tyr Pro Val Val Arg Tyr Glu
        195                 200                 205

aat ggt cct tgt gtg gat gat act aaa ttt tgc aat cct gtc aaa ctt     672
Asn Gly Pro Cys Val Asp Asp Thr Lys Phe Cys Asn Pro Val Lys Leu
    210                 215                 220

cag tta gag gat att gag aag ctt ctc aat gaa atc cca gat gca ccc     720
Gln Leu Glu Asp Ile Glu Lys Leu Leu Asn Glu Ile Pro Asp Ala Pro
225                 230                 235                 240

ggg gtt aac caa aga cag ttt gat gag ttt gtt ggt gtt cca cag ggt     768
Gly Val Asn Gln Arg Gln Phe Asp Glu Phe Val Gly Val Pro Gln Gly
```

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                245                     250                     255

aat agt gca gaa gtg ata cag agc aca ttg ctg aat aat tct tct gga      816
Asn Ser Ala Glu Val Ile Gln Ser Thr Leu Leu Asn Asn Ser Ser Gly
            260                     265                     270

gag tat att gac cct cgg acg aat gga atg ttc ttg cca aat ggc cag      864
Glu Tyr Ile Asp Pro Arg Thr Asn Gly Met Phe Leu Pro Asn Gly Gln
        275                     280                     285

cta tac aac agg gac tcg agt ttt cag tcc cat ttg aat tca ttt gag      912
Leu Tyr Asn Arg Asp Ser Ser Phe Gln Ser His Leu Asn Ser Phe Glu
    290                     295                     300

gct acc tct ggt atg gca cct ctt cta gat aat gag aag gag gag tac      960
Ala Thr Ser Gly Met Ala Pro Leu Leu Asp Asn Glu Lys Glu Glu Tyr
305                     310                     315                     320

att gaa atg aat gat ctt ctg atc cct gag ctc ggt gct tct tca aca      1008
Ile Glu Met Asn Asp Leu Leu Ile Pro Glu Leu Gly Ala Ser Ser Thr
                325                     330                     335

gag aaa tcc aca gag ttc ttg aac cat ggt gaa ttt ggt gat gtt aat      1056
Glu Lys Ser Thr Glu Phe Leu Asn His Gly Glu Phe Gly Asp Val Asn
            340                     345                     350

gaa tac gac caa ttg ttc aat gac ata tct gtt ttt cag gga act tct      1104
Glu Tyr Asp Gln Leu Phe Asn Asp Ile Ser Val Phe Gln Gly Thr Ser
        355                     360                     365

aca gat ctg tct tgt ctg agt aat ttt act aat aac aca tca ggc caa      1152
Thr Asp Leu Ser Cys Leu Ser Asn Phe Thr Asn Asn Thr Ser Gly Gln
    370                     375                     380

aga cag caa tta ctt tat gaa cag ttc cag tac cag aca cct gag aac      1200
Arg Gln Gln Leu Leu Tyr Glu Gln Phe Gln Tyr Gln Thr Pro Glu Asn
385                     390                     395                     400

cag ctt aat aac tac atg cat cct agt acc act ctt aat cag ttc act      1248
Gln Leu Asn Asn Tyr Met His Pro Ser Thr Thr Leu Asn Gln Phe Thr
                405                     410                     415

gac aat atg tgg ttt aaa gat gat cag gct gct ctc tat gtt caa cca      1296
Asp Asn Met Trp Phe Lys Asp Asp Gln Ala Ala Leu Tyr Val Gln Pro
            420                     425                     430

cca caa tct tct tct gga gca ttc act tca cag tca aca ggt gtg atg      1344
Pro Gln Ser Ser Ser Gly Ala Phe Thr Ser Gln Ser Thr Gly Val Met
        435                     440                     445

cct gag tct atg aat ccc act atg agt gta aat ccc caa tac aag gaa      1392
Pro Glu Ser Met Asn Pro Thr Met Ser Val Asn Pro Gln Tyr Lys Glu
    450                     455                     460

gga caa aat ggt ggt gga aca agg agc cag ttc tca tca gct ctg tgg      1440
Gly Gln Asn Gly Gly Gly Thr Arg Ser Gln Phe Ser Ser Ala Leu Trp
465                     470                     475                     480
```

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gaa tta ttg gaa tca ata cca tca aca cca gcc tct gcc tgt gag ggt    1488
Glu Leu Leu Glu Ser Ile Pro Ser Thr Pro Ala Ser Ala Cys Glu Gly
                485                 490                 495

cct ctt aac cag acc ttt gtg cgt atg tct agc ttc agc cgc atc agg    1536
Pro Leu Asn Gln Thr Phe Val Arg Met Ser Ser Phe Ser Arg Ile Arg
            500                 505                 510

ttc aat gga acg tca gtg act agt aga aaa gtc act gta gca aag aag    1584
Phe Asn Gly Thr Ser Val Thr Ser Arg Lys Val Thr Val Ala Lys Lys
        515                 520                 525

cgt atc agt aac aga ggt ttt ctt ctg tta tca att atg ggt gct ttg    1632
Arg Ile Ser Asn Arg Gly Phe Leu Leu Leu Ser Ile Met Gly Ala Leu
    530                 535                 540

tgt gct atc ttc tgg gtg ttc aaa gcc acc gtt gga gtt atg gga aga    1680
Cys Ala Ile Phe Trp Val Phe Lys Ala Thr Val Gly Val Met Gly Arg
545                 550                 555                 560

cct ctc ttg tcg tga                                                1695
Pro Leu Leu Ser  *
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<210> 240
<211> 564
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (17)...(188)
<223> Conserved domain

<400> 240

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Met Val Asp Ser Ser Arg Asp Ser Cys Phe Lys Ala Gly Lys Phe Ser
 1               5                  10                  15
Ala Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Val Tyr
            20                  25                  30
Tyr Leu Lys Arg Lys Ile Cys Cys Lys Lys Leu Arg Val Asn Ala Ile
        35                  40                  45
Gly Val Val Asp Val Tyr Lys Val Asp Pro Ser Glu Leu Pro Gly Leu
    50                  55                  60
Ser Met Leu Lys Thr Gly Asp Arg Gln Trp Phe Phe Phe Thr Pro Arg
65                  70                  75                  80
Asn Arg Lys Tyr Pro Asn Ala Ala Arg Ser Ser Arg Gly Thr Ala Thr
                85                  90                  95
Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Val Ile Glu Tyr Asn Ser
            100                 105                 110
Arg Ser Val Gly Leu Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala
        115                 120                 125
Pro Asn Gly Glu Arg Thr Asp Trp Val Met His Glu Tyr Thr Met Asp
    130                 135                 140
Glu Glu Glu Leu Gly Arg Cys Lys Asn Ala Lys Glu Tyr Tyr Ala Leu
145                 150                 155                 160
```

```
Tyr Lys Leu Tyr Lys Lys Ser Gly Ala Gly Pro Lys Asn Gly Glu G
                165                 170                 175
Tyr Gly Ala Pro Phe Gln Glu Glu Glu Trp Val Asp Ser Asp Ser Glu
            180                 185                 190
Asp Ala Asp Ser Val Ala Val Pro Asp Tyr Pro Val Val Arg Tyr Glu
        195                 200                 205
Asn Gly Pro Cys Val Asp Asp Thr Lys Phe Cys Asn Pro Val Lys Leu
    210                 215                 220
Gln Leu Glu Asp Ile Glu Lys Leu Leu Asn Glu Ile Pro Asp Ala Pro
225                 230                 235                 240
Gly Val Asn Gln Arg Gln Phe Asp Glu Phe Val Gly Val Pro Gln Gly
                245                 250                 255
Asn Ser Ala Glu Val Ile Gln Ser Thr Leu Leu Asn Asn Ser Ser Gly
            260                 265                 270
Glu Tyr Ile Asp Pro Arg Thr Asn Gly Met Phe Leu Pro Asn Gly Gln
        275                 280                 285
Leu Tyr Asn Arg Asp Ser Ser Phe Gln Ser His Leu Asn Ser Phe Glu
    290                 295                 300
Ala Thr Ser Gly Met Ala Pro Leu Leu Asp Asn Glu Lys Glu Glu Tyr
305                 310                 315                 320
Ile Glu Met Asn Asp Leu Leu Ile Pro Glu Leu Gly Ala Ser Ser Thr
                325                 330                 335
Glu Lys Ser Thr Glu Phe Leu Asn His Gly Glu Phe Gly Asp Val Asn
            340                 345                 350
Glu Tyr Asp Gln Leu Phe Asn Asp Ile Ser Val Phe Gln Gly Thr Ser
        355                 360                 365
Thr Asp Leu Ser Cys Leu Ser Asn Phe Thr Asn Asn Thr Ser Gly Gln
    370                 375                 380
Arg Gln Gln Leu Leu Tyr Glu Gln Phe Gln Tyr Gln Thr Pro Glu Asn
385                 390                 395                 400
Gln Leu Asn Asn Tyr Met His Pro Ser Thr Thr Leu Asn Gln Phe Thr
                405                 410                 415
Asp Asn Met Trp Phe Lys Asp Asp Gln Ala Ala Leu Tyr Val Gln Pro
            420                 425                 430
Pro Gln Ser Ser Ser Gly Ala Phe Thr Ser Gln Ser Thr Gly Val Met
        435                 440                 445
Pro Glu Ser Met Asn Pro Thr Met Ser Val Asn Pro Gln Tyr Lys Glu
    450                 455                 460
Gly Gln Asn Gly Gly Gly Thr Arg Ser Gln Phe Ser Ser Ala Leu Trp
465                 470                 475                 480
Glu Leu Leu Glu Ser Ile Pro Ser Thr Pro Ala Ser Ala Cys Glu Gly
                485                 490                 495
Pro Leu Asn Gln Thr Phe Val Arg Met Ser Ser Phe Ser Arg Ile Arg
            500                 505                 510
Phe Asn Gly Thr Ser Val Thr Ser Arg Lys Val Thr Val Ala Lys Lys
        515                 520                 525
Arg Ile Ser Asn Arg Gly Phe Leu Leu Leu Ser Ile Met Gly Ala Leu
    530                 535                 540
Cys Ala Ile Phe Trp Val Phe Lys Ala Thr Val Gly Val Met Gly Arg
545                 550                 555                 560
Pro Leu Leu Ser
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<210> 241
<211> 2104
<212> DNA

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<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (93)...(1874)

<400> 241
tcgatcttta accaaatcca gttgataagg tctcttcgtt gattagcaga gatctcttta 60
atttgtgaat ttcaattcat cggaacctgt tg atg gac acc acc att gat gga    113
                                    Met Asp Thr Thr Ile Asp Gly
                                     1               5

ttc gcc gat tct tat gaa atc agc agc act agt ttc gtc gct acc gat    161
Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp
        10                  15                  20

aac acc gac tcc tct att gtt tat ctg gcc gcc gaa caa gta ctc acc    209
Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr
    25                  30                  35

gga cct gat gta tct gct ctg caa ttg ctc tcc aac agc ttc gaa tcc    257
Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser
40                  45                  50                  55

gtc ttt gac tcg ccg gat gat ttc tac agc gac gct aag ctt gtt ctc    305
Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu
                60                  65                  70

tcc gac ggc cgg gaa gtt tct ttc cac cgg tgc gtt ttg tca gcg aga    353
Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg
            75                  80                  85

agc tct ttc ttc aag agc gct tta gcc gcc gct aag aag gag aaa gac    401
Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp
        90                  95                  100

tcc aac aac acc gcc gcc gtg aag ctc gag ctt aag gag att gcc aag    449
Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys
    105                 110                 115

gat tac gaa gtc ggt ttc gat tcg gtt gtg act gtt ttg gct tat gtt    497
Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val
120                 125                 130                 135

tac agc agc aga gtg aga ccg ccg cct aaa gga gtt tct gaa tgc gca    545
Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala
                140                 145                 150

gac gag aat tgc tgc cac gtg gct tgc cgg ccg gcg gtg gat ttc atg    593
Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met
            155                 160                 165

ttg gag gtt ctc tat ttg gct ttc atc ttc aag atc cct gaa tta att    641
Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile
        170                 175                 180

act ctc tat cag agg cac tta ttg gac gtt gta gac aaa gtt gtt ata    689
```

```
Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val Val I
    185                 190                 195

gag gac aca ttg gtt ata ctc aag ctt gct aat ata tgt ggt aaa gct    737
Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala
200                 205                 210                 215

tgt atg aag cta ttg gat aga tgt aaa gag att att gtc aag tct aat    785
Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn
                220                 225                 230

gta gat atg gtt agt ctt gaa aag tca ttg ccg gaa gag ctt gtt aaa    833
Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys
            235                 240                 245

gag ata att gat aga cgt aaa gag ctt ggt ttg gag gta cct aaa gta    881
Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val
        250                 255                 260

aag aaa cat gtc tcg aat gta cat aag gca ctt gac tcg gat gat att    929
Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile
    265                 270                 275

gag tta gtc aag ttg ctt ttg aaa gag gat cac acc aat cta gat gat    977
Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp
280                 285                 290                 295

gcg tgt gct ctt cat ttc gct gtt gca tat tgc aat gtg aag acc gca    1025
Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala
                300                 305                 310

aca gat ctt tta aaa ctt gat ctt gcc gat gtc aac cat agg aat ccg    1073
Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro
            315                 320                 325

agg gga tat acg gtg ctt cat gtt gct gcg atg cgg aag gag cca caa    1121
Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu Pro Gln
        330                 335                 340

ttg ata cta tct cta ttg gaa aaa ggt gca agt gca tca gaa gca act    1169
Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr
    345                 350                 355

ttg gaa ggt aga acc gca ctc atg atc gca aaa caa gcc act atg gcg    1217
Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala
360                 365                 370                 375

gtt gaa tgt aat aat atc ccg gag caa tgc aag cat tct ctc aaa ggc    1265
Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly
                380                 385                 390

cga cta tgt gta gaa ata cta gag caa gaa gac aaa cga gaa caa att    1313
Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile
            395                 400                 405

cct aga gat gtt cct ccc tct ttt gca gtg gcg gcc gat gaa ttg aag    1361
Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys
```

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        410                 415                 420

atg acg ctg ctc gat ctt gaa aat aga gtt gca ctt gct caa cgt ctt    1409
Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu
    425                 430                 435

ttt cca acg gaa gca caa gct gca atg gag atc gcc gaa atg aag gga    1457
Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly
440                 445                 450                 455

aca tgt gag ttc ata gtg act agc ctc gag cct gac cgt ctc act ggt    1505
Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly
                460                 465                 470

acg aag aga aca tca ccg ggt gta aag ata gca cct ttc aga atc cta    1553
Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu
            475                 480                 485

gaa gag cat caa agt aga cta aaa gcg ctt tct aaa acc gtg gaa ctc    1601
Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu
        490                 495                 500

ggg aaa cga ttc ttc ccg cgc tgt tcg gca gtg ctc gac cag att atg    1649
Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met
    505                 510                 515

aac tgt gag gac ttg act caa ctg gct tgc gga gaa gac gac act gct    1697
Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala
520                 525                 530                 535

gag aaa cga cta caa aag aag caa agg tac atg gaa ata caa gag aca    1745
Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr
                540                 545                 550

cta aag aag gcc ttt agt gag gac aat ttg gaa tta gga aat tcg tcc    1793
Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly Asn Ser Ser
            555                 560                 565

ctg aca gat tcg act tct tcc aca tcg aaa tca acc ggt gga aag agg    1841
Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly Gly Lys Arg
        570                 575                 580

tct aac cgt aaa ctc tct cat cgt cgt cgg tga gactcttgcc tcttagtgta 1894
Ser Asn Arg Lys Leu Ser His Arg Arg Arg  *
    585                 590

atttttgctg taccatataa ttctgttttc atgatgactg taactgttta tgtctatcgt 1954
tggcgtcata tagtttcgct cttcgttttg catcctgtgt attattgctg caggtgtgct 2014
tcaaacaaat gttgtaacaa tttgaaccaa tggtatacag atttgtaata tatatttatg 2074
tacatcaaca ataaaaaaaa aaaaaaaaaa                                  2104

<210> 242
<211> 593
<212> PRT
<213> Arabidopsis thaliana

<220>
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<221> DOMAIN
<222> (2)...(593)
<223> Conserved domain

<400> 242
Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser
1 5 10 15
Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu
20 25 30
Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu
35 40 45
Leu Ser Asn Ser Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr
50 55 60
Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His
65 70 75 80
Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala
85 90 95
Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu
100 105 110
Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val
115 120 125
Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro
130 135 140
Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys
145 150 155 160
Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile
165 170 175
Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp
180 185 190
Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu
195 200 205
Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys
210 215 220
Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser
225 230 235 240
Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu
245 250 255
Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys
260 265 270
Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu
275 280 285
Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala
290 295 300
Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala
305 310 315 320
Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala
325 330 335
Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly
340 345 350
Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile
355 360 365
Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln
370 375 380
Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln
385 390 395 400
Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala
405 410 415

```
Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg
            420                 425                 430
Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met
        435                 440                 445
Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu
    450                 455                 460
Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys
465                 470                 475                 480
Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala
                485                 490                 495
Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser
            500                 505                 510
Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala
        515                 520                 525
Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg
    530                 535                 540
Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn
545                 550                 555                 560
Leu Glu Leu Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser
                565                 570                 575
Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg
            580                 585                 590
Arg


<210> 243
<211> 1292
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (46)...(960)

<400> 243
agaaaagata agagcctttt aaagtttttt ttttaccttc tcttc atg gac ttg tct 57
                                                  Met Asp Leu Ser
                                                   1

gta ctt gat agg ctt aag tgg ctg caa cag caa caa atg gtt tca cct   105
Val Leu Asp Arg Leu Lys Trp Leu Gln Gln Gln Gln Met Val Ser Pro
 5                  10                  15                  20

gag ttt ctt cag ata ctt ggc tca gat ggg aga gaa gag ctc aaa aga   153
Glu Phe Leu Gln Ile Leu Gly Ser Asp Gly Arg Glu Glu Leu Lys Arg
                25                  30                  35

gtt gag agt tac ttg gga aac aac aat gat gag ctg cag agt ttc aga   201
Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu Gln Ser Phe Arg
            40                  45                  50

cat ttt ccc gaa ttc gga ccg gat tat gat act act gat ggc tgc att   249
His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr Asp Gly Cys Ile
        55                  60                  65

tct agg aca agt agc ttc cat atg gag cca gtg aag aat aat gga cac   297
```

```
Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys Asn Asn Gly His
     70                 75                   80

agc aga gcc att acc ttg cag aac aag aga aaa cca gag ggt aag aca    345
Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro Glu Gly Lys Thr
 85                 90                   95                  100

gaa aag aga gag aag aag aag atc aaa gca gag gat gaa aca gag cca    393
Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp Glu Thr Glu Pro
                105                 110                 115

agc atg aaa ggg aaa tca aac atg agt aac aca gag aca tct tca gaa    441
Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu Thr Ser Ser Glu
            120                 125                 130

att cag aaa cca gat tac att cat gtt agg gct aga cga ggt gaa gcc    489
Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg Arg Gly Glu Ala
        135                 140                 145

acc gac aga cat agc tta gca gag agg gca aga aga gaa aag ata agc    537
Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser
    150                 155                 160

aag aag atg aaa tgt cta caa gat att gtt cct gga tgc aac aaa gtt    585
Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val
165                 170                 175                 180

act gga aaa gct ggt atg ctt gat gag atc atc aac tat gtc caa tct    633
Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser
                185                 190                 195

ctg caa caa caa gtc gag ttc ttg tcg atg aaa ctc tct gtc ata aat    681
Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu Ser Val Ile Asn
            200                 205                 210

cca gaa ctt gag tgt cat atc gat gat tta tcc gca aaa cag ttt cag    729
Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala Lys Gln Phe Gln
        215                 220                 225

gct tac ttc aca ggt cct cca gaa ggt gac tcg aag cag tca atc atg    777
Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys Gln Ser Ile Met
    230                 235                 240

gcg gat ttt cgg tct ttt cca tta cat cag caa gga tct tta gat tac    825
Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly Ser Leu Asp Tyr
245                 250                 255                 260

tca gtc ata aac tca gac cac acc aca tct ctc ggc gct aaa gat cat    873
Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly Ala Lys Asp His
                265                 270                 275

aca tca tca agc tgg gaa act cac tca cag tgt ctt tac aac agc ttg    921
Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu Tyr Asn Ser Leu
            280                 285                 290

aga acc gat tct gtt tcc aat ttc ttc agc ctc aag taa aaaaattagg     970
Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys  *
```

```
        295                 300

gatagcctca ttaaaaaaat cgcggttttt tgttgttgtc ttatccattt atctatctta 1030
tctgaaattt gaaccagaaa gacagaggaa accaatccaa agatctttct caatctatta 1090
tcttcataca aatatagtga tttacatata ttccagggga tatgtatatg tgtagaagaa 1150
agagaaaaaa ctcttgtggt catagcaatt cctttttttg tacattgtag aatcaaactc 1210
ttgtggtcgt aacaattatt tccttcacaa attacaacta cacttgtatt aatggagatg 1270
ccttttggcc ctgggatcaa ca                                          1292

<210> 244
<211> 304
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> DOMAIN
<222> (140)...(204)
<223> Conserved domain

<400> 244
Met Asp Leu Ser Val Leu Asp Arg Leu Lys Trp Leu Gln Gln Gln Gln
 1               5                  10                  15
Met Val Ser Pro Glu Phe Leu Gln Ile Leu Gly Ser Asp Gly Arg Glu
            20                  25                  30
Glu Leu Lys Arg Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu
        35                  40                  45
Gln Ser Phe Arg His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr
    50                  55                  60
Asp Gly Cys Ile Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys
65                  70                  75                  80
Asn Asn Gly His Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro
                85                  90                  95
Glu Gly Lys Thr Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp
            100                 105                 110
Glu Thr Glu Pro Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu
        115                 120                 125
Thr Ser Ser Glu Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg
    130                 135                 140
Arg Gly Glu Ala Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg
145                 150                 155                 160
Glu Lys Ile Ser Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly
                165                 170                 175
Cys Asn Lys Val Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn
            180                 185                 190
Tyr Val Gln Ser Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu
        195                 200                 205
Ser Val Ile Asn Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala
    210                 215                 220
Lys Gln Phe Gln Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys
225                 230                 235                 240
Gln Ser Ile Met Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly
                245                 250                 255
Ser Leu Asp Tyr Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly
            260                 265                 270
Ala Lys Asp His Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu
        275                 280                 285
Tyr Asn Ser Leu Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys
```

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    290                 295                 300

<210> 245
<211> 1231
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (107)...(1084)

<400> 245
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ccacttcccc cccaccaaag cttcgatcat catcatcatc atcatc atg gat ccg    115
                                                   Met Asp Pro
                                                    1

gat ccg gat cat aac cat cga ccc aac ttc cct ctc cag ctt ctt gat   163
Asp Pro Asp His Asn His Arg Pro Asn Phe Pro Leu Gln Leu Leu Asp
    5                  10                  15

tct tct acc tcc tcc tct tcc act tcc tta gcc atc atc tct act act   211
Ser Ser Thr Ser Ser Ser Ser Thr Ser Leu Ala Ile Ile Ser Thr Thr
 20                  25                  30                  35

tcc gaa cct aac tcc gaa cct aag aag cct cct cct aaa cga acc tct   259
Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys Arg Thr Ser
                 40                  45                  50

act aaa gac cga cac acc aaa gtc gaa ggc cga ggc cgt cgg atc cgt   307
Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg
             55                  60                  65

atg cct gcc atg tgt gct gca cgt gtc ttt cag ctc aca cgt gag ctt   355
Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu
         70                  75                  80

ggt cac aaa tcc gac ggt gaa act att gag tgg cta ctc caa caa gca   403
Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala
     85                  90                  95

gaa cca gcg gtt ata gcc gct aca ggg act gga acc att ccg gct aac   451
Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn
100                 105                 110                 115

ttc act tct tta aac atc tca ctt cgt agc tca aga tct tct ctc tct   499
Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser Ser Leu Ser
                120                 125                 130

gct gct cat ctt cgt aca act cct agt agc tat tac ttt cat tca cca   547
Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe His Ser Pro
            135                 140                 145

cat cag tcc atg act cat cat ctt caa cat cag cat cag gtt cgt ccc   595
His Gln Ser Met Thr His His Leu Gln His Gln His Gln Val Arg Pro
        150                 155                 160
```

```
aag aac gag tca cat tct tcg tct tct tct tct tca cag ctt tta gat    643
Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln Leu Leu Asp
    165                 170                 175

cac aac caa atg ggt aac tat cta gta caa tca act gct gga tct tta    691
His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala Gly Ser Leu
180                 185                 190                 195

cct acg agt cag agt cct gca acg gca ccg ttt tgg agt agt ggt gac    739
Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser Ser Gly Asp
                200                 205                 210

aac aca cag aat ctt tgg gct ttt aat att aat cct cat cat tcc ggt    787
Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His His Ser Gly
            215                 220                 225

gtt gtc gcc gga gat gtt tac aac ccc aac agt ggt ggt agt ggc ggc    835
Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly Ser Gly Gly
        230                 235                 240

ggt agt gga gtt cat ttg atg aat ttt gca gct cct att gct ttg ttt    883
Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile Ala Leu Phe
    245                 250                 255

tct gga cag cct ttg gct tct ggt tat gga gga gga gga ggt ggc ggt    931
Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly Gly Gly Gly
260                 265                 270                 275

gga gaa cat agc cat tat gga gtt tta gcg gcg ttg aat gct gct tac    979
Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn Ala Ala Tyr
                280                 285                 290

cga ccg gtg gcg gag acg ggg aac cat aac aac aac cag caa aac cgt    1027
Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln Gln Asn Arg
            295                 300                 305

gac gga gat cat cat cac aac cat caa gaa gat gga agc acc agt cat    1075
Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser Thr Ser His
        310                 315                 320

cat tcc tag gcaaacatac acaaacaaat atattctgtg agatttattt            1124
His Ser  *
    325

ttcttttttt gtcctttcgt ttgtttgttt gttcttaaca agcgtgtttt ttttgcattg 1184
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Ser Thr Thr Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys
        35                  40                  45
Arg Thr Ser Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg
    50                  55                  60
Arg Ile Arg Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr
65                  70                  75                  80
Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu
                85                  90                  95
Gln Gln Ala Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile
            100                 105                 110
Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser
        115                 120                 125
Ser Leu Ser Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe
    130                 135                 140
His Ser Pro His Gln Ser Met Thr His His Leu Gln His Gln His Gln
145                 150                 155                 160
Val Arg Pro Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln
                165                 170                 175
Leu Leu Asp His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala
            180                 185                 190
Gly Ser Leu Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser
        195                 200                 205
Ser Gly Asp Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His
    210                 215                 220
His Ser Gly Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly
225                 230                 235                 240
Ser Gly Gly Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile
                245                 250                 255
Ala Leu Phe Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly
            260                 265                 270
Gly Gly Gly Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn
        275                 280                 285
Ala Ala Tyr Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln
    290                 295                 300
Gln Asn Arg Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser
305                 310                 315                 320
Thr Ser His His Ser
                325
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